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General General Copyright (c) 1993 - 2000 Compugen Ltd.
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oM protein , protein search, using sw model

Run on. July 2, 29°2, 15;33.62 ; Scarch time 19.99 Scannuds (without alianments) 2619.734 Million cell updates/sec

5-599-409-80 SD

Porfrect score: 2144 September: 1 MISLAQUEQRIALPQSPASE...........CQREEDQLEETVLORPEQSYPT 2144

Scoring table: 0LD0 Gaper 5000 Gapext 60.0

Sourched: 2316.28 seqs, 24425594 residues

Word size : 6 Total number of hits satistying chosen parameters:

2393

Minimum DB seq length: 0 Maximum DB seq length: 2000000009 Post-processing: Listing first 45 summaries

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

		æ			SUMMAKIES	
Result	Score	Ouery Match	onery Match Length	DB	ID	Description
-	· x	7.0	144	-	US-08-284-393B-11	Sequence 11, Appl
~	æ	4.0	144	_	-697	6
~	æ	4.0	144	ca	US 08 905 513 G	2
**	æ	0.4	144	4	US-08-759-628-6	Sequence 6, Appli
רט	æ	4.0	144	**	ns-09-522-217-114	114
٤	æ	4.0	144	٠,٦	PrT-US95-08950-11	_
.,	æ	0.4	678	4	US-09-413-814-105	105,
æ	7	0.3	1.2	~	US-08-740-069 6	Sequence 6, Appli
2	۲-	* · O	1.2	++	US-09-282-501-6	Sequence 6. Appli
10	7	9 . 0	-	4	US-08-640-915A-79	79,
11	7	¥ . 0	7.1	47	US-08-905-223-311	3.1
24	r·	0	8	-1	US-08-211-202-130	130,
1 4	7	~ ⊊	117	~,	-08-545-	139,
1.4	7	(f. 3	1.1%	13	US-08-475-000-16	16, A
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16,	7	4.0	5]]	~	US-08-484-508-16	Sequence 16, Appl
1.7	7	÷ :	143	-	US-08-254-696B-10	10,
ж. Т	7.	¥ . 0	1 1 3	~	US-08-902-513-10	10,
1.9	7	¥ . 0	1.44	-	US-08-133-979A-11	Sequence 11, Appl
97	7	10	1.14	7	115-08-436-890-11	1.1,
7.7	۲.	† : ⊖	1.14	•	05-08 451 213 11	Sequence 11, Appl
77	ŗ.	f . c	178	~1	08 08 929 692 57	Sequence 57, Appl
¥ 7	7	\$. O	17.4	-		8, A
77		* '0	1.73	~	-09 041-	Sequence 8, Appli
5.7	7	₹. ©	714	-1	05-08-217-327-4	Sequence 4. Appli
5.5	7	¥ '0	2.28	~	03-09-079-981 1	Sequence 1, Appli
2.7	r.	÷.	~	-	DS 08 961 083 12	Sequence 12, App1

Sequence 1, Applit		Sequence 25, Appl Sequence 17, Appl	÷.	Sequence 3, App.1 Sequence 3, Appli	~	.~4	Sequence 5, Appli	Sequence 1, Appli	Sequence i, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 6, Appli	.0.7	Sequence 10. Appl
US-07-729-099-1 US-08-257-392-1	US-08-770-035-1	US-08-978-741-17	US-09-333-729A-13	US-U8-843-993-3 US-09-059-520A-3	US-09-334-275-3	US-08-978-741-2	US-09-333-729A:3	US-08-724-948-1	US-080-080-238-1	US-08 978 741 6	US-09-333-729A 1	US-09-347-833:6	US-08-665-966-10	US-09-041-780-10
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8 6 7 8 8 7 8	30	32 32	E .	5 KJ	36	3.7	38	36	040	4.1	42	43	44	4.5

ALIGNMENTS

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APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
HIGH: ED INVENT: MELTENS OF MAMMATIAN SYLCHINES
HIGHER OF SPECIFICIES: 16
CORRESPONDENCE ARCHESS:
                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.40
                                                                                                                                                                                                                                                                                                                                                                                               O1-AUG-1994
                                                                                                                                                                                   DNAX Research Institute
                                 ; Sequence 11, Application US/08284393B; Patent No. <u>56</u>96234
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DX0389
                                                                                                                                                                             ADDRESSEE: DNAX Research
THFEE 431 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGNEY/AGENT INFORMATION.
NAME: Ching, Edwin D. P. P. REGISTRATION NUMBER: 34.090
REFERENCE/ONCKET NUMBER: DX031
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-452-9196
TELEPHONE: 415-465-1200
                                                                                                                                                                                                                                                                                                                                      1BM PC compatible
                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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INFORMATION FOR SPO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-284-3938-11
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                     Abbres.
SibeEt 491 c.
7:17 1915 A1:3
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FILING DATE: 01-AUG
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                                                                                                                                                                                                                                                                              94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
             US-08-284-393B-11
                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE
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RESULT
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Ouery Match 0.4%; Score 8; DH 1; Length 144; Hrst Local Similarity 100.6%, Fred. Ro. 22; Matches 8; Conservative 0; Mismatches 0; Indels 0;

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TITLE OF INVENTION: DNA ENCODING CANINE GRANULOCYTE
TITLE OF INVENTION: MACROPHAGE COLONY STIMILATING FACTOR (AS amended)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; thength 144,
                                                                                                                                                                                                            E: Christensen, O'Connor, Johnson and Kindness
1420 Filth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0, Indels
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APPLICANT: Storb, Rahit
TILLE OF INVENTION: CANING GRANILLWEYTE MACROPHAGE
TITLE OF INVENTION: COLONY STIMULATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Scote 8; DB T
100.0%; Prcd. No. 22;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein DESCRIPTION: Human GMCSF, Figure 5
                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/259,696B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHSP17718
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                   Sequence 9, Application US/08259696B Patent No. 5702919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Sequence 9, Application US/08902513
// Patent No. 5925343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Shelton, Dennis K. REGISTRATION NUMBER: 26,997 REFERENCE/DOCKET NUMBER: FILTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 9:
                                                                                             APPLICANT: Nash, Richard A. APPLICANT. Storb, Ranir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206-224-0718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 144 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 0.4%
Best Local Similarity 100.0
Matches 8; Conservative
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Washington
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FILING DATE: 14-JU
                                                                                                                                                                                                                                                                        Washington
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                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LLLLGTVA 13
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                    US-08-259-696H 9
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US-08-902-513-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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RESULT
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0; Gaps
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APPLICANT: Bock, Pernando L.
APPLICANT: Bazan, J. Fernando L.
APPLICANT: Bazan, J. Fernando L.
APPLICANT: Kastclein, Robert A.
TITLE: PINVENTION: MITTATIONAL VARIANTS OF MAMMIJAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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COMPUTER- IRM PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%, Score 8, DB 2, 100.0%; Pred. No. 22; tive 0; Mismatches
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FHSP111036
TELECOMMUNICATION INPORMATION:
TELEPHORE: 206-224-0718
TELEFAX: 206-24-0779
INFORMATION FOR SEQ IN NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
DESCRIPTION: Human GMCSF, Figure 5
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                                                                             APPLICATION NUMBER: US/08/902,513
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                                                                                                                                                           08/259,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08759628 Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,090
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                                                                                                                                                                                                                                                          26,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1995
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                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
PEGISTPATION NUMBER: 26,6
                                                                                                                                                                            14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                   144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%
Best Local Similarity 100.0
Matches 8; Conservative
                                                        CHRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHAPACTERISTICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                        PPIOP APPLICATION DATA:
                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                   435
                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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APPLICANT:
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                                                                                                                                                                                                                           DOTATION: 18,.144

OTHER INFORMATION: /note- "peptide of Figure 1"
OS 08 759 628 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hammond, Angela K.
1111E OF INVENTION: NOVEL CYPOKINE ZALPHALL LIGAND
FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 8; DB 4;
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0; Mismatches
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EARLIER APPLICATION NUMBER: US 60/123,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1939-03-11
STATLER PELLING DATE: 1939-03-11
FARLIER FILING DATE: 1939-07-01
NUMHER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: US 60/123,547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114, Application US,799522217
Patent No. 6307024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zarawski, Sandra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190.06;
           TELEFAX: 415 496-1200
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FOSTET, Donald C. APPLICANT: HOLLY, BICHARD D. APPLICANT: GROSS, Jane A. APPLICANT: Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nelson, Andrew J.
Dillon, Stager R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                         single
                                                                                                                                             TOPOLOGY: linear
MOLECULE LYPE: protein
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: ORGANISM: Homo sapiens
US-09-522-217-114
                                                                                                                                                                                                         NAME/KEY: Poptide
                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
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APPLICANT Zaraws)
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6 11111GIVA 13
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TELEPHONE:
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APPLICANT:
APPLICANT:
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APPLICANT: Muclify Joachim
APPLICANT: Muclify Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
FILTLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Wyers Squibb, Co.
APPLICANT: Beyer. Stetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
               TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 8; DB 5
100.0%; Pred. No. 22;
Live 0; Mismatches
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EARLIER FILLING DAIE: 1998-10-09
NUMBER OF SEQ ID NOS- 107
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                                                                                     ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PC /US95/08950
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,393
FILLING LATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DX0389
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                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
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Zurawski, Gerard
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APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Goldberg, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Boile, Gerbard
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 852-9196
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Best Local Similarity 100.
Matches 8: Conservative
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TELEFAX: 415-496-1200
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                                                                                                                                    Palo Alto
California
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ZIP: 94304-1104
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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                                                                                                                     0.4%; Score 8; DB 4; Length 829; 100.0%; Pred. No. 1e+02, ative 0, Mismatches 0, indels
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Best Local Similarity 100.0%, Fred. No. 21,
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANGIOGENESIS INHIBITOR NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wenderoth, Lind & Ponack
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                                                                                                                                                                                                                                                                                                                         , Sequence 6, Application US/08740059; Patent No. 6057290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            October 24, 1996
                                                                                                                                                                                                                                                                                                                                                                               Chiho FUKIAGE et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warren M. Cheek, Jr. RATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                  CONGANISM: Sorangium cellulosum US-09-413-814-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: MORDELECTECT 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/
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PEPPPENCE/POCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 amino acids
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                                                                                                                           Ouery Match
Best Local Similarity 100.
Matches 8, Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE, peptide US-08-740-069-6
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                                                                                                                                                                                                                                  309 LLSALAAL 316
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US-09-282-501-6
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                   LENGTH: 829
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SEC ID NO 105
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                                    TYPE: PRT
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APPLICANT: FOWIKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPERTIDES HAVING A FUNCTIONAL.
TITLE OF INVENTION: FOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                              Wenderoth, Lind & Ponack, L.L.P
                                                                                                                                                                                                   CALF: ....CALF: EVEN:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
                APPLICANT: Chiho FUKIAGE et al.
TITLE OF INVENTION: ANGIOGENESIS INHIBITOR
NUMBER OF SEQUENCES: 8
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1155 Avenue of the Americas
                                                                                                           2033 K Street, N.W., #800
Washington
                                                                                                                                                                                                                                                                                                                             US/09/282,501
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HOFFMAN. No. 6309820h
KAY, Brian K
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: October 24, 1996
PPIOP APPLICATION DATA:
APPLICATION NUMBEP: 09/243,822
                                                                                                                                                                                                                                                                                                                                                                                                          08/740,069
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/740,065
FILING DATE: OCLOBER 24, 1996
                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IS/IN9/28.
FILING DATE: April 9, 1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren M. Cheek, Jr. ATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: February 3, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEG ID NO. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-09-282-501-6
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                                                                          CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
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                                                                                                ADDRESSEE:
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APPLICANT:
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                                                                                                                                                                         COUNTRY
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                                                                                                                                      CITY: V
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REFERENCE/DOCKET NUMBER: 28111/31960
  LENGTH:
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                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edwards, Jean-Haptiste D.
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SETPETED PROTEINS
CORRESPONDENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 URRENI APPLICATION DAIA:
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                                                                                                                         03. VC
03. APR-1996
18. 536
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1101 174
TELECOMMUNICATION INFORMATION:
TELEPRINE: (212) 969-9864/9741
TELEFAX: (212) 969-8864/9741
TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
                                                                                             OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 411, Application US/08905223 Patent No. 6222929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE CONTRICT NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (619, 2.55.8550
TELEFAX: (619, 2.55.9126
INFORMATION FOR SEQ. 10 NO. 311:
SEQUENCE CHARACTERISTICS:
                                                                             IBM PC compatible
                                                                                                                                                                                                                                       NAME: Misrock, S Lestie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PG COmpatible OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRALLON NUMBER: 29,655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 West Broadway
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy Disk
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    41 amino arids
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POPULOGY: unknown
Molecule PYPE: peptide
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MEDIUM TYPE: Floppy |
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                                                                                                                                                            APPLICATION NUMBER:
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                10036-2711
                                                                                                                                                                             FILING DATE: 0 CLASSIFICATION:
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COUNTRY: USA
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US - 08 - 905 - 223 - 411
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                                                                             COMPUTER:
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CITY: S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of chimeric antibodies - a combinatorial approach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT HOUGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: BAIER, Laurent Stephane Anne Therese
APPLICANT: JESPERS, Laurent Stephane Anne Therese
                                                                                                                                                                                                                                                                                                                                                0: Indels
                                                                                                                                                                                                                                                                                                         Length 71:
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CURRENT APPLICATION DATA:
APPLICATION NIMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                       Query Match 0.3%; Score 7; DB 4; L
Bost Local Similarity 109.0%; Prcd. No. le:02;
Matches 7; Conservative 0; Mismatches 0
                                                                                                                                                                 LOCATION: -69..-1
IDENTIFICATION METHOD: Von Heljne matrix
                                                                                                                                                                                           OTHER INFORMATION: SCOTE 6.7 OTHER INFORMATION: SCOTE 6.7 OTHER INFORMATION: SCOTE FKLLLLGAMCSG/AR US-08-905-223-311
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APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
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YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 130, Application US/08211202
; Patent No. 5565332
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: David W. Clough
REGISTRATION NUMBER: 3
                                                                                                                                            NAME/KEY: sig_peptide
                                           PROTEIN
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                                                                                                   TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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AMINO ACID
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                     LINEAR
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CLASSIFICATION:
               TOPOLOGY: LINE
MOLECULE TYPE: P
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
                                                                                                                                                                                                                                                                                                                                                                                       151 LKINNSK 157
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                                                                                                                                                                                                                                                                                                                                                                                                                             39 LKINNSK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-211-202-130
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82 KFQERVT 88
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                                                                      US-08-475-000-16
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                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITILE OF INVENTION: HUMAN EMMUNOGLOBULIN VH GENE
TITILE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
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                                                                                                                                                                                                                                          0.3%; Score 7; DB 1; hength 98; 160.0%; Pred. No. 1.38+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSkO for Windows Version 2.0
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE, TROCKET NUMBER 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/JP93/00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/545,809A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson, P.C. STREET, 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 139, Application US/08545809A; Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 139:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24,066
                  TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-385
INFORMATION FOR SEQ ID NO: 130:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 amino acids
                                                                                                                                                                                                                            Oucry Match
Best Local Similarity 100.v
Best Local 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Freeman, John W. REGISTRATION NUMBER: 2
                                                                                                                98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 617-542-500,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                            SHOUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE IYPE: protein
                                                                                                                                            ; TOPOLOGY, linear; MOLECULE TYPE: protein US-08-211-202-130
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COMPUTER PEADABLE FORM-
MEDIUM TYPE: Diskell
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                                                                                                                                    amino acid
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STREET. 22.
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Gaps
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                                                                                       TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 3%; Score 7; DR 2; Length 119;
100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
                                                                                                                                                                            ADDRESSEE: CHLRON CORPORATION
STREET: INTELLECTUAL PROPERTY P440 - P O. ROX 8097
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                         SOMTWARE: Patentin Release #1.0, Version #1.25 CUPPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.33
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/475,000 FILING DATE: 07-HHV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08483199; Patent No. 5849877.; GENERAL INFORMATION:
Sequence 16, Application US/08475000 Patent No. 2811267 Patent INFORMATION: GENERAL INFORMATION: APPLICANT FING, DAVID B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTOKNEY/AGENT INPORMATION:
NAME: SAVEREIDE, PAUL
REGIETRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 088
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ 1D NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                            CORRESPONDENCE ADDRESS:
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SOFTWARE: Fatentic Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/483,199,
FULLING DATE: U7-UN-1995
GUASSIFICATION: A44
ATTORING MATTER I INFORMATION:
NAME: SAVEREIDE: 86,914
REGISTRATION NUMBER: 36,914
RECISTRATION OF SEQ 15 No.: 16:
RECUENCE GHARATTERISTICS:
LENGIH: 119 amino acids
INPERIOR ATTOR OF SEQ 15 No.: 16:
SEQUENCE GHARATTERISTICS:
LENGIH: 119 amino acids
INPERIOR TYPE: protein
US-OB 48:-199 16
WALEOULE TYPE: protein
US-OB 48:-199 16
REST LOCAL SUMILATITY 100:08: Prod. No. 1:69:02;
Matches 7: Conservative 0: Mismarches 0: Indels 0: Gaps
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Search completed: July 2, 2002, 15:36:40 Job time: 218 sec

Oy 1544 KVVESGG 1549
DE 1411111

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demiore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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M protein protein search, using SW model

July 2, 2002, 15:36:43 ; Search time 20.46 Seconds (without alignments) 4057.415 Million cell updates/sec Kun on:

US 09+503-655-5 2144 1 MISLAUQ-QKLALPQSDASH..... Dorter Score: Sequence:

.....COKTIĞOLETVLGERLQSYF 2144 Scoring table:

105224 seqs, 48719550 residues oLIGo Gapop 60.0 , Gapext 60.0 Searched

Total number of hits satisfying chosen parameters: Word size :

4252

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing linst 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

STOPE Match Long 15 15 15 15 15 15 15 1	±		* 0.000				
1764 82.1 2144 1 BP28 10 MAN 095583 10	Ž	Score	Match	Lend h	8	a	Description
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10 0.5	7	511	5.4	45B	_	HP28 MACEA	_
9 0.4 2096 1 HP2B BROME Q94m25 1 4.4 1 GSF2_HUMAN P04141 1 4.4 1 GSF2_HUMAN P04141 1 4.4 2.5 1 KR5_CAREL P14445 1 0.4 2.5 1 KR5_CAREL P14427 1 0.4 2.4 1 KR5_CAREL P24277 2 0.4 1 KR5_CAREL P24277 P2427 8 0.4 1 KR5_CAREL P24277 P2427 8 0.4 1 KR5_CAREL P24277 P2437 9 1 KR5_CAREL P2447 P2447 P2447 9 1 KR5_CAREL P2447 P2478 P2447 9 1 KR5_CAREL P2447 P2447 P2447 9 1 KR5_CAREL P2	~	10	0.5	1453	_	Y 3 7 3_BOVIN	
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7 0.3 1.5 1 YK95 ARCFU 028.885 7 0.4 124 1 GALA_BUVIN P01242 7 0.4 124 1 GALA_BUSIN P01242 7 0.4 142 1 YHAW_RCGLL 090H75 7 0.4 187 1 VA4_SCLLR 090H75 7 0.3 140 1 CSF2_CAVPG 06481 7 0.4 141 1 CYTS_RAT P10313 7 0.4 144 1 CHSY_RRAT P1032	7.5	7	. 0	1 5	-	OV39_ONCVC	P31730 onchocerca
7 0.4 124 1 GALA BOVIN P11242 7 0.3 124 1 GALA_PIG	17	7.	0.3	1.5	-	YK95_ARCFU	028185 archaeoglob
7 0.4 1.24 1 GALA, PIG P074180 7 0.4 142 1 YHAM, EDGILI P77712 7 0.4 142 1 YHAM, EDGILI P77712 7 0.3 147 1 VA4_SOLIN P163577 7 0.3 141 1 CSF2_CAVPG, 960481 7 0.4 141 1 CSF2_BAT P19313 7 0.4 144 1 CSF2_BAT P19313 7 0.4 144 1 CSF2_BOVIN P19313	7.7	7	0.3	1.24		GALA_BOVIN	P11242 bos taurus
7 0.4 142 1 YHAM_ECOLI 1 177712 7 0.4 137 1 VAA_SOLGE 090h775 7 0.3 140 1 GSF2_CAVPS 960481 7 0.4 141 1 GYTS_RAT 7 0.3 144 1 GSF2_RAY 7 0.4 144 1 GSF2_RAY 811052 7 0.4 144 1 GHY REGAR 11052 7 0.4 144 1 GHY REGAR 11052 7 0.4 144 1 GHY REGAR 11052	57	7	- C	1.2.5		GALA_PIG	
7 0.4 187 1 VA4_SOLGE 09th 75 7 0.3 187 1 VA4_SOLGE 05th 75 7 7 0.3 140 1 CSF2_CAVPG 05th 7 0.4 141 1 CYTS_RAT	7.6	į.	(1)	1.42		YBAW_ESOLI	P77712 escherichia
7 0.3 137 1 VA4_SOLIN F-85277 7 0.3 140 1 CSF2_CAVPC, 960481 7 0.3 141 CYTS_RAT P19313 7 0.4 144 1 CYF2_BOVIN P1052 7 0.4 144 1 CYF2_BOVIN F-996126 7 0.4 144 1 CYF2_POPER F-996126	17	7	· . 0	1 3.7	-	VA4_SOLGE	09nh75 solenopsis
3 140 1 GSF2_CAVPs 060481 3 141 1 CYTS_RAT P19313 4 144 1 GSF2_BOVIN P1052 4 144 1 CHYY_INGRA P96126 4 144 1 GSF2_CEREI F51748	78		0.3	1.47	-	VA4_SOLIN	P45777 solenopsis
141 CYTS_RAT P19313 P19413 P19413 P1941 P1052 P141 CHYP_TRUMA P1052 P144 CSF2_CREE1 P51748 P164 CSF2_CREE1 P51748 P164 P	6.7	7	F. O	140		CSF2_CAVPO	Q60481 cavia porce
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3 144 1 CHEY_TREEDA 3 144 1 CSF2_CERREL 151748	7	7	で. ○	14 4		CSF2_BOVIN	P11052 bos taurus
.3 144 1 CSF2_CBREL. P51748	~	Ĺ	0.4	144		CHEY_TRUBA	P96126 treponema p
	~	7	~∵ਂ	144		CSF2_CERRIL	cervus ela

	P28774 ovis aries	PO1795 mas mascula	Sontain appropriate m	P47339 mycoplasma	US8904 methanocoec	O9knz8 vibric chol	P04494 human adenso	P43147 mus musculu	Q57593 methanococc	P51646 rattus norv	P29996 hepatitis d
CSF2_PIG	CSF2_SHEEP	HV26_MOUSE	$DUT_{\overline{z}} YMMC$	RL9_MYCGE	YF09_MELJA	RS7_VIBCH	E3G1_ADE05	LIT1_MOUSE	Y129_MET.IA	ARL5_RAT	AANT_HDVD3
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ALIGNMENTS

VARIANT 1854 1854	VARIANT 1854 1854		VARIANT 1694 1694	TOUR TOUR BUILDING	REPEAT 2106 2142	Follymorphism.			-: SIMILAKIII: CONIMINS + HEAI KEFEAI.	
	PROSTIE, PSS0077, HEAT-REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694 1694	PROSTIE, PSS0077; HEAT_REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694 1694						this SWISS FROT entry is copyright. It is between the Swiss Institute of Highforthe European Highline Institute of Highforthe European Highline Institutions as lost modified and this statement is not removerables requires a license adrenment (Sour send an email to licensedisb-sib.ch). EMBL; AX067150; CAC26776.1; EMBL; AX061221; BAA91564.1;		
InterPro; IPR000357; HEAT_REPPROSITE, PSS0077; HEAT_REPEAT POLYMORPHISM. REPPRAT 2106 23.42 VARIANT 1694 1694	InterPro: IPRG00357: HEAT_REPEAT POLYMORPHISM. PRIVAT 2106 2142 VARIANT 1694 1694	InterPro: IPRU00357; HEAT_REPEAT POLYMORPHISM. 2106 2142 VARIANT 1694 1694								
EMBL. ANOULZI, BARATIOGALITA INLEFPRO, IPROGOST, BEATLEPP PROSITE, PSSOOTT, HEAT_REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694 1694	EMBL: ANOULE: BARNFIDGA.I: A InterPro: IPR000357; BEAT_rep PROSITE, PSS0077; HEAT_REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694 1694	EMBL. ANOUGEST: MARCHEST FOR INTERPRET PROSITE, PSS0077; HEAT_REPEAT POLYMORPH NR. 2106 2142 VARIANT 1694 1694				,	 -			
EMBL; AK001221; BAA91564.1; A Interpro; PR000357; HEAT_REPEAT POSTIE, PS50077; HEAT_REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694	EMBL: AK001221; BAA91564.1; A InterPro; IPR000357; HEAT_REPEAT PROSITE, PS50077; HEAT_REPEAT POLYMORPHISM. REPEAT 2106 2142 VARIANT 1694 1694	EMBL: AK001221; BAA91564.1; A InterPro; IPR000357; HEAT_REPEAT PROSITE, PS50077; HEAT_REPEAT POlymorphism. REPEAT 2106 2142 VARIANT 1694 1694					-			
EMBL: AL136105; CAC15948.1; EMBL: AK001221; BAC1564.1; InterPro; IPR000137; HEAT_REPEAT PROSITE; PS50077; HEAT_REPEAT POLYMORPH'SM. REPEAT 2106 2142 VARIANT 1694 1694	EMBL: AL136105; CAC15948.1; - EMBL: AK001221; BAS01564.1; A InterPro; IPR000357; HEAT_REPEAT POLYMOrphism. REPEAT 2106 2142 VARIANT 1694 1694	EMBL; AL136105; CAC15948.1; EMBL; AK001221; BAA91564.1; A InterPro; 1PK000377; HEAT_REPEAT POLYMORPHISM. POLYMORPHISM. 2106 2112 VARIANT 1694 1694								
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										: SIMILARIII: CONIAINS + HEAI KEFEAI.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THFPFAIRVESLLQKKIKKLESVITAVEIPSEWHIELMLDRGIPVELWAHYVEELNSTQR 780
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                                                                                                                                                                                                                                                  SFEQFEAPLFSQLAKILEKSVQTKAVNKQLDENISLFLIHLSPYFLLKPAQKCLEWLIHR 120
                                                                                                                                                                                                                                                                                   SFEQFEAPLESQLAKTLEPSVQTKAVNKQLDENISLFLJHLSPYFLLKPAQKGJEWIJHP 120
                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                  1 MTSLAQQLQRLALPQSDASLLSRDEVASLLFDPKKAATIDRDTAFAIGCTGLEELLGIDP 60
                                                                                                             82.3%; Score 1764; DB 1; Length 2144;
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                                                         D66816BE78D809R7 (18064)
/FTId-VAR_010941.
                                          /FTId-VAR 010942
                                                                                                                                            0; Mismatches
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                                                            2144 AA; 242455 MW;
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Matches 1964; Conservative
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                                                        1021 VLQGVNGEMVLSQLLPMAEQTLEKTQKEPTAVLKDEAMVLHLTLGKYNEFSVSLLNEDPK
                                                                       EADTEFWFSVCCEFSVQHQ1QSLMN1LQYLLKLPEEKEFT1PKAVSFNKSESQEEMLQVF
961 SKAPELESDAAYV IQILATLEPELQEPEKKLKSHQKLSFELKN: LSPVYSTPSYTAKLIME
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958 AA

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STANDARD;

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This SWISS-PPOT entry is depyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the BMBL outstation—the brropean Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and to commercial entities requires a literar agreement (See http://www.isb-sib-ch/announce/or send an email to license*isb-sib-ch).
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                                                                                                                                                                                                                                                                                                                                                      Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 UTHHHALLLGTVAGIFPDKVLHNIMSIFTFMGANVMRLDDTYSFQVINKTVKMVIPALI 172
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Mammalia; Eutheria; Catartiodactyla; Ruminania; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1359 @SPSGDSIEVSPNVEFIVVKIISVFVDALPHVPEHRPLPHLV@LVDTLGAEKFLW 1413
                                                                                                                                         Macaca fascicularis (Trab eating macaque) (Cynonolgus monkey).
Enkaryota: Metazoa: Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia: Eutheria; Erimates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 QSDSGDSTEVSKNVEETVVKTTSVFVDALPHVPERFELPTLVQLVDTLGAERFUW 227
                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of full length opna clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 115; DB i; Length 958; 100.0%; Pred. No. 4.4e-107; ive 0, Mismatches 0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (ocl. 2000) to the EMBL/Gormank/AppR databases
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16 oct.2001 (Rel. 40, Orested)
16 oct.2001 (Rel. 40, Last sequence update)
16 oct.2001 (Rel. 40, Last anaotation update)
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16-0XT-2001 (Rel. 40, Last sequence update)
16-0XT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0373.
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Matches 115; Conservative
                                                                                       Protein BAP28 (Fragment).
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                                                                                                                                                                                                                                 Cercopithecinae; Macaca.
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09TU2 3;
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RECEINE_20196006; PubMed=10731132;

RECEINE_20196006; PubMed=10731132;

RA Adams N.D. Celniker S.E. Bolt R.A. Evans C.A. Gocayne J.D. Adams N.D. Celniker S.E. Bolt R.A. Schorror M., Hondorson S.N.,

RA Goorge R.A. Lowis S.E. Richards S. Ashburnor M., Hondorson S.N.,

RA Goorge R.A. Lowis S.E. Richards S. Champe W., Chon G. Worthman J.K.,

RA HTMAN G.G. Worthman J.K., Yandell M.D., Zhang O., Chon L.X.,

RA AFILL J.F. Adapayah A. M. H.-J., Andrews Plannkoon C. Baldwin D.,

RA HTMAN G. Boyle C. Faxrer E.G. Helt G. Nelson F. R. Mikros G.L.G.

RA AFILL J.F., Adapayah A. M. H.-J., Andrews Plannkoon C. Baldwin D.,

RA HOTKON S.C., Botchan M.R., Bouck J., Horkstarchull L.D. Beasley E.M.,

RA BUTKS K.C., Busam D.A. Butler H.D. Bhandari D., Holshakov S.,

RA BUTKS K.C., Busam D.A. Butler H.D. Bhandari D., Holshakov S.,

RA BUTKS K.C., Busam D.A. Butler H.D. Bhandari D., Holshakov S.,

RA BUTKS K.C., Busam D.A. Butler H.D. Byen I., Dietz S.M.,

BODORN K.J. Evangelista C.C., Fortract S., Plotschantu W.,

RA BUTLS K.C., Busam D.A. Butler H.D. Gabron E.D. Daw I., Dietz S.M.,

BODORN K.J. Evangelista C.C., Fortract S., Plotschantu W.,

RA Goden K.J. Evangelista C.C., Fortract S., Plotschantu W.,

RA Harris N.L., Barvey D., Helman T.J., Hernandez J.R., House C.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., House M.C.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., House M.C.,

RA Harris N. Watter M.K. House M. Werley M. M. Mollon D.L.,

RA Harris N. Watter M. K.A. Hovaland T.J., Well M. H., Theowam C.,

RA Harris N. Watter M. K.A. Hovaland T.J., Well M. H., Marlon D.L.,

RA Harris N. Matter M. K.A. Hovaland T.J., Well M. H., Marlon D.L.,

RA Harris N. Watter H., McIntosh T.C., McHool M. W., McHool D. L.,

RA Harris N. Watter H., McIntosh T.C., McHool M. W., McHool D. M., Millen D. L.,

RA Harris N. Watter H., McIntosh T.C., Steherler E., Spendh H.,

Rabor D. L., Siden H., Sunders R., Venter E., Wang A., H. Willen S.M., Watoley H., Watsarman D.A., Wellon D., Williams S. W., Watter H., Wellon E., Shon H., W
                  use by mon-profit institutions as long as its content is in no way modified and this statement is not removed. Base by and for commercial entities Lequizes a license attendent (see http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch).
  There are no restrictions on
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Ephydroidea, Drosophilidae, Drosophila,
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                  0.5%; Score 10; DR 1; Longth 1453;
100.0%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                        169934 MW: 03CBA02A64CF4139 CRC64;
                                                                                                                                                                     Hypothetical protein; Coiled coil.

OMAIN (7 1426 COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                  100.0%; Pred. no.
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the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 OCT 2001 (Rel. 40, Created)
                                                                                                                                                EMBL.; AF175816; AAF00990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein CG10805.
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIANDARD;
                                                                                                                                                                                                                          SECUENCE 1453 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HP28_DROME
Q9VM75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                     Owery Match
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Chena X.H., Zhona E.N., Zhona W., Zhona X., Zhi S., Zho X., Smith H o Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila metanogaster.",
Science 287:2185-2195(2009)
-1. SIMILARITY: BELONGS I HEAP PAMILY.
-1. SIMILARITY: CONTAINS I HEAP REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cantroll M.A., Anderson D., Cerretti D.P., Price V., McKoreghan K., Tushinski R.J., Mochizuki D.Y., Parson A., Grabstein K., Cosman D.; "Clouing, sequence, and expression of a human granalocyte/macrophage colony-stimulating factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
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LeCT-2-UDI (Rel 40, Last annovation update)
Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
(Colony-stimulating factor) (CSF) (Sargramostim) (Molgramostin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Wokarvola, Mctazoa, Chordata, Chaniata, Vertebrata, Enteleostomi;
Womanaka, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colony-stimulating factor by functional expression in mammalian
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Arai K.-I., Rennick D.,
"Isolation of cDNA for a human granulocyte-macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%, Score 9, DB 1,
100.0%; Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box; 1.
PROSITE; PS50077; HEAT_REPEAT; FALSE_NEG.
                                                                                                                                                                                                                                                                                          or send an email to licensewish-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDILINE+85242684; Pubmed-3925454; G.m.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86205844; PubMed=3486413;
                                                                                                                                                                                                                                                                                                                                                       FlyBase, FBgn0031864, CG10805.
InterPro, IPR001810, F-box.
InterPro, IPR000357, HEAT_repeat.
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                                                                                                                                                                                                                                                                                                                                      EMBL; AE003615; AAF52447.2; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
REPEAT 2058 209
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Best Local Similarity
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PO4141:
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CSF2_HUMAN
CSF2_HUMAN
CSF2_HUMAN
UT 01-NOV
UF 02-Z
COS MARMAN
KN MEDILIN
KN ACAI
KN CC10N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaushansky K., Lopez J.A., Brown C.B.; "Role of carbohydiate modification in the production and secretion of human granulocyte macrophage colony-stimulating factor in genetically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M., Davis C A., Kather K., Miguel T., Pitluck S., Pollard M., Rojeski H., Subramanian S., Martin C.H.; Sobramanian S., Martin C.H.; Sobramanian S., Martin C.H.; EMBL/GenBauk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stimulating factor. comparison of the mouse and human genes.";
EMBO 7. 4.2561-2568(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOCKAPHY (2.8 ANGSTROMS).
MELLINE-92235844; PubMed-1569568;
Walter M.P., Cook W.J., Balick S.E., Nagabhushan T.L., Trotta P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- DOLYMOPPHISM: VAPIANT LLF-117 MAY RE A PISK FACTOR FOR ATOPIC
                                                                                                        MPNINE=87218749; bubMnd-3923623; Wilkens K M. Irary A C., Will G G Witck J S., Temple D A . Wilkens K M., Orr E.C., Clurenberg D P., Indones S S., Brown F I., Kay R M., Orr E.C., Shoemaker C., Golde D W., Kaulman R I, Hewick R.M., Wang E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Thiee-dimensional structure of recombinant human granulocyte
                                                                                                                                                                                                                                                                                                                    'Human GM·CSF; molecular clouing of the complementary DNA and
                                                                                                                                                                                                                                                                                                                                                 purification of the natural and recombinant proteins.";
Science 228:810-815(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Novel fold and putative receptor binding site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte-macrophage colony-stimulating factor Science 254:1779-1782(1991).
11.S.A 82-6250 F254 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       engineered and normal mesenchymal cells.";
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Diederichs K., Boone T., Karplus P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92144609; Pubmed-1737041;
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EMBL; M11220; AAA52578 1;
    Proc. Natl. Acad. Sci.
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                                                                                                                                                                                    GRANULOGYTE-MACROPHAGE COLONY-STIMULATING
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                                                                                                                                                     Cytokine: Growth Tactur: Glycoprotein; Signal; 3D-structure;
Polymorphism: Pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 144
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01-001-1994 (Rel. 30, Last sequence update)
16-001-2001 (Rel. 40, Last amnotation update)
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Pred No R I;
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MEDLINE-95189110: PubMed-7881192;
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                                                                                                                                                                                                                                                O-LINKED.
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EMHI, X04021; CAA26822.1;
EMHI: M10663; AAA52121.1; C
EME, X000451; AAC08707.1;
PIR; A01854; FQHUGM.
PIP; C24636; C24646
                                                                                                           PRINTS, PRODEST, CMCSFACTOR.
                                                                                                                                            PROSITE: PS00702; GM_TSF; 1.
                                                                                                                        Probom; PD007349; GM_3SF; 1
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103
                                                                                          InterPro; IPR000773; Gl
Pram; PF01109; GM_CSF;
                                                                                                                                                                                                                                                                                                                                                                                         101
                                                              PDB; 1050; 31-1AN-94
PDB; 20MF; 08-NoV-96;
                                                                                                                                  SMOODAD: CSF2
                                                    PIR: A25169; A25169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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NGBI_faxID-1488;
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DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                       HELIX
STRAND
HELIX
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                                                                                                                                                                          SIGNAL.
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TURN
                                                                                                                                                                                                                                                                                                                                                                                                             HELIX
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                                                                                                                                                                                                                                           New Hills II. Reston S., Gmels Denk, M.V., Makathera K.S., Zeng O., Gibson P., Lee H.M., Dubois J., Qiu D., Hitti J., Molf Y.L., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Rennert G.W., Konin E.V., Smith D.F., Soucaille P., Daly M.J., "Genome sequence and comperative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3. Bacteriol. 176:6572-6582(1994).
FIRE SIGMA FACTOR IS AN INITIATION FACTOR HAT PROMOTES ATTACHMENT OF THE WAR DOLYMPASE TO SPECIFIC INITIATION SILES AND THEN IS RELEASED. THIE SIGMA FACTOR IS RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporulation and primary sigma factor homologous genes in Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription requiation; Sigma factor; DNA-directed RNA polymerase; DNA-binding; Sporulation; Complete proteome.

BO POLYMERASE CORE BINDING (POTENTIAL).

DNA_BIND 202 221 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U; Gaps
                                                    SEQUENCE FROM N.A. STRAIN 192 / VKM B-1787; STRAIN-AFCC 824 / ESM 792 / VKM B-1787; Santangelo J.D., Kuhn A., Treuner A., Durre P.; "Special 4thus and time routse expression of signa factor homologous genes in Clostridium acceptobutylicum."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sauer U., Treuner A., Buchholz M., Santangelo J.D., Durre P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSION OF SPORULATION SPECIFIC GENES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L -> P (IN REF. 4).
C726E18E6C93A903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. no.
                                                                                                                                                                                                         SIRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
Neclling 1 , Breton G , Cach Lenko M V ,
                                                                                                                                                                                                                                                                                                                                                                                                                       STEAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-95050216; Pubmed=7961408;
Clostridium acetebutylicum ATCC 824.";
Gene 153:89:92(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.48; Score 8;
                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 183:4823-48:8(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00140; sigma70; 1.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR000943; Sigma_70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26969 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U07420; AAC43309.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 46-235 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, Z23079, CAA80617.1, -. EMBL, AE007679, AAK79661.1, PIR, S34309, S34309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 VEDLISVG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YK67_CAFEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YK67_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ċ
                                                                                                                                                                                      Wilson P., Ainscough P., Anderson K., Baynes C., Berks M., Bonfield J., Burton I., Conceil M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin F., Favello A., Fraser A., Inchanton L., Jones M., Kershaw J., Kirsten J., Laisster I., Jier M., Introllo L., Jones M., Kershaw J., Kirsten J., Laisster I., Lightning J., Lioyd C., Mortimore B., Gaurders D., Shawkaen R., Berrott D., Percy C., Piffern J., Rought M., Sounders D., Shawkaen R., Sims M., Smaldon N., Smith M., Soundenmer B., Staden K., Sulston J., Thierry-Mieg J., Thomas K., Vandin M., Vaughan K., Materston P., Walson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Phabditoidea;
                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Ehabditida; Ehabditoidea;
                                                                                                                                                                                                                                                                                                                                                                      Mb of contiguous nucleotide sequence from chromosome 1:1 of C.
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C
                                                                                                                                                                                                                                                                                                                                                                                                     NATUTO 368:32 38(1224).
-i- SIMILARITY: BELONGS TO THE GST SUPERFAMILY, OMEGA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 8; DB 1; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FER-1994 (Pel 28, Lasi sequence update)
01-MAR-2002 (Fel. 41, Last annotation update)
Hypothetical 42.8 kba protein 00205.3 in chromosome 111.
01-FEB-1994 (Rel. 28, Tast Sequence update)
01-MAR-2002 (Rel. 4), Tast annotation update)
Hypothetical 28.5 kPa profein C24E4 / In chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
4EB0E85351217C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 O%; Pred. No. 13;
tive O; Mismatches
                                                                                               Rhabditidae, Peloderinae, Caenorhabditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transferase.
ACT_SITE 33 33 BY SI
SEQUENCE 250 AA; 28477 MW; 4EB
                                                                                                                                                            STPATN-RPISTOL N2;
MEDLINE-94150718; Pubmed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z¤, ∵reated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 1,23651; AAA27959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004046; GST_C.
InterPro; IPR004045; GST_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, S44768, S44768,
HSSP, P78417, IEEM
WormPep, C29E4 7, CERRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00043; GST_C; 1
Pfam; PF02798; GST_N; 1
                                                               Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1121 EKVQQKLL 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 EKVQQKLL 116
                                                                                                                                             SECUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1444 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6239;
                                                                                                              NCB1_Tax1D=6239;
                                                                                                                                                                                                                                                                                                                                                        Wohldman P :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FER-1994
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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P34277;
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                                                                                                                                                                                                                                                                                                                                                                                       elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                Coulson A.,
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
Wilson F., Ainsongh F., Anderson K., Faynes C., Berks M.,
Wilson F., Ainsongh F., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Garden A., Greyn P., Hawkins T., Hillor L., Jier M.,
Johnston L., Joues M., Kershaw J., Kirsten J., Halsster N.,
Latreille P., Lightning J., Lloyd C., Mortimoro R., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Sims M., Smaldon N., Smith M., Sannhammer E., Staden R.,
Salston J., Thierry-Mieg T., Thomas K., Vaudin M., Vauqiban R.,
Waterston R., Warson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                2 Mb of contiguous nucleotide sequence from chromosome 111 of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 20460 / W29,

In Dall M -T, Nicaud T.-M, Treton B Y, Gaillardin C.;
Submitted (XXX-1942) to the EMBL/GenBank/DDBJ databases.

-: CATALYTIC ACTIVITY. ATP + 3 phospher-0-glycerate - ADP + 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospho.D-glyceroyl phosphate.
-1- parhway. SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-1- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Score 8; DB 1; Length 379; 100 0%; Pred No. 19; (ive 0; Mishatches 0; Indels tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AA; 42Hill MW; 894hhRilBROWAA7R CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APF-1993 (Rel 25, Created)
01-APP-1993 (Pel 25, Last sequence update)
01-0XI-1996 (Rel 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 417 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarcharomyretales; Dipodasrareae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yarrowia lipolytica (Candida lipolytica).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoglycerate kinase (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 1.16622; AAA27915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   Nature ann: 12 - 18 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004046; GST_C.
InterPro; IPR004045; GST_N.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00043, GST_C; 1.
Pfam, PF02798; GST_N; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR: S44745; S44745
HSSP; P78417; 1EEM.
WormPep; CD2D5.4; CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1121 EKVQQKLL 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APE-1993 (Pel
01-APE-1993 (Pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 EKVQQKLL 40
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                                                                                                                                                                                                                                                                                                           Wohldman P ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGK_YARL1
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50 AALQKVVE 57

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      entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license*isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
use by non-profit institutions as long as its content is in-modulied and this statement is not removed. Usage by and for co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHELICAL LIPOPROFEIN MPN097.
N-ACYL DIGLYCERIDE (PUEENLIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macteria, Firmicutes: Barrings/Clostridium group, Mollicates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Match 0.4%; Score 8; DB 1; Length 541; Local Similarity 100.0%; Pred. No. 26; or Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.4%; Score 8: DB i; Length 417; Best Local Similarity 100.0%; Pred. No. 21; Matches 8: Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 oct. 2001 (Ref. 40, Created)
16 oct. 2001 (Rel. 40, Last sequence update)
16 oct. 2001 (Rel. 40, Last amotation update)
Hypothetical lipoprotein MPNO97 precursor (R02_ort541)
MPNO97 OR MP057.
                                                                                                                                                                                                                                                                                                                                                                    44772 MW; 3F308467FCC730BF CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD2FCB2B826B1F9C CRC64;
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F. SIMITAPITY: RELOWES TO THE MORRS / MG260 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license disb-sib.ch).
                                                                                                                                                                                                                                                                   PROBLE; PROBA77; PHOLYCKINASE.
PROSTIE; PSOULLI; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AFCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                          Transferase: Kinase: Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 23 N
541 AA; 53153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae; Mycoplasma.
                                                                                                                                                   EMBL: M91598; AAC47504.1: ..
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                                                                                                                                                                                                          LuterPro; IPR001576; PGK.
Ptam; PF00162; PGK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
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                                                                                                                                                                                                                                                                                                                                                                 417 AM:
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                                                                                                                                                                                   P00560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piam; PF02552; Lactate_perm; 1.
Hypothetical protein; Transport; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 8; DB 1; Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1997) to the EMFL/Genhank/DDBJ databases
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                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group, Bacillus.
                                              01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                      Putative L-lastate permease YVFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%,
100.0%; PYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 51-563 FROM N.A.
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  STANDARD;
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177
214
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Best Local Similarity
Matches 87 Conserv
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                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCB1_Tax1D=1423;
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                                                                                                                                                                                                                                                                                                                                                                  Denizot F.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168;
YVFH_BACSU
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98384019; PubMed-9719514; Redpath M.B., Carrall M., Amorim A., Guther M.L., Cardon M.B., Carrall N., Webb H., Courel M., Amorim A., Guther M.L., Cardon de Almeida M.L., Carringron M. Conservation of genetic linkage between heat shock protein 100 and 91ycosylphosphatidylinositol-specific phospholipase C in Trypanosoma brucei and Trypanosoma eruzi. 1 MMOL. Hotohem. Parasitol. 94:113-12(1998).
                                                                                                                                                                                                             Eukaryota: Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCHI_TaxID-5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                               MEDLINE-90239044; PubMed 2185473; Dichersky B., Carrington M., Hobbs M., Portosman S., Squires C., Pichersky B., Carrington M., Hobbs M., Mattick T. S., Dalrynple B., Kuramitsu H., Shiroza T., Foster T., Clark W.P., Ross B., Squires C.L., Maurizi M.R.; "Conservation of the regulatory subunit for the Cip AFP-dependent protease in protease in protease in protease in S. A. 8773512-3512.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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7E06D4AFE46E1881 CRC64;
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                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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100 0%; Prod No.
Live O; Mismatch
                                                                                                                           Heat shock protein 100 (CLP protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR003959, AAA_subfam.
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PROSITE; PSOOR71; CLPAB_2; 1.
Chaperone, ATP binding, Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96904 MW;
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InterPro; IPR004176; Clp_N.
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PIR, E35905, E35905.
Interpro, IPPO03593, AAA
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Pfam; PF02861; CIP_N;
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                         ARTHROPODS.
CONTAINS TWO COPPEP ATOMS PEP FUNCTIONAL UNIT EACH SUBMINIT: DECAMEPS OF LARGE TOENTICAL SUBMINITS (350 kDa), EACH CONTAINING 7 GLUBULAR OXYGEN-BINDING DOMAINS: GDA, GDB, GDD,
                                                                                                 SEQUENCE OF 1-834 FROM N.A. MEDLINE-91095437; PubMed-1898774; Lang W H , van Holde K E ; "Cloning and sequencing of Octopus doffein! hemocyanin cDNA: derived sequences of functional units ode and Odi."; Proc. Natl. Acad. Sci. H S.A. 88:244-248(1991).
                                                                                                                                                                                                                           "CDM cloning of the Octopus dofleini hemocyanin: sequence of the carboxyl-terminal domain.":

Blochmistry 27:775-7282(1988).

*1-FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING PREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                     Hemocyanin A.type, units ODE to ODG (Fragment).
Octopus dofleini (Glant octopus).
Eukaryota, Metazoa, Moilusca, Cephalegoda, Colceides, Octopoda;
Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                                                                                                                                                                         ODE, ODF, AND ODG.
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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MEDLINE-89088084; Pubmed-3207675;
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Ċ Saps Ċ Score 8: DB 7; Length 1233: Indole 543 o: Mismatches Pred. No. 100.0%; 0.4%: Conservative Host Local Similarity Matches 8: Conserv Ouery Match

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Eukaryota, Motazoa, Cherdata, Craniata: Vertebrata, Euteleostomi, Mammalia, Eutheria, Cytartiodactyla: Ruminantia, Pecora, Boyoidea, 01-AUG 1991 (Ref. 19, Created) 01-07F-1994 (Ref. 30, Last sequence update) 15-07F-2001 (Ref. 40, Last annotation update) STANDARD; Bovidae; Caprinae; Ovis. Ovis aries (Sheep). NCBL TaxID - 9940; rrichobyalin. TRHY SHEEP P22793; TRHY_SHEEP THH.

First M.J., McLaughlar C.J., Campbell M.L., Rogers G.E., Analysis of the Sheep Ericholyalin gene: potential structural and calcium-binding roles of trichohyalin in the hair follicle."; J. Cell Biol. 121:855-865(1994). MEDLINE-9326(0)18; PubMed-7684041; SECUENCE FROM N.A.

SEQUENCE OF 1016-1549 FROM N.A. STRAIN-MERINO-DOKSET JORN X BORDER LEICESTER; TISSUE-WOOL FOLLICLES;

MEDLINE-90140642; PubMed-2294812; Fielz M.J., Presland R.B., Roders G.E.: "The CDNA deduced amino acid sequence for trichohyalin, a differentiation marker in the hair follible, contains a 23 amino acid Cell Biol, 110:427-436(1990) repeat.";

, CONFIGURED AS A SERIES OF PEPTIDE REPEATS AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS, DOMAIN 6 IS THE MOST FEEBLAR AND MAY HIND KIE DIRECTLY BY TONIC INTERACTIONS DOMAINS 5 AND 7 ARE LISS WELL ORGANIZED AND MAY INDICE FOLDS IN THE MOLECULE, DOMAIN 9 CONTAINS THE C-LEMMINUS, CONSERVED AMONG ENTIRELY ALPHA-HELLICAL, OF VARYING REGULARITY DIFFERENT SPECIES.

- PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100 FAMILY.
- -!- SIMILARITY: CONTAINS 2 PF-HAND CALCIUM-BINDING DOMAINS.

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EF-HAND 1 (LOW AFFINITY) (POTENTIAL). EF HAND 2 (HIGH AFFINITY) (POTENTIAL). 14 X 28 AA APPROXIMATE TANDEM KEDEATS. S-100 LIKE. PROSITE: PS00303; S100_CARP; FALSE_NEG. InterPro; IPR002048; EF-hand. InterPro; IPR001751; S100_CaBP. Pfam; PF00036; efhand; 1. Pfam; PF01023; S_100; 1. PROSITE; PS00018; EF_HAND; 1. EMBL; Z18361; CAA79165.1; -. EMBL; X51695; CAA35992.1; -. Repeat; Calcium binding. DOMAIN 1 91 PIR; A34209; A34209. PIR; S32633; S32633. PIR; A40691; A40691. HSSP; P02633; 31CB. CA_BIND

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    This SWISS-PROT entry is cepylight. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence of the Octopus doflein! hemocyanin subunit, structural and evolutionary implications.",
I. Mol. Biol. 278:827-842(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **ARY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF SUBUNIT ONG.
MEDINE-98271752. PubMed-9614977;
Cuff M.E., Miller K.L., von Holde K.E., Hoodstickson W.A.,
"Crystal structure of a functional unit from Octopus hemoryanin";
J. Mol. Ball, 278-855-870(4398).
: FUNCTION: HEMORYANINS ARE COFFED-TONIALINING CXYGEN CARPIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMMH OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: CONTAINS TWO COPPER ATOMS PER FUNCTIONAL UNIT. SUBUNIT: DECAMERS OF LARGE IDENTICAL SUBUNITS (350 kDa), EACH CONTAININS 7 SLOBILAR OXYGEN: BINCINS FUNCTIONAL UNITS. ODA, ODE, ODE, ODE, AND OFG. DETAMEP FORMATION REQUIRES THE PRESENCE OF MAGNESIUM 10NS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Octopus dolleini (Giant octopus).
Eukarysta, Metazoa: Moilusca, Orphalopodu, Coleoidea; Octopoda:
Incirrata; Octopodidae, Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Branchial gland;
MEDLINE-98277150: PubMed-9614945;
Miller K.I., Cuff M.E., Lang W.F., Varga-Weisz P., Field K.G.,
van Holde K.E.;
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2-21.
2-22.
2-33.
MISSING (IN SHOPT FORM)
MISSING (IN SHOPT FORM)
E G G (IN FFF 2).
MW. E72FB9FF1326E5AE CRC64;
                                                                                                                                                                                     DB 1; Length 1549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interire, IFR002227, Tytosinase.
Ffam; PF00264, Lyrosinase; 8.
PRINTS, PR0092; TYROSINASE.
PROSITE, PS00497, TYROSINASE.
PROSITE, PS00497, TYROSINASE.; 4.
Oxygen transport; Transport, Copper, Glycoprotein, Hemolymph; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                        Pred. No. 66;
0, Mismatches
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                                                                                                                                                                                       Score 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemocyanin G type, units ODA to ODG.
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                                                                                                                                                                                                                              8; Conservative
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                   1462 148
1485 150
1145 110
1251 127
1399 130
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Best Local Similarity
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N-LINKED (GLCNAC. ...) (POTENTIAL).
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0 0; Gaps Ouery March 0.4%; Score B; DH 1; Length 2896; Hest Local Similarity 100.0%; Prod. No. 1.1c.02; Matches B; Conservative 0: Mismatches 0; Indels

<u>a</u>

Search completed: July 2, 2002, 15:42:58 Job time: 375 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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protein search, using sw model M protein July 2, 2002, 16:04:01; Search Lime 44-R5 Secrets (Without alignments) 106.198 Million cell updates/sec Вчп оп:

US 09 603-665 5_COPY_1950_2144 195 Title: Pertect score.

I LETLFAGHLVKPFADILXQV.......QKIIQQLEIVLGEPLQSYF 195 Sequence

Capop 60.0 . Sapovr 60.0 Scoring table:

241628 seqs, 24425594 residues Word size : Searched.

169 lotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Latabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		9			SUMMARIES	
Result No.	Score	Querry Match	Query Match Length DB	$\tilde{\Xi}$	9	Description
		. ¥. . ∓			US:08 636 915A 79	Sequence 79, Appl
73	Ĺ	4.5	98	-1	-08-211	
~	7	4.5	117	₹,		
4	7	÷.	178	~	US-08-928:692-57	Sequence 57, Appl
r.	7	4.6	428	4	US-09-347 833 6	Sequence 6, Appli
÷	7	9.6	655	~	US-09-347-833-4	-
7	7	3.6	729	4	US-09-230-196-2	(1
œ	7	4.6	911	.7	US 08-928 692-59	59,
6	7	4.6	916	.71	US-08-928-692-58	Sequence 58, Appl
10	7	3.6	1045	-	US-07-596-467-6	1 '4
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12	7	3.6	1045	-	US-U7-783-861C-6	Sequence 6, Appli
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77	æ	7.7	18		US-08-432-691-1	ì
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7.7	ę	- -	18	~	US-08-940-093-244	

Querry Match 3.6%; Score 7; DB 4; Length 41; Best Local Similarity 100.(%; Pred. No. 4.2;

LENGIH: 41 amino acids

TYPE: amino acid STRANDEDNESS: TOPOLOGY: unknown MOLECULE TYPF: peptide US-08-630-915A-79

3.1 18 3 0 3.1 18 3 0 3.1 18 4 0 3.1 18 4 0 3.1 18 4 0 3.1 18 4 0 3.1 165 2 0 3.1 167 1 0 3.1 167 1 0 3.1 161 5 0 3.1 181 2 0 3.1 181 2 0 3.1 181 2 0 3.1 181 4 0	
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6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	TELERHONE: (212) 790-9090 TELERA: (212) 869-8864/97 TELEX: 66141 PENNIE: RMATION FOR SEQ ID NO: 79: QUENCE CHARACIFRISTICS:
28 6 6 8 8 9 9 6 8 8 9 9 6 8 8 9 9 6 8 9 9 9 6 8 9 9 9 6 9 9 9 9	TELLETHONE: (212) 790-712 TELEX: (212) 869-889 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

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Gaps
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                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Production of chimeric antibodies - a TITLE OF INVENTION: combinatorial approach NUMBER OF SECUENCES: 144
                                                                                                                                                                                                                      APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIEM, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6%; Score 7; DB 1; Length 98; Best Local Similarity 100 0%; Prod No 9 5; Matches 7; Conservative 0; Mismatches 0; Indels
Indels
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Mismatches
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FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLING DATE: 23-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GR 9206372 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 ; Sequence 130, Application US/08211202; Patent No. 5565332; GENERAL INFORMATION:
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INFORMATION FOR SHO ID NO: 130:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-MAP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/G
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APPLICATION NUMBER: GB 91
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
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7; Conservative
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MEDIUM TYPE: Floppy
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                                   33 ENDPEKC 39
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                                                                                                                                     SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods for Modifying the Production of TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%; Score 7; DB 3; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0, Indels
                                                                            APPL:CANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CC
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CC
                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 11;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP93/00603 FILLING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HS/08/545,809A
                                                                                                                                                                                                 Fish & Richardson, P.C.
                  Sequence 139, Application US/U85458U9A Patent No. 6096878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/08928692
Patent No. 5958727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-542-8906
TELEX: 200154
INFOPMATION FOR SEQ ID NO: 139:
                                                                                                                                                                                    Windows95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brody, Howard APPLICANT: Yaver, Deborah S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0v
Best Local Similarity 100.0v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lamsa, Michael APPLICANT: Hansen, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 617-542-5070
617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                             CUPPENT APPLICATION DATA - APPLICATION NUMBER - HS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Freeman, John W
PEGISTPATION NUMBEP: 2
                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein HS-08-545-809A-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 COMPUTER PEADARLE FORM:
                                                                                                                                                         NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                        GENERAL INFORMATION:
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US-08-545-809A-139
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                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
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MOLECULE TYPE: protein
Patent No. 6294658
                                                                                                                                                                                                                        SEQ ID NO 4
LENGTH: 655
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                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ouery Match 3.6%; Seore 7: DB 2; Length 178; Hest Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March 3.6%; Score 7; DB 4; Length 428; Local Similarity 100 0%; Pred, No. 37; Conservative 8, Mismatches 6; Indels 1044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Famodu, Layo O.
APPLICANT: odell, Joan T.
TITLE OF INVENTION: Factors Involved in Gene Expression FILE REFERENCE: HH-1172
                                                                                                          COMPUTER: 14M Compatible OFFICE STREAM TO SYSTEM TO SOFTWARE: Fast SEQ for Windows Version 2.7 CURRENT APPLICATION DAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/347,833 CURRENT FILING DATE: 1939-07-02 FARITER APPLICATION NUMBER: 60,0042,415
                                                                                                                                                                                                                                                                                              4944.200-US
                                                                                                                                                                              Characterist 645
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: Patent No. 6294658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: July 16, 1998
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                          REFERENCE/IXXXEET NIMBER: 494
HELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
FELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                             44,728
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
FENGH: 178 amino acids
                                                                                                                                                                              APPLICATION NUMBER: US 20 PER FILLING DATE: 12-SEPF-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : MOLECULE TYPE: No. 5958727e
US U8:928-592:57
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                           NAME: Lambiris, Elias J
REGISTRATION NUMBER: 43
                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                        COMPUTER READABLE FORM:
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US-09-347-833-6
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CITY: New York
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357 PLVIQUE 363
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                                     VSO
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                                   COUNTRY:
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Best Local S
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                 SIATE
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APPLICANT: Rauscher III, Frank J.
APPLICANT: Jensen, David E.
TITLE OF INVENTION: BRCAL Associated Protein (BAP-1) and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SPOURDERS: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 7; DH 4; Length 655;
100.0%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (c) Indels
                APPLICANT: Famodu, Layo O.
APPLICANT: Famodu, Layo O.
TITLE OF INVENTION: Factors Involved in Gene Expression
FILE REFRENCE: H8-1172
CURRENT APPLICATION NUMBER: US/09/347,843
CURRENT FILM ODATE: 1999-07-02
EARLIER APPLICATION NUMBER 60/092,415
EARLIER FILMS DATE: July :0, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: MICROSOFT OFFICE 97
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Spring House Corporate Chil., Po Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-TAGS
SOFTWARE: Patentin Release #1.0, Version #1.36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/230,196
                                                                                                                                                                                                                                                                                                                                                                           WSISBUSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/022,997
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Sequence 2, Application HS/09230196
// Patent No. 6307035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 31,215
FEFFEN-LOSKET NUMBER: WE
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215-540-9200
215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: 729 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                  ; ORGANISM: Oryza sativa
US-09-347-833-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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GENERAL INFORMATION:
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Lamsa, Michael
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Chappell, J.
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                                                                NUMBER OF SEQUENCES:
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Bost Local Similarity
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                                                                                                                                                                                                                                    OPERATING SYSTEM:
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APPLICANT: Wolf,
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                                                                                                                             New York
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   APPLICANT:
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                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                       APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Lamsa, Michael
APPLICANT: Harsen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 7; DR 2; Length 911;
100.0%; Pred. No. 74;
Live 0; Mismatches 0; Indels
                                                      DB 4; Length 729;
                                                                                      0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                       Ouery Match 3.6%; Score 7, DB 4;
Best Local Similarity 100.0%; Prod No. 61;
Matches 7; Conservative 6, Mismatches
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FILING DATE: 12-SEPT-1997
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Patent No. 5958/27
GENERAL INFORMATION
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
                                                                                                                                                                                                                                 Sequence 59, Application US/08928692
Patent No. 5958727
                                                                                                                                                                                                                                                                                                                                                                                                                           405 Lexington Avenue
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INFORMATION FOR SEQ ID NO: 59:
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US-08-928-692-59
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Rest Local Similarity 100.0
....ches 7; Conservative
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REGISTRATION NUMBER: 33
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                                                                                                                                                                                                                                                                                   Brody, Howard
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637 1.1.1.QF11, 643
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448 LAEKLIKE 454
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APPLICANT:
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                US-09-230-196-2
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COPPESPONDENCE ADDRESS:
ADDRESSEE. No. 99547270 No. 5958727413k of No. 69587274 h America, Inc.
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Chicago
APPLICANT: Hansen, Kim TITLE OF INVENTION: Methods for Modifying the Production of TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Method and Composition for increasing TITLE OF INVENTION: Sterol Accumulation in Higher Plants NUMHER OF SKOUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 916;
3. 75;
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APPLICATION NUMBER: BS/07/596,467
                                                                                                                                                                                                                                                                                                                               SOFTWARE. FASTSHO for Windows Version 2 0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,6%, Score 7; DB 2
100 O%; Pred. No. 75;
ative 0; Mismatches
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                                                                                                                                       405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFOPMATION-
NAME: LAMBITIS, Ellas J
REGISTRATION NIMHER: 33,728
REFERENCE/DOCKET NIMHER: 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saunders, Court A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: No. 5958727e
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 18M Compatible
                                                                                                                                                                                                                                                                                                                                                                                                           12-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212-857-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      916 amino acids
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Wolf, Fred P.
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A Method and Composition for Increasing the Accumulation of Squalene and Specific Sterols in Yeast
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                                                                                                                                                                                                                                                                                                                                          Amogo Corp., Patents and Licensing Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Levine, Daniel M.; Parker, Thomas S.;
APPLICANT: Rubin, Albert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods Useful in Endotoxin
Prophylaxis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/783,861C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Galloway, NO. 5460949vall B. TELECOMMUNICATION: TELEPHONE: 312 856-7180
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APPLICATION NUMBER: US 07/613,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Sequence 3, Application US/07928930A
; Patent No. 5344822
                                                                                                                   ; Sequence 6, Application US/07783861C
; Patent No. 5460949
                                                                                                                                                                                                                                                                                                                                                       : 200 East Randolph St.
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Saunders, Court A.
APPLICANT: Wolf, Fred R.
                                                                                                                                                                                                                       APPLICANT: Mukharji, Indrani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                    10 HLVKPFA 16
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                                                                                                  US-07-783-861C-6
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                                                                             RESULT 12
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STREET: 180 N Ste son St
                                                                                                                                                                                                                                                                                                               9.6%; Score 7; DB 1; Length 1045; Best Local Similarity 100.0%; Prod. No. 84; Matches 7; Conservative 0; Mismatches 0; Indels
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19920814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29,381
                                                                         TELECOMMUNICATION INFORMATION: IELECHONE: 412-616-5400 iFLECTAX: 412-616-5450 incommation for SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chappell, J.
APPLICANT: Sannders. Court A.
APPLICANT: Chellar, 3.
APPLICANT: Woll, Fred R.
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                  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 29
                                                            Gamson, Edward P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE CHARACTERISTICS:
FILING DATE: 19901012
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: MOLECULE TYPE: protein

US 07 596 467-6
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illino
COUNTRY: USA
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US 07 934 324-6
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Gaps

New York

STATE:

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RESULT 15
US-08-487-461-3
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                                                                                                                             US-08-288-568-3
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                                                                                          TYPE:
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APPLICANT: Rubin, Albert L; Gordon, Bruce K; Saal, Stuart D.
TITLE OF INVENTION: Methods Useful in EndoLoxin Based
TITLE OF INVENTION: Prophylaxis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1%; Score 6; DB 1; Length 17; Jun um; prod No. 19; tive 0; Mismatches 0; Indels
                                                 Diskette, 5 25 inch, 360 kb storage
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
MEDIUM TYPE: Storage
                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,530A
FILING DATE: 19920812
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REFERENCE/DOCKET NUMBER: ROGO 211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/288,568 FILING DATE: 10-AUGUST-1994
                                                                                                                                                                                                                             Hanson, No. 5344822man D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/UB288558
; Patent No. 5506218
                                                                                                                                                                                                                                                   30,946
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FILING DATE: 9-ANGHST-1993
                                                                                                                                                                                                                                                                                                             (212) 688-9200
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OPERATING SYSTEM: PC-DOS
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805 Third Avenue
                                                                                        PC-D08
                                                                                                                                                                   FILING DATE: 19920812
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3884 INPORMATION POR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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AMINO ACID
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CORRESPONDENCE ADDRESS:
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New York
                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                     IBM PS/2
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                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                       MEDIUM TYPE:
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COUNTRY.
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APPLICANT: Rubin, Albert Li, Gordon, Bruce R; Saal, Stuart D.
TITLE OF INVENTION: Methods Useful in Endotoxin Based
TITLE OF INVENTION: Prophylaxis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outry Match 3.1%, Score 6, 198-1; Longth 17; Best Local Similarity 100.0\$; Pred. No. 19; Marches 6; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                      0; Indols
                                                                                                                                                                                                                  Query Match 3.1%; Score 6; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 19; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 5-25 inch, 360 kb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROCO 211.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/487,461
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5587366man D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08487461 Patent No. 5587366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30,946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9-AUGUST-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 688-9200
TELEFAX: (212) 838-3884
INPORMATION FOR SEQ ID NO: 3:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPPRATING SYSTEM: PO-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: June 7, CLASSIFICATION: 514 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 9-AUGUST PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER PRADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                 amino acid
                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Jol 7 - 20.50 -

Gemiore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

M protein - protein search, using sw model

Run on:

July 2, 2002, 14:08:03 ; Search time 117 for seconds (Without alignments) 189.862 Million cell updates/sec

US 09-603-665-5_00PY_1867_2067

Perfect score:

CIAQESVAMADDSLWKPLNY 201 1 LTAFFLEALDFRAGHSENDL. Sequences

otigo Gapop 60.0 , Gapoxt 60.0 Scoring table:

747574 sets, 111074796 residues Sear-hed:

Word size :

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481

Minimum DB seq lenath: 0 Maximum DB seq length: 2003000000

Post processing: Listing First 45 summaries

Database .

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

	Description		Protein encoded by	Human protein sequ	Homo sapiens BAP28	A dyrase protein o	Peptide #7963 enco	Human brain expres	Human bone marrow	Peptide #8214 enco	Dp-74 VH1 gene hea	Buman immunoqlobul	B. vulgaris NIM1 h
SUMMARIES	41		AAB85029	AAH92729	AAW54099	AAY 2 8 7 % 8	ARB40457	AAM51274	AAM74002	AAM34177	AAR 34 27 :	AAR66345	AAB27314
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æ			0.86	49.8	¥ . ¥	0.4	₹.	ت ~	ر م	ý.,	\$.5	\$ 1 +	ت ج
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Motant Asperaillus A. oryzae P7:14.1	Human protein sequ	Helicobactor pylor	Peptide #3629 enco	Peptide # 4574 enco	Novel human diagno	Human protein sequ	Human polypeptide	ATP specific succi	Human protein sequ	DNA encoding hyman	Buman polypeptide	Dropouphild melanod	B. vulgaris NIM1 h	Rice poly (A) band	Buman JRFX JRF2246	Human H37 anino ac	Yeast HMG CoA redu	Class A amphipathi	Fragment of human	Human hervous syst	Novel human secret	Peptide #11578 enc	Peptide #81 9 enco	Buman immune/haema	Arabidopsis thatla	Human immune/haema	Human polypeptide	Zea mays protein t	Human diqestiv⊷ sy	Zea mays protein f	Novel human diagno	Human polypeptide
AAW37995 AAY39876	AAB95232	AAU35868	AAM17195	AAM04892	ABG27639	AAB92979	AAM39688	AAG6.6.5.0.1	AAH93393	AAB70163	AAM4 14 74	ABB59537	AAH27 +24	AAE1 4001	AAB42482	AAB03758	AAR58611	AAY42447	AAY76326	ABB15816	AAU31446	ABB44072	AAM21705	AAM85086	AAG13000	AAM90052	AAO04594	AAG22312	AAM92148	AAG22686	ARC02711	AA007992
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ALIGNMENTS

RAP28; prostate; tumour; canger; diagnostic; genetic analysis. Protein encoded by BAP28 cDNA consisting of exons 1 to 45. AAB85029 standard; Protein; 2144 AA. Location/Qualifiers /label- Ser or Asn /label- Asp or Asn /label- Gly or Glu /label- Ala or Val U6-AUG-2001 (first entry) Misc-difference 1694 Misc-difference 1854 Misc-difference 1967 Misc-difference 2017 HUMO Sapiens AAHPS029; AAH85029 RESULT

WOZUNTUNK69-AZ

04 - JAN - 2001.

23 JUN 2000, 2000WO-IB01183.

25-JUN-1999; 990S-0141323. 18-JAN-2000; 2000US-0176880.

(GEST) GENSET

09-1MTN-2000; 2000JP-0241899.

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The invention is directed to RAP2R polypeptides, RAP2R polynucleotide sequences and regulatory region located at the 3' and 5' ends of the MAP2B couldny region. The MAP2B polypeptides can be expressed by standard recombinant methodology. BAP2B polynucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP2B expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP2B polypeptides are useful in genetic analysis, the present sequence represents a protein encoded by a first cDNA sequence of the BAP2B gene consisting of the exons 1 to 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DAPKDRELTFYNLADGIAEKERGEFTLFAGHLVKPFADTLXQVNISKTDEAFFDSENDPE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KCCLLI QPILINCLYK I FLFOTTORF I SKFPRAXALMMPLVDQLENPLGGEBEKFOMRVTKHLI 180
                                                                                           New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2144;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1997 - D6 22; Longth 21/
Pred. No. 4.7e-197;
Pred. Tohes - 0; Indels
             Bouqueleret L, Chumakov I, Cohen-Akenine A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:11159.
                                                                                                                                                        Ciaim 14; Page 297-304; 349pp; English.
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100.08; Pre
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99JP-0300253.
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                                                            N-PSDB; AAF83909, AAF83910.
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                                          2001-367032/38
                                                                                                                                                                                                                                                                                                                                                                                                     2144 AA;
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27-AUG-1999;
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02-MAY-2000;
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In gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the profesors the constitution of the full length cDNAs. The primers allow obtaining of the full length cDNAs casily without any specialised methods. AAH03166 to AAH18628 and AAH1863s to AAH8472 to present human cDNA sequences; AAH374 to AAH3852 to AAH3853 represent human amino acid sequences, and AAH3369 to AAH3832 to AAH3832 and AAH3843 represent human amino acid sequences, and AAH3369 to AAH3832 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oliqoral primer and an oliqoral complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides of (b) a combination of an oligonucleotide comprises at least 15 nucleotides of (b) a combination complementary strand or a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 1'-end sequence and an oligonucleotide comprising a sequence defined the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3' and sequence is selected from those defined in the specification. The primer sets can be used in antisense thereby and
                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                  Yamamoto J;
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100 0%; Pred No 3 6e-95;
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                                                                                                                                                        Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                              Saito K,
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                                                                                                                           Hayashi K,
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                                                                                                                              Isogai T, Nishikawa T,
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the present invention.
                                                             (HELLI -) HELLIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs
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(MARI-) MARINE BIOTECHNOLOGY INST CO 1.TD.
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27-SEP-2000; 200005 0236359.
04-YCT-2000; 2000GB-0024263.
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20000S-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 SENDPEKC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proportion of the recombinant breast cancer antiaen, BRCA1, binding proportion of a BARD1, BL23, BE2, RE14, BE31 or BE445, or a composition for the detection of a BARD1, BL23, BE2, BE14, BE31 or RE445 inclpication for the sequence, specification of BRCA1, useful to identify a patient having, or at its of developing cancer. HARD1 can be used in the preparation of an anti-RARD1 antibody, and in the detection and purification of a BECA1 protein. BARD1, BL23, BE2, BE14, BE31 or BE445 can used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identification of a binding protein agonist or aniagonist that alters the binding of MARDI, BL23, BE24, BE31 or BE445 to BRCA1 or the biological activity of the HKCA1 BARDI, BL23, BE2, BE34 or BE445 complex. The aniibodics can be used to defect BARDI, BL23, BE14, BE31 or BE445, a specific anti-BARDI antibody can be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence encoding BARDI, B123, BE14, BE31 or BE445 - which as breast cancer antiqen, BRCAI, binding proteins are useful to identify patient having or at rick of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification; defection; microbe; gyrase gene; gyrase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guery Match
Best Local Similarity 100.0%; Pred. No. 5.2e.95;
Matches 100; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a protein which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a patient having or at risk of developing cancer.
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9788-0042611.
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97WO - HS16842.
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                                                                                                                                                                                                                                                                                                            Baer R. Bowcock AM;
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                                                                          04 - APR 1997;
19 SEP 1997;
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                                                                                                                   13.46
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human factal liver. The single exon nucleic acid probes may be used for predicting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; geng expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sapt.
                                                                                                                                                                                                      The specification describes a method for the identification or detection of a microbe, using the gyrase quee as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then identified or detected depending on its base sequence. The method can be used to classify and identify an unidentified microbe stain rapidly and with high precision. The present sequence represents a gyrase protein.
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                                                                                                       - by detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #7963 encoded by human toetal liver single exon probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4.0%; Score 8; 5B 20; Lenath 220;
100.0%; Pred. No. 5.4;
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                                                                                                     Identification and detection of a microbe
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
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                                                                                                                                                                  Example 3; Page 14-15; 42,pp; Japanese
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                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe encoded protein SEQ ID NO: 33384.
measuring and displaying gene expression in samples derived from human tetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                               Human, brain expressed exen, gene expression analysis, probe,
microarray, Alzhelmer's disease, multiple sclerosis, schisophrenia,
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C
                                                                                                                   3.5%, Score 7, DB 22; Length 36; 100_104, 9x \pm d - Nz, 11, 11, o. 1 Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0207456.
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2000US-0236359.
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                                                                                                                                             7; Conservative
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                                                                                                                                 Best Lucal Similarity
                                                                                    36 AA;
                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer.
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                                                                                     Sequence
                                                                                                                       Query Match
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DB 22; Length 36;

3.5%; Score 7; DB 2: 100.0%; Pred. No. 11;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID No. 34308, 658pp / Sequence histing; English.
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  0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7; DB 22
.00.6%; Pted. No. 11;
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  0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM34177 standard; Protein; 36 AA.
                                                                                                                                                                                                              AAM74002 standard, Protein; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-00r-2000; 20000B 0024263.
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2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-ATG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2001 (first entry)
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%
Query Match
Best Local Similarity 100.0
Matches 7; Conservative
    7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GGEEKFQ 172
                                               166 GGREKFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ggeekfg 10
                                                                                            4 gycekfg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04 FeB 2000;
26-MAY 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-3HV-2000;
                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM34177;
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                                                                                                                                                                                                                                                              AAM74002;
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AAM34177
    Matches
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AAR66345
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                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single even nucleic acid probes (SENP-see AAI315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antendfal diagnosis of human quentic disorders.
       Poptide #8214 encoded by probe for measuring placestal gove expression.
                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                           Human genome derived single exon nucleic acid probes useful for analyzing qene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                       Probes microarrays humans placentas antenatal diagnesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; monoclonal antibody; anti alobilin reaponse;
chimeric; mouse numan antibodies; antibody; prevention
                                                                                                                                                                                                                                                                                                                                                                                lou.0%; Pred. No. 11; ive 0; Mismatches
                                                                                                                                                                                                                                                                    "Laim 27; SEQ 10 No :4446; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 7; 1
du.0%; Pred. No.
                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W, Rank DR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR 44.271 Standard; Protein: 89 AA.
                                                                                                                                                                                        (MOLE ) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-GB01755.
                                                                                                                   2000US 0180312.
2000US-0207456.
                                                                                                                                                              200005-0246459.
                                                                                                                                                                       04 OCT-2000; 2000GB-0024263.
                                                                                                    40 JAN-2001; 2001WO USOU663.
                                                                                                                                     20000BS-0608408.
                                                                                                                                             200001S-0632366
20000JS-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp 74 VHl gene heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 JHL-1994 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 190.7
                                                                                                                                                                                                                           WPI: 2001 488897/53.
                                                                                                                                                                                                                                                                                                                                                16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          166 GGERKPO 172
                                 qenetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                    Wo200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SEP 1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saprens
                                                 Homo Sapiens
                                                                                                                           2000;
                                                                                                                                                               SEP-2000:
                                                                                                                                     JUN-2000;
                                                                                                                                              AUG -2000;
                                                                                                                                                       SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01 APR-1994.
                                                                                  09 AUG-2001
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR (4271;
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR 14271
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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Primer, PCR, amplify, human; immunoqlobulin; variable; heavy chain; cosmid; placenta; vector; pJR81; F.coli; mammalian,
                                                                                                                                                                                                                                                                                                                                    comprises use of chain shiffing using phage expression, useful
for reducing auti-globulin responses in humans for increased
human characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragment comprising human immunoqiobalin Vh genes - for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
5
                                                                                                                                                                                                                                                                                                               Producing human antibody polypeptide dimer specific for antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which may be used as part of a method of producing chimeric monse-human anibodies or fragments which have the same binding specificity as a parent Ab but have increased human characteristics, preventing anti-globulin response in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.5%; Score 7; DB 14; Length 89; 100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of the DP-74 VIII qene heavy chain
                                                                                                                                                                                                               Winter GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunoglobulin variable heavy chain #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note "encoded by ACA codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.3%; Prod. no.
Tivo 0; Mismatches
                                                                                                                                                                                                               Baier M, Hoogenboom HRJM, Jespers LSAI,
                                                                                                                                           (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR66345 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Fig 11; 109pp; English.
91CB-0020252.
91GB-0020377.
92GB-0006318.
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                                                                                                                                                                  (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-JP00603
                                                                    92GB-0006372
                                                                                                92WO-GB00883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Host Local Similarity
7, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-006791/01.
                                                                                                                                                                                                                                                             WPI; 1993-117534/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 KFQEPVT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 kfgervt 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 MAY-1993;
                                                                                                15-MAY-1992;
                                                24-MAP-1992;
                                                                    1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04 - AUG - 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09426895-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR66345;
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Caps

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WPI; 1998-207372/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 AA;
                                                                                                                                                                                                               165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV31842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 LLLQFIL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 111qfil 110
                                                                                                                                                                                                                                                                                                                                                                                       115 dapkdrl 121
                                                                                                                                                                                                                                                                                                                                                  61 DAPKDRL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09811203-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brody H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW37995
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                                                                                         chain sequences encoded by novel isolated genes. The genes of cosmitted sequences encoded by novel isolated genes. The genes of cosmitted sequences: You's YOU HE SEQUENCES COSMITTED THE BOWN THE PART THE PART OF THE TARREST YOU'S YOU'S YOU HE EAST THE TARREST YOU HE TARREST YOU'S YOU WANT Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention is concerned with the isolation of NIM1 homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, NICOLiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          Protein sequences (AAR66295:51) are novel human immunojlobulin heavy chain sequences encoded by novel isolated genes. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Systemic acquired resistance; SAP, signal transduction cascade; disease resistance, tobacco, tomato, canola; sunflower; sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16, Length 117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
production of human immunoglobulin in mammailan hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmeron JM, Weislo LJ, Willits MG, Mengiste I,
                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7, DB 16
100.0%; Pred. No. 33;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.
                                       Disclosure; Page 105-107; 130pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. vulgaris NIM1 homologue SEQ ID NO: 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologues of Arabidopsis NIM1 gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB27313 standard; Protein; 165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 111; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2000; 2000WO-EP01978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 JAN 2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-594322/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA97216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 KPQERVT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 kfgervt 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB27313;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB27313
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signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The protein and gene can be used to produce transgeric plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, indispot virus, pelargonium haf cul virus, rad clorar mettle virus, temato bushy stunt virus, fungi, including Phythophthora parasitic and Perchospora tabacia, bacteria such as Pseudomonas sytingae and P. Meloidogyue incounting aphids and lepidoptera and nematodes such as Meloidogyue incounting aphids and lepidoptera and nematodes such as organisms of maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of a rescued locus from the mutant Aspergilius oryzae P7 14.1, used in the method of the invention which involves the use of a mutant cell with a nucleic acid construct introduced into a locus. The methods can be used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide production - using a matant cell with a nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant Aspergillus oryzae P7-14 I resound locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lamsa MH, Yaver DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fiq 32, 195pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rescued locus; mutant; metabolite.
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Matches 7, Conservative
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This sequence is encoded by an Aspergillus organe DNA locus. The invention relates to a method of prodicing a polypeptide, comprising; (a) cultivating a mutant cell under conductive for production on the polypeptide, where: (i) the mutant cell is related to a parent cell. Which comprises a first DNA sequence encoding the polypeptide, by the introduction of a nucleic acid construct into the genome of the parent cell at locus which is not within the first DNA sequence, and not within a second ENA which encodes a protein that negatively regulates transcription, translation or secretion of the polypeptide, and not within a third DNA sequence encoding a protein that negatively regulates within a third DNA sequence, encoding a protein that cell and not within a the polypeptide under the conditions; and (ii) the mutant cell produces more of the polypeptide than the parent cell when both cells are cultivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     under the conditions; and (b) recovering the polypeptide. The method is useful for producing polypoptides encoded by a LNA sequence which does not contain the mutation.
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                                                                                                                                                                              Protein production; mutant protein; DNA locus.
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lu0.0%; Pred. No. 49;
ative 0: Mismatches
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                                                                                                                                           A. oryzae P? 14.1 locus protein seguence
                                                                                                                                                                                                                                                                                                                                                                                                           Lamsa M, Hansen K, Yaver DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:17369.
                                              AAY 19876 standard: Protein; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Fig 33; 129pp; English.
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Hest Local Similarity 100.0-
                                                                                                            04-DEC 1999 (tirst entry)
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                                                                                                                                                                                                             Aspergillus orygan
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             RESULT 14
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                           AAY 19876
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The present invention describes primer sets for synthesising 5602 full length coMs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonurcheotide complementary to the complementary strand of a polynneleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides, of (b) a combination of an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide mapping a sequence complementary to the sequence and an oligonucleotide mapping a sequence comprises a 5'-end sequence and an oligonucleotide mapping a sequence of polynneleotide mapping a sequence of polynneleotide comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gone therapy. The primers are useful for synthesising polynocleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining on the full-length cDNAs casily without any specialised methods. AAR03165 to AAR13628 and AAR13647 to AAR13742 represent human clind sequences; and AAR1343 represent human amino acid sequences; and AAR1345 to AAR13332 represent oligomicleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 5' end sequence/3' end sequence is selected from those defined in the specification. The primer sets can be used in antiscuse therapy and in gene therapy. The primers are useful for synthesising polynocleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detrection and/or diagnosis of the abnormality of the proteins encoded by the
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Human; primer; detection; diagnosis; antisense therapy; gene therapy
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100.0%; Pred. No. 65;
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Ishii S. Sugiyama I, Makamatsu A, Nagai K, Otsuki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 17369; 2537pp + CD ROM; English.
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                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116136.
                                                                                                                                                                                                                                                                                                                                                                                     441P-0248036.
                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0300253.
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Best Local Similarity
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                                                                                 Homo sapiens.
                                                                                                                                                      EP1074617-A2.
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Helicobacter pylori cellular proliferation protein #181.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the converse their use in the discovery of movel antibiotics, the essential genes themselves and the discovery of movel antibiotics, the essential genes themselves and the discovery of movel antibiotics, the essential genes themselves and the checked proteins. The proteins are sendenced are considered to the protein antibiotic and Enferonce, and potential new targets for antibioris also useful for the identification of potential new targets of or antibiotic development. The antiscosmologic stress these proteins, and to obtain antibodies capable of binding to the express these proteins. The proteins can be used in proliferation, to express these proteins. The proteins can be used to screen compounds in alticular dispute in screen conformance. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an escential prokaryotic cellular proliferation protein.

Con the printed specifical on, but was obtained in electronic contraction in the printed specifical ion, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; druq design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Seq ID No 11461; 511pp; English.
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                                                                                              Helicobacter pylori.
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26-MAY-2000;
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22 - DEC - 2909;
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241528 scqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters:

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Minimum DH seq length: 0 Maximum DH seq length: 200000000

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Squ2 hcft-data? SquaFA_WH prg:*

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yequ2 yptodata/2/laa/AA_CAMB.ppg:*

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Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Kesnit No.	t o. Score	_	Ouery Match Length	DB	ID	Description
	1 7	4.5	41	4	US-08-630-915A-79	Sequence 79, Appl
	C4	3.5	86		08 08 211 202 130	130,
	4	5.4	1117		-08-545	139,
	7	5°. ≁	178	~	05-08-928-692-57	57, /
	5 7	3.5	4.28	4	US-09-347-833-6	Sequence 6, Appli
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-	4 6	1.0	1.33	4	US-U9-085-761A-47	Sequence 47, Appl
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	17	⊒.*	101	L^	PCI -US95 - 05741 - 11	Sequence 11, Appl
-	æ	D. *	178	~1	US 08-477-451-46	Sequence 46, Appl
	ч 5:	0.1	180	-	US-08-328-254-7	7, 1
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•	¥.	3.0	195	~1	US-08-882-704A-2	2, A
7	9 77	0.4	202	~	US-08-469-486-56	Sequence 56, Appl
7	55 h	≎.*	707	7	118-08-464-658-56	Sequence 56, Appl
•	97	3.6	TO CT	٠,	84 08 533 525 15	15,
•	4	3.€	807	^1	US 08 531 525 17	17,

3.5%, Score 7; DB 4; Length 41; 100.0%, Pred. No. 3.2;

Query Match Best Local Similarity

LENGTH: 41 amino acids

TYPE: amino acid
STRANDIDINES:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

Sequence 15, Appl Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 1, Appl Sequence 2, Appl	IDENTIFY ING AND	
US 08 718 270A 15 US 09 718 270A 17 US 09 718 270A 17 US 08 718 270A 16 US 08 718 270A 16 US 08 718 270A 18 US 09 718 1525 18 US 09 718 1734 1 US 09 718 1734 1 US 09 88 20 706 88 US 09 88 200 A 125 US 09 88 207 A 125 US 09 88 207 A 125 US 09 89 207 A 125 US 09 88 207 A 125	ALIGNMENTS PHICATION: SPARKS, Andrew B. HOFPMAN, NO. 0309820h. HOFPMAN, NO. 0309820h. MCCONNELL. SLEPHEN J. MCCONNELL. SAME. WORNICON: USING SAME. WORNICON: WARNICON: WARNICON	6 69741 9:
33.00 3.00	ALIG SULI 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TELEPHONE: (212) 869-8864/97 TELLER: 6611 PRINTE TELLEX: 6611 PRINTE TELLEX: 6617 PRINT TELLEX: 6617 P
82001101244444 820011012455676764444 000010124567676000000000000000000000000000000000	US-08-60-915A-79 Sequence 79 Application of Patent INCORMATION: APPLICANT: SPARKS, And APPLICANT: SPARKS, And APPLICANT: MOFFMAN, WALLICANT: HOFFMAN, MALLICANT: HOFFMAN, MARS ADDRESSED: POMPRES ADDRESSED: ADDRESSED	TELEPHONE

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NUMBER OF SEQUENCES:
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Best Local Similarity
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             63 KPORRVT 69
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Caps
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 0, Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25 (FPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            6300 Sears Tower, 233 South Wacker Drive
   6; Mismatches
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APPLICATION NUMBER: GB 9206372.6
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APPLICATION NUMBER OR 9120252 3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                / Sequence 130, Application US/08211202
/ Patent No. 5565332
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INFORMATION FOR SEQ ID NO: 130:
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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   7; Conservative
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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                                       116 ENDPEKC 122
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                                                                                                                                                    APPLICANT: Honjo, Tasuku
APPLICANT: matsuda, Fumihiko
TITLE DE INVENTION: HUMAN HMUNOGLOHULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
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100.0%; Pred. No. 8.3;
Live 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                          2: Fish & Richardson, P.C. 225 Franklin Street
Sequence 139, Application US/08545809A; Patent No. 6096878; GENERAL INFORMATION:
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TELEPHONE: 617-542-5070
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INFORMATION FOR SEQ ID NOS
SEQUENCE CHARACTERISTICS:
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Patent No. 6294658
GENERAL INFORMATION:
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583 PLVDQLE 589
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100 0%: Pred. No. 12;
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                                                                                                              SOFTWARE: FastSEC Correlations Version 2.0 CURRENT APPLICATION DAIN: APPLICATION NUMBER US/08/2008 60:
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                                                                                                                                                                                                                                  33,728
FP: 4944,200·US
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EARLIER FILING DATE: Joly 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARF: Microsoft Office 97
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Patent No. 6294658
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                                                                                                                                                                                                                      NAME: Lambiris, Elias J
REGISTRATION NUMBER: 84,728
REFERENCE/DOCKET NUMBER: 494
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-4655
INFORMATION FOR SEC ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                     : MOLEGULE TYPE: NO. 5958727e
US-08-928-692-57
                                                                                                                                                                        12-SEPT-1997
                                                                              MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    212-867-0124
212-878-4655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Hest Local Similarity Toese.
                                                                                                                                                                                                                                                                                                                                                      178 amino acids
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Best Local Similarity 100.0-
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                        single
                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : TYPE: PRT
; ORGANISM: Glycine max
US 09-347-833-6
                                                                                                                                                                                                                                                                                                                                                                       amino arid
                                                                                                                                                                                                                                                                                                                                                                                                      linear
CITY: New York
                                                                                                                                                                                         CLASSIFICALION:
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357 PEVIOLE 353
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                                                                                                                                                                          FILLING DATE:
                                            10174
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                            COUNTRY:
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               STATE
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No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
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APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
CORRESPONDENCE: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  3.5%; Score 7: DH 4; Length 655; 100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                 θ; Indels
APPLICANT: Famodu, Layo O.
APPLICANT: Gdell, Joan T.
TITLE OF INVENTION: Factors Involved in Gene Expression
FITLE OF INVENTION: Factors Involved in Gene Expression
FILE REPERENCE: BB-1172
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 69/092.415
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: PasisEQ for Aindows Version 2.0
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 4944.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/38928692; Patent No. 5958727; GENERAL INFORMATION:
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Gruppy, 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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Yaver, Deborah S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNISS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5958727e
US-U8-928-672-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 212-867-0123
212-878-9655
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Best Local Similarity 100.0%
7: Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
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                                           इत्रहरू (त
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                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Methods for Modifying the Production of TITLE OF INVENTION: a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method and Composition for Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 3.5%; Score 7; DH 2; Length 916; Best Local Similarity 100.0\%; Prod No 54; Matches 7; Conservative 0; Mismatches 0; Indels
Query Match 3.5%; Score 7; DB 2; Longth 911; Best Local Similarity 100.0%; Pred. No. 54; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: 18/08/94/8,692 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4944.200-US
                                                                                                                                                                                                                           ; Sequence 58, Application US/08928692; Patent No. 5958727
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Patent No. 5306862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 494
TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Saunders, Court. A. APPLICANT: Cuellar, R. APPLICANT: Wolf, Frod R. TITLE OF INVENTION: Method and
                                                                                                                                                                                                                                                                                   APPLICANT: Brody, Howard APPLICANT: Yaver, Deborah S. APPLICANT: Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: NO. 59587270
US-08-928-692-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212-867-0123
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APPLICANT: Chappell, I
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hansen, Kim
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                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SECHENCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                         US-08-928-692-58
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TITLE OF INVENTION: Process and Composition for Increasing TITLE OF INVENTION: Sterol Accumulation in Higher Plants
                                           E. Dressler, Goldsmith, Shore, Sutker & Milnamow
180 N Stelson St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1045;
  Sterol Accumulation in Higher Plants
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                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
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Best Loral Similarity 100 0%; Pred. No 61;
Matches 7; Conservative 0, Mismatches
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/07/596,467
FILING DATE: 19901012
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19920814
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                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence b, Application US/U7934374
Palent No. 349126
SENEPAL INFOPMATION:
APPLICANT: Chappell, J.
APPLICANT: Chappell, J.
APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
                                                                                                                                                                                                                1BM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                        NAME: Gamson, Edward P. TELECOMMUNICATION :
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312 616-5460
INFORMATION FOR SEQ 10 NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1045 amino acids
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                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                312 616-5460
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MOLECULE TYPE: protein
US-07-596-467-6
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                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                     CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SHQUENCES:
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                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                            ADDRESSEE:
                                                                                                                                                                                                                  COMPUTER.
                                                                                                                                       COUNTRY:
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                                                                                               CITY: C
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CITY:
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APPLICANI: Woll, Fred R.
APPLICANI: Mikhari, Indendani
IIILE OF INVENTION: A Method and Composition for Increasing
FITLE OF INVENTION: the Accumulation of Squalome and Specific Storois in
                                                                                                                                                                                                                                         Gaps
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O
                                                                                                                                                                                                    Length 1045;
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                                                                                                                                                                                                                                         0) Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Amoro Corp., Patents and Licensing Dept. STREET: 200 East Randolph St. Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentir Release #1.0, Version #1.25
                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                  Ouery Match 1.5%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/783,861C
FILING DATE: 19911028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Galloway, No. 5460949vall B.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/613,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: THM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07783861C.
Patent No. 5460949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                       1045 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1045 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 856-7180
312 615 5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IELEFAX: 312 616-5460
INFORMATION FOR SEQ ID NO:
                                                                                                                       : MOLECULE TYPE: protein
US-07-934-374-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19911028
CLASSIFICATION: 4 · 5
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                        TYPE: AMINO ACID
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMING ACID
                                                                                                             inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 50580-0703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         91 HIVKPFA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 HLVKPFA 97
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 TELEPHONE:
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                                                                         LENGTHE
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                                                                                                                                                                                                                                                                                                                                                                  RESULT
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STREET: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HITLE OF INVENTION: Regulatory Proteins that Elective with FITLE OF INVENTION: Mad or Max
NUMBER OF SEQUENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.0%; Score 5; DH 1; Length 34; Best Local Similarity 100.0%; Pred. No. 29; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                            TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2026-4103US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: US-JAN-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/07/617,910
                                                           GENERAL INFORMATION:
APPLICANT: WU, CARL; CLOS, JOACHIM:
APPLICANT: WLSTWOOD, J. TIMOTHY.; R
                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
WORDPERFECT 5.1
                    Sequence 28, Application US/08178477B
Patent No. 5756343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/03252966H
Patent No. 5624818
                                                                                                                                                                                                  ADDRESSER: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eisenman, Robert N. APPLICANT: Hurlin, Peter J. APPLICANT: Ayer, Donald S.
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,341
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                                                                                                                                                                                                                                                                                                                                      FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT : CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CAROL M. GRUPPI
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-178-477B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                              NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING DATE: 20
                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                 10154
US-08-178-477B-28
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                                                                                                                                                                                                                                                          STATE: N
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                              US-09-085-761A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US 09 087 465 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 22
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE. PRT
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APPLICANT: Turner, Raymond J.
APPLICE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR 1: Length 35;
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                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECOLE TYPE: peptide
DESCRIPTION: MAD-1 peptide; see Figure 15A
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSER: Medlen & Carroll, .....
STREET. 220 Montgomery Street, Suite 2200
CITY: San_Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.0%; Score 6; DR 1;
Best Local Similarity 100 0%; Prod. No. 29;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,837
REFERENCE/INGCKET NUMBER: UALR-03356
                                                                                                                                                                                                                                                                      PEGISTRATION NÜMRER 26,447.
PRECEDENIE, PAN KET UMBEEF FUFF17594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEPHONE: (206) 244-0779
INFORMATION FOR SEQ 10 NO 9.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         US/08/257, 966B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 47, Application HS/090R5761A ; Patent No. 6335178
                                                                                               IBM PC compatible
                                                                                                                                                                                 01-JUN-1994
01-JUN-1994
0N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                   COMPUTER READABLE FORM-
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   NAME: Shelton, Dennis K. PEGISTRATION NUMBER: 2h,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Carroll, Peter G. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                              35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                         APPLICATION NUMBER.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                 98101-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION.
                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 EKLKGL 84
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                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-085-761A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM:
US-08-252-9668-9
                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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APPLICANT: Vinkemeier, Uwe
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Darnell Jr., James E
APPLICANT: Mariyan, John
TITLE OF INVENTION: A CPYSTAL OF THE CORP. PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-229
CURRENT APPLICATION NUMBER: US/09/087,465A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O, Gaps
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                                                                                                                                                                                                                                                                                         Length 103,
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Best Local Similarity 100.0%; Pred. No. 82;
Matches 6, Conservative 0, Mismatches
                                                                                                                                                                                                                                                                                         Query Match 3.0%, Score 6, DB 4, Best Local Similarity 100.0%; Pred No 79; Matches 6, Conservative 6, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scarch completed: July 2, 2002, 16.34.00 Job time: 57 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09087465A Patent No. 6160092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHRPPNI FILLING DATE: 1998-05-29 NUMBER OF SEQ ID NOS: 37
TELEPAX: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  not relevant
                                                                                                 LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                     MOLENIE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-087-465-22
                                                                                                                                                                      ToPoLoGY. unknown
                                                                                                                       TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 FISKER 149
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2000 Compugen Ltd. Gendore version 4.5 Copyright (c) 1994 -

protein search, using sw model M protein

Run on:

July 2, 2002, 16:15:19; Search time 57:09 Seconds

(Without alignments) 338.307 Million cell updates/sec

US-09-603-665-5, COPY_1867, 2067 fitte: Ferteet score;

.....CIAQESVAMADDSUWKPLNY 201 1 LIAPFLEALDFRAĞHSENDI... Sequence

Gapop 60.0 , Gapext 60.0 Scoring table:

283138 seqs, 96)89334 residues

Total number of hits satistying chosen parameters:

710

Maximum DR seq length: 20000000000 Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PTR 71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHWMARTES

		200			SUMMARTES	
Result	,	Ouer 7				
္ရ	Score	Match	Match Longth	E.	9	Description
1	œ	O. 4	467	~	AG0546	probable terminal
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~	œ	0 · 4	875	~	T 40023	hypothetical prote
4	Œ	€	935	Ç4	668673	
Ϋ́	7	3.5	86	7	S26914	
9	7	3.5	2 10	୍ୟ	T12480	hypothetical prote
7	į.	نا *	2.52	C4	JC7706	
αr	7	3.5	251	~	H87692	conserved hypothet.
5	7	ν. Υ	254	~	E64716	conserved hypothet
9	7	٠.	276	~	AG 1305	23S ribosomal RNA
Ξ	7	٠. ۶	296	~	A87 311	hypothetical prote
1.2	7	\$. *	458	~	JC5964	apoptosis inhibito
1 -	7	\$. *	359	C 4	T22950	h, pothetical prote
14	7	5-7	472	~1	AE 1184	alcohol dehydrogen
	7	٠.٠	376	.74	014140	hypothetical profe
-	7	3.5	397	2	307675	acetoacetyl-CoA re
17	7	٠,٠	400	~4	CB2213	conserved hypothet
<u>x</u>	7	۶.۶	414	_	H69963	DNA-damage repair
51	7	3.5	422	^;	D87550	hypothetical prote
70	.;	· ·	443	<u> 1</u> 4	683759	cytochrome d (bd-t
7.7	7	1.5	453	?	F86846	ABC transporter pe
7.7	7	٠٠٠٠	537	~1	A38170	cytochrome d compl
7.7	7	3.5	284	~	S77647	mobilisation prote
7.4	7	3.5	601	C4	102633	hypothetical prote
52	۲.	ر. م	683	-1	F69280	iron (II) transpor
56	7	3.5	651	?	T06979	polyadenylate-bind
27	7	٠.	847	~3	F8 4517	probable penicilli
28	7	۲. ۳	875	Ω4	T20429	hypothetical prote
29	7	٠. ٢	211	7	JC6016	chitin synthase (E

	916 2 JO2315 C 10.42 2 H30239 h 1612 2 H30239 h 4558 2 CR2199 F 4558 2 CR2199	3.0 38 2 A21851 22K factor - human 3.0 40 2 T06840 photosystem chai 3.0 67 2 H82490 hypothetical prote 3.0 68 2 G64027 hypothetical prote	72 2 874974 1 72 2 87451 1 84 2 764172 6 85 2 897348 1	3.0 87 164127 alutaredoxin - Hao 3.0 87 2 84288 hypothetical prote 4.0 87 2 895890 hypothetical prote
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RESULI

probable terminal oxidase chain I [imported] - Salmonella enterica subsp. enterica se Gispecies salmonella enterica subsp. enterica servovar Typhi A. Note: this species has also been called Salmonella typhi Gibate: na-Nov-2001 asequence_revision 09-Nov: 2001 #text_chainate 27 Nov: 2001 Gibate: na-Nov-2001 sequence_revision 09-Nov: 2001 #text_chainate 27 Nov: 2001 Gibate: na-Nov-2001 sequence_revision 09-Nov: 2001 #text_chainate 27 Nov: 2001 H; T.; Connection, D.; Grodin, A.; Davis, P.; Pickard, D.; Wain, J.; Church th, T.; Connection, D.; Crodin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parr Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherlord, K.; Simmonds, M.; Skelton, J.; Stevens, A.Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A.Reference number: AB0502; PM.D:11677608

A:Status: preliminary A:Molecule type: DNA A:Residues: 1-467 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08815.1; PID:q16501629; GSPDB:GN00176 C; Genetics:

A:Gene: STY0392

C; Superfamily: cytochrome d complex terminal oxidase chain 1

o: Caps 4.0%; Score 8; DB 2; Length 467; 100.0%; Pred. No. 4.1; U. 100.0%; Pred. No. 4.1; Guery Match Best Local Similarity 100.09 Matches 8, Conservative

102 LTAFFLEA 109 qq

1 LTAFFLEA 8

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RESULT

eyanide insensitive terminal oxidase chain cioA (imported) - Pseudomonas aeruqinosa

C.Species: Pseudomonas aeruginosa

CigRectess resonances attractions
CigRectess resonances attractions
CigRectession 74777; 683155
Cigrectession 74777; 683155
Cigrectession 74777; 683155
Mol. Microbiol. 24, 579-591, 1997
Mol. Microbiol. 24, 579-591, 1997
Miller The cioAB genes from Fseudomonas aeruqinosa code for a novel cyanide insension 747273
Ascreterence number: 22446; MU.D:97323403
Ascretession: 747273
Ascreterence primary: translated from GH/EMHL/DDBJ
Ascrete type: DNA
Ascrete type: DNA .; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

.; 0

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C; Species: Homo saplens (man)
C; Species: L2-Nov-199; #sequence_revision io-Nov-1995 #text_change 21-Jan-2000
C; Late: L2-Nov-199; #sequence_revision io-Nov-1995 #text_change 21-Jan-2000
C; Accession: S26914
A; Mol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(II) sequences reveals about lifty groups on A; Reference number: S26885; MUID: 93021117
A; Reference number: S26885; MUID: 93021117
A; Reference number: S26914
A; Ascession: S
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C.barror 2: 50171999 #sequence_revision 23 Jul-1999 #text_change 52 Jun 2000
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R.Rlum, H.; Rauersachks, S.; Mawes, H.W.; Gassanhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A.Reference number, 217526
A.Reference number, 217526
A.Reference number, 217526
A.Status: preliminary
A.Molecule Lype: mRNA
A.Residues: 1-230 CBLL/>
A.Residues: 1-230 CBLL/>
A.Residues: 1-230 CBLL/>
A.References: EMBL:AL080096
A.Reserimental source: feta: brain, clone DRFTp554P2062
C.Genetics:
A.Note: DRFZp564P2062.1
C.Superiamily: sucrinale--CoA Ligase (ADP-Louning) beta chain
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lun c*; Pred. No. 25;
Lve. 0; Mismatches 0; Indels
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                                                                                                                             Length 935
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                                                                                                                        4.0%; Score 8; DB 2;
100.0%; Pred. No. 7.4;
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                                                                                                                                                                                                             0, Mismatches
A; Introns: 40/2; 143/3; 218/3; 883/2; 923/3
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beta crystallin Bl protein - zebra fish
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                                                                                                                                                       Best Local Similarity
Matches 8, Conserva
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                                                                                                                    Query Match
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                          A,Title. Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathd
A,Reference number: AK2450; MHTD:2043733
A,Accession: G83155
                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004A10; 0;R-AE004B041; NID:g4950106; P10N:AA007317,1; 6SP0H;6N001
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A;Residucs: 1-875 ANDE JORES; PILIN AAHGELGG L; GSEDREGNUUD.2, GESPEKORPII.2
A;Experimental source: strain Bristol N2; clone KORPII
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A)Experimental source: Strain Bristol N2; clone K08D10
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C;Species: Caenorhabdilis elegans
C;Daler 15:Oct.1999 #sequence_revision 15:Oct.1999 #fext_change 15:Oct.1999
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C.Date: 15-60-1999 #sequence.revision 15-60-1999 #Lext_change 15-00-1999
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C;Suputfamily, cytochrome d complex terminal oxidase chain I
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R.Murray, J., Wohldmann, P. submitted to the EMBL Data Library, September 1996 A. Description. The sequence of C. elegans cosmid KOBFII. A.Pelenene number: 220723 A.Pecession: 130023 A.Stolus, preliminary: Liauslated from GB/EMBL/DDBJ

LUB 2,

4,0%, Sivite B, L 100.0%; Pred No tive 0, Mismatich

Best Local Similarity 100 o Matches 8, Conservative

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696 ENDLEEVG 703

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17 ENDLEEVG 24

A;Gene: CESP:KOBF11.2 A;Map position: 4 A;Introns: 97/3; 172/3; 837/2; 875/2

Mismatches

hypothetical protein KOBELL.2 - Caemorhabditis elegans

C;Accession: T30023

4 0%; Score 8; DB 2; 100 0%; Pred No 4 2; ive 0; Mismarches

Query Match Best Local Similarity Tuo . Loc 8: Conservation

103 LTAFFLEA 110

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1 LTAFFLEA 8

A:Experimental source: strain PAO1 C:Genetics:

A; Molecule type: DNA A; Residues: 1-488 <STO>

A;Status: preliminary

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A; Description: The sequence of C. elegans cosmid Kükülü

A; Reference number: \$20mls

A; Accession: T29390

R;Geisel, C.; Bradshaw, H. submitted to the EMBL Data Library, April 1996

C; Accession: T29390

A:Status: preliminary; translated from GB/EMBL/DDBJ

A, Molecule type: DNA A, Residues: 1-935 <CEI>

A; Gene: CESP: K08D10.1

A; Map position: 4

C; Superfamily: hypothetical protein H10454

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A: Experimental source: strain 16M
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A;Residues: 1-276 <KUR>
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Ajgene: BMEI0429
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A.Acression: E64716
A.Stalus: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Molecule ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conserved hypothetical protein 03378 [imported] - Caulobacter crescentus Cispecies: Caulobacter Caulob
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                                                                                                                                                                                                                                                A lifte: Molecular cloning, developmental empression, and hormonal regulation of rebrafi
A:Reference number: JC7706: MULD:21331298; PMID:11437379
A:Acression: JC7706
A:Residues: 1-242 * CHES
A:Cross-relerences: GB:AJ317957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
C:Species: Brachydanio rerio (?cbra fish)
C:Date: 09-Nov-2001 #sequeice_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Acression: JC776
Acres 3.V.: Chang, B.E.: Chet, Y.H.: Lin, C.J.F.: Wu, J.L.; Kuo, C.M.
Biochem. Biophys. Res. Commun. 285, 105-116, 2001
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C.Date: 09-Aud-1997 *Sequence_revision 09-Aug-1997 *tevt_change 29-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obsome one in this protein is involved in requiation by growth factors essuperfamily: beta erystallin E:20:25/Requon; active proline, and alanine-rich motif #status predicted
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00.0%; Pred, No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Matches 7, Conservative
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Nature 388, 539-547, 1997
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Best Local Similarity
Matches 7: Conserv
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R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Lanb, M.T.; DeBoy, R.T.; Dodson, R.J.; Durklin, A.S.; Gwinn, M.L.; Hatt, D.H., Ro in, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc., Natl. Acad. Sci. U.S.A. 98, 416-4141, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;DelVecchio, V.G.; Kapatral, V.; RedKar, P.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; G'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
AJiller The aproper sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                           23S ribosomal RNA methyltransferase (EC 2.1.1.–) [imported] – Brucella melitensis (st
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                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01 Fcb-2002 #text_change 01 Fcb 2002
C;Accession: AG3305
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C.Date. 20.Apr.2961 #sequitive revision 29 Apr. 2961 #text_Jhange Lo Apr.2001
C.Accession: A87311
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                                                                           9; indels
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              Length 254;
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AjAccession: A87311
          58 2:
. 27;
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100.0%; Pred. No. 29;
ative 0; Mismatches
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Query Match 3.5%; Score 7; EB 2
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0, Mismatches
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337 DRIJIFY 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                         Ristchlik, C.; de Martin, R., Binder, B.R., Lipp, J.
Blochem Riophys Pes Commun. 243, 827-832, 1998
A:Tille: Cytokine induced expression of porcine inhibitor of apoptosis protein (lap) fam
A:Reference number: Jc5964: MUID:98152522
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A;Authors: Yoo, H.: Tao, Y.: Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alcohol dehydrogenase (benzyl; xyik [imported] - Agrobacterium tumefaciens (strain C58, C;Specias: Agrobacterium tumefaciens (C;Specias) despecial tran-2002 #sequence_revision 11 Jan 2002 #fext_change 01-Peb-2002 (C;Accession: AE3184)
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apoptosis inhibitor - pig
Cispecies: Sas scrola domestica (domestic pig)
Cibatus ud-Sup-1998 #sequence_revision u4-Sep 1998 #text_change 02-Sep-2000
CiAccession: JC5964
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                            A)Residues: 1-358 <STE>
A)Cross-references: GB:H79142; NID:q2957174; PIDN:AAC39171.1; PID:q2957175
C)Supertamily: RING finger homology
E;307-351/Domain RING finger homology <ERN.>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.5%; Score 7; DB 2;
100.0%; Pred. No. 36;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, Derember 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Matches 7; Conservative
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Matches 7; Conservative
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A;Accession: T22950
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                                                                                                                                                                                                                           A;Accession: JC5964
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 LLLOFIL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KDRLLTF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KDRLLTF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: F58G6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T22950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A.C.noss-references: EMBL:X63974
C.Superfamily, VH1-type dual specificity phosphoprotein phosphatase homology
F/63-182/Domain VH1-type dual specificity phosphoprotein phosphatase homology vVH1>
A.Accession: AE3184
A.Status: preliminary
A.Molecule Type: DNA
A.Molecule Type: DNA
A.Rosidues. 1 372 - KURN
A.Cross references: GR.AE008687, PIEN AAL45891 1: FIE:q17743636; GSPLR-GND)188
A.Experimental source: strain G58 (Dupont)
A.Genetics:
A.Gene: xyls
A.Gene: xyls
A.Gene: xyls
A.Gene: xyls
A.Gene: xyls
A.Gene: xyls
A.Genericy: alrohol dehydrogenase; long-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein B - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                              3.5%, Score 7; DB 2; Length 372;
100.0%, Pred. No. 38;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%; Score 7; DB 2; Length 376; 100 0%; Pred No 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S19740
R; Kelly, D.J.
submitted to the EMBL Data Library, February 1992
A; Reference number: S19739
A; Accession: S19740
A; Status: pretiminary
A; Mouleule type: DNA
A; Residues: 1:376 <KEL>
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Matches 7, Conservative 0, Mismatches
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                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.05
7: Conservative
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Genéric version 4 \pm Copyright (c) 1993 - 2600 Compugen Ltd.

ÓM protein - protein search, ysing sw model

July 2, 2002. 16:19:06 : Search time 30:19 Seconds (without alignments) 257.788 Million cell updates/sec Run on:

US-09-60 (-565-5_C)UY_1857_2067 201 1 LIAFFLEALDFRAUHSENDL........CIAQESVAMADDSLWKPLNY 201 Diffe: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

105224 seqs, 38719550 residues Word size : Searched:

255 Total number of hits satistying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post processing: Listing lirst 45 summaries

SwissProt_40:* Dafabase : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		œ				
Result No.	Score	Ouery Mateh	Length DB	DB	(11)	Description
. :				:		
	100	43.8	2144	Н	BP28_HUMAN	09h583 homo sapien
zų	ą.	37.3	856	٠.	HF28 MACEA	
~	7	· 5	358	-	PIAP_PIG	062640 sus scrofa
₹	7	3.5	414	-	YOUH_BACSU	P54545 bacillus su
r.	7	<.5 .5	537	-	CYDA_AZOVI	009049 azotobanter
æ	7	٠٠٠	8.45	-	CHS3_EXODE	P30602 exophiala d
7	7	3.5	911	-	CHSG_ASPFU	P54267 aspergillus
x	7	ړ. *	916	-	CHSB EMENI	000757 emericella
÷	7	\$. *	1045	_	HMD2_YEAST	
10	7	3.5	1612	~-	ATG4_YEAST	
1.1	S.	3.0	0.	-	PSA.I_CYAPA	_
12	4	0.4	3.8	~	YE02_HAEIN	P44177 haemophilus
1.	ç	3.0	14	-	EX78_HAEIN	P43314 haemophilus
† 1	-	0.7	47		GLRX_HAEIN	
· ·	y	0.4	57	-	LA FA_ECOL1	065948 escherichia
7.	ę	○. ~	1.04	-	CYF2_MOUSE	P35174 mus musculu
1.7	4	3.0	113		RL24_MICES	P33193 Kitchoomens
Ξ	٢	4.0	125	~-1	MERR_SIRLI	P30346 Streptomyce
<u>. 1</u>	ď	(· · ·	1 44		YUBL_BACSU	P45928 bacillus su
13 74	·,	⊕. ~	1 3.5	٠.	E314_ADE97	715135 human adeno
7	£	0.*	_	-	SODM_MYCPH	P53648 mycobacteri
7.7	ŝ	9°4	118	-	V105_FOWPV	9935b5 fowlpox vir
17	ď	ુ.	158		FRDA_SCHPO	074831 schizosacch
77	ď	C . •	_	-	DEST_CHICK	P18359 gallus gall
57	Ţ	0.₹	_	-	DEST_HUMAN	P18282 homo sapien
5.6	ď.	0.₹	_	-	DEST_MOUSE	O9rOp5 mus musculu
, , ,	w.	0.*	176	٠.	YLS7_ARCFU	028125 archaeoglob
28	42	3.0	1.38	-	YESU METIA	_
5.4	t,	3.0	1 16	-	UIDR_ECOLI	Q59431 escherichia
()+	£	3.0	1.59		RAB2_DICDI	P36409 dictyosteli
. 1	ď,	9.0	202	-4	TETN_HUMAN	P05452 homo sapien
1.2	£	0.*	21)6	-	SODM_MYCFO	Q59519 mycobacteri
~ ~	ۍ	⊕.~	807	-	VEP_NPVOP	OlO318 orgyia pseu

P49104 70a mays (m	P49104 703 mays (m	P08886 homo sapien	Q05975 lymna+a sta	P51994 Mus Austulu	Q01971 Oryctolagus	P05712 raftus norv	Q39570 chlamydomon	P36863 VOlvox cart	044741 homo sapien		P43973 haemophilus
HHZA_MAIZE	RB2B_MAIZE	RAB2_BITMAN	RAB2_LYMST	RAB2_MCUSE	RAH2_RAHIT	RAB2_RAT	YPT4_CHURE	YPT4_VOLCA	ER23_HUMAN	RPSD_SERMA	Y256_HAEIN
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209	210	212	212	212	212	212	213	213	214	215	215
3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0
9	ø	9	ع	9	9	9	9	Q	وا	Q	9

ALIGNMENTS

<pre>KW FOLYMOTECHISM. FT REPEAT 2:06 2:142 HEAT. FT VARIANT 1694 N -> S. FT VARIANT 1854 V -> N -> FT FT VARIANT 1854 V -> N -> FT FT VARIANT 1854 V -> N -> FT FT VARIANT 1854 V -> N -></pre>	TARES DOCCOCCCCA A SANTA	16-oct-2001 (Rel. 40, Created) 16 oct 2001 (Rel. 40, Last sequence) 16-oct-2001 (Rel. 40, Last sequence) Protein HAP28. HAP28. HAP28. Eukarycta: Metaca: Chordata: Crania Mammalia: Eutheria: Primates; Catarri NCHLTAXID-9605. NCHLTAXID-9605. NCHLTAXID-9605. A novel BAP28 gene and protein "; Patent number W00100669, u4-JAN-2001 [1] [2] SEQUENCE OF 1534-2144 FRON N.A. SEQUENCE OF 1534-2144 FRON N.A. SEQUENCE OF 1777-2144 FRON N.A. NUSHIKAWA T., NAYAMALS N., NAXAMULA NOTO NUMBAR N., Chiba Y., Ifhida S., M. Watanabe S. Kimura K., M. Nakamura Numoniya K., Iwayanaqi T.; Takahashi M., Chiba Y., Ifhida S., M. Natoninted (FEB-2000) to the EMBLA, Geni Consider Released Noto Informatice of Hioli the Buropean Hiolioformatice of Hioli the Buropean Hiolioformatice adtenment BMBL; ARO01221; RAA91564.1; ALT_INIT Interprof Proj. IFFO00157; HEAT FREAT: FALSE	16 OCT 2001 (Re) 16 OCT 2001 (Re) 17 OCT 2001 (Re) 18 DT 2001 (Re) 19 DT 2001 (Re) 19 DT 2001 (Re) 19 DT 2001 (Re) 10 DT 2001	uman). Label Labe	Ccreated Last and Last Last Last Last Last Last Last Last	sequence annotation sequence annotation set; Catarr Catarr Catarry Cote EMBL/Gen N. A. Sugiy M. A. Sugiy Gano. S., S. Sano. S., S., S. Sano. S., S., S., S., S., S., S., S., S., S.	09f158; 09MR23; 16 cc77 2001 (Rel; 40, Last sequence update) 17 cc77 2001 (Rel; 40, Last annotation update) 18 cc77 2001 (Rel; 40, Last annotation update) 18 cc77 2001 (Rel; 40, Last annotation update) 18 cc77 2001 (Rel; 40, Last annotation update) 19 cc77 2001 (Rel; 40, Last annotation last last annotation last annotation last annotation last last annotation last annotation last annotation last last annotation last annotation last last last last last last last last	The CCT 2001 (Rel. 40, Created) 16 OCT 2001 (Rel. 40, Last annotation update) 18 AND 28 18 AND 28 AND	Mi. 2017. 2017. rhi S., R., R., roundation outstation in no way reunderial rheunounce/
VARIANT 1854 1854	KW FT FT	Polymotph Repeat Variant	ism. 2:06 1694	2142 1694		HEAT.			
7961 7961 TNATGAV	EEEE	VARIANT	1854	1854	., \	/FTIG-V V -> A. /FTIG-V	AR_010939. AR_010940.		

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                                                                                                                                                                                                                                          1867 LTAFFLEALDFRAQHSENDLEEVGKTENGIIDGLVAMVVKLSEVTFRPLFFKLFDWAKTE 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osada N., Hida M., Kusuda J., Tanuma P., Iseki K., Hirai M., Terao K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Caps
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                                                                                                                                                             ů; ďaps
                                                                                                                                                                                                    1 LTAFFLEALDFRAQHSENDLEEVGKTENCTIDCLVAMVVKLSEVTFPPLFFKLFDWAKTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDAA clones from macaque brain cDAA
                                                                                                                       Length 2144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%; Score 75; DB 1; Length 958; 100 0%; Pred No 1.2e-70; tive 0; Mismatches 0, Indels
                                                                                                                                                             Indeis
                                                         2144 AA; 242355 MW; D66816FE78D8C9B7 CEC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     libraries.";
Submitted (OCT-2000) to the FMHI/SenBank/NNBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    920 956 HRAT.
958 AA; 108644 MW; 3DHD95C3623CFB31 CRC64;
                                                                                                                                                                                                                                                                                                      1927 JASKORIZIERYNIALG IAFRINGIETTE ASHLVKIFFALLE 1966.
                                                                                                                                                                                                                                                                                   61 DAPKDRILITEYNLADCIAEKLKGLETLEAGHLVKPFADTL 100
                                                                                                            49.8%, Soure 100, DR 1, 1
for Dw. Dred No 1 3e-96;
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                                      /FTId-VAR_010942.
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16-0CT-2001 (Pel. 40, Last annotation update)
/FTId-VAP_010941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE RAP28 FAMILY
-1- SIMILARITY, CONTAINS I HEAT REPEAT.
                                                                                                                                                             U; Mismatches
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                                                                                                                                      Pred No
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InterPro; IPR000357; HEAT_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
                                                                                                                       Query Match
Best Local Similarity 100 0%;
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Matches 75; Conservative
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766 TLFAGHLVKPFADTL 780
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                                                             SHOUFINGE
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                     VARIANT
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                                                                                                                                                                                                                                 Eukaryota; Merlážoa; Chordata, Craniata. Vertebrata; Euteleostomi;
Mammalia; Eutheria; CetarLiodactyla; Suina; Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ċ
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 358;
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                                                                      15-bic-1998 (Rel. 37, Created)
15-bbc-1998 (Rel. 37, Last sequence update)
15-br-12001 (Rel. 40, Last annotation update)
Putative inhibitor of apoptosis.
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01-0CT-1996 (Rel. 34, Last sequence update)
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RING-TYPE.
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                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; Zinc-finger; Repeat.
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311 346 R
358 AA; 40977 MW;
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InterPro: IPR001315: CARE
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SM00114; CARD; 1.
                             STANDARD;
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Pfam: PF00619; CARD: 1
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Matches 7; Conserv
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                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                     NCBI_TaxID-9823;
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                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Aorta;
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P54545;
                           PIAP_PIG
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ZN_FING
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PIAP_PIG
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CHARACTERIZATION.

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16-001 (Rei. 40, Last annotation update)
Hypothetical 47.0 KDa protein in qing-ansF interpenir region
                                                                                                                                                                                                                                                                                                       , Mizano M., Masuda S., Takemaru K., Hosono S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%; Score 7; DB 1; Length 414; 100.0%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases ++ SIMILARITY: BELONSS TO THE IMPB/MUCB/SAMB FAMILY.
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01-NvV-1997 (Rel. 35, Last sequence update)
01-NvV-1997 (Rel. 35, Last annotation update)
Cytochrome D ubiquinol oxidase submuit I (EC 1.10.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0824062080B8448F CRC64;
                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                        Bacillus/Staphylococris group: Bacillus.
NCBL_TaxID-1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macteriol, 173:6230-6241(1991).
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Hest Local Similarity 100.0v
Hest T. Conservative
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InterPro; PPR001126; SMUC
Pfam; PP00817; HMS; 1.
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                                                                                                                                                                                                                                                                                                                                   Takeuchi M.;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-168 / JH642:
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                                                                                            Bacillus subtilis
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                                                                                                                                                                                                                                  entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                   Exophiala dermatitidis (Wangiella dermatitidis).
Eukarpota, Fungi, Ascompcota, Pericomycotina, Chactothyrionycetes;
Chactothyriales, Herpotrichiellaceae; mitosporic Herpotrichiellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHS3_EXONE STANDADD; PPI; 885 AA.
P30602; 074678;
01-APP-1993 (Rel. 25, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chitin synthase 3 (RC 2.4 1.15) (Chitin-Ungacety)-gluccsaminyl
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Pfam; PF01654; Bac_Ubq_Cox; 1.
           MEDLINE-91008979; PubMed-2170336;
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Asperqillus nidulans.";
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                                                                                                                                                                                                                                                                                                                                                                                                            "Classification of fungal chitin synthases.";

Proc. Natl. Acad. Sci. II. S.A. 89·519-523(1992)
-!- FUNCTION: PLAYS A MAJOR FOLE IN CFIL WALL REGENESIS.
-!- CATALYTIC ACTIVITY: UDP-Nacety1-D-glucosamine + {(1,4)-(N-accty1-beta-D-glucosaminy1)}(N) = UDP+ {(1,4)-(N-acety1-beta-D-glucosaminy1)}(N) = UDP-4 (1,4)-(N-acety1-beta-D-glucosaminy1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qlucosaminyl){(N+I).
-!- SUBCELLULAR LOCATION- Plasma membrane-bound.
-!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                   "Characterization and expression studius of WdCHS3, a gene that encodes a class III chitin synthase and contributes to virulence in Wangiella (Exophiala) dermatitidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Foricomycotina, Eurotiomycotus,
Eurotialus, Trichocomaceae, Mitosporie Trichocomaceae, Aspergillus.
NCRI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIANE-96347138; PubMed-8736545; Mellado E., Aufauvro-Hrown A., Gow N A P., Holdon D W.; Mellado E., Aufauvro-Hrown A., Gow N A P., Holdon D W.; The Aspergilius fumigatus chick and chsG genes encode class III chilin syntheses with dillerent functions.", Mol. Microbiol. 20.667-679(1996)
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15-JUD-1999 (Rel. 38, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chitin synthase G (EC 2.4.1.16) (Chitin CDP acetyl-glucosaminyl
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                                                                                                                                                                                                                                                                                                                                      Chen-Wu III, Momeny M., Young R., Seamiselo P. J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002998; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5%; Score 7; DB 1; Length 885;
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                                                                                                                                                                                                      Submitted (MAR-1998) to the EMBL/GenBank/DDRT databases
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R \to S \text{ (IN REF. 2)}.
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...tive 0, Mismatches
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                                                                  Wang Z., Graybil! J.R., Szaniszlo P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; 1PR002923; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
                                                                                                                                                                                                                                                                            SEQUENCE OF 214-410 FROM N.A.
MEDLINE-92115692; Pubmed-1731323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF053314; AAC35278.1; -.
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Matches 7, Conservative
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P54267: Q09031: Q06032;
01-0CT-1996 (Rel: 34, Crs
15-JUL-1999 (Rel: 38, Las
16-OCT-2001 (Rel: 40, Las
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family, 215
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SEQUENCE FROM N A.
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                                                                                                                                                                                                                                                                                                                                                                                   Robbins P.W.;
                                 STRAIN-8656;
                                                                                                                                                                                                                                                                                                                                              HOWON A R .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H237
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REPRESENTANT OF THE PROPERTY O
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS natitute of Hioinformatics and the EMH, outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Thanks and this statement is not removed. There exists equires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     -!- SURCELLUIAP LOCATION: Plasma membrane-bound.
                                                                                                                        -i- FUNCTION: PLAYS A MAJOR FOLE IN CELL WALL DIOGENESIS.
-i- CATALYTIC ACTIVITY- UDP-N-acety1-D-qlucosaminc + {(1,4)-(N-acety1-beta D-glucosaminy1)}(N) = UDP + {(1,4)-(N-acety1 beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caps
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"Isolation and characterization of two chitin synthase genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHISB_EMENI STANDARD, PRI, 916 AA. 000757; P87326, 15 Jul.-1999 (Rel. 38, Created) 15 Jul.-1999 (Rel. 38, Last sequence update) 15 Jul. 1999 (Rel. 38, Last annotation update) 15 Jul. 1999 (Rel. 38, Last annotation update) Chitin synthase B (EC 2.4.1.16) (Chitin-UDP acetyl glucosaminyl transferase B) (Class-III chitin synthase B).
                                  Borgia P.E., lartchouk N., Riggle P.J., Winter N.K., Koitin Y.,
Bulawa C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Eurotiales; Trichocomaceae, Emericella.
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IV -> MM (IN REF. 2; AAB07679).

F > N (IN REF. 2; AAB07870).
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                                                                                                Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
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BC893F8BA00BE48D CRC64;
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R -> C (IN REF. 2; AAB076
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100.0%, Pred. No. ...
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MEDLINE-95072312; PubMcd-7765508;
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EMBL; U39479; AAB07679.1;
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                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY, SUBFAMILY CLASS
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01 NoV-1997 (Rel. 35, Last annotation update)
3-hydroxy-3 methylqlutaryl-coenzyme A reductase 2 (EC 1.1.1.34) (HMG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Basson M.E., Thorsness M., Finer-Moore J., Strond R.M., Riner J.;
"structural and functional conservation between yeast in 3-
"structural and functional conservation between yeast in 3-
mydroxy-amethylquiaryl conservane A reductases, the ra illina
enzyme of sterol biosynthesis.".
Mol. Cell. Biol. 8:3797-3898(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fanai, Ascomycota, Saccheromycotina, Saccha, omycetes, Saccharomycetales, Saccharomycetaceae, Saccharomycetales,
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Than: PO1644: Chilin_synth. L.
Probon: P00248; Chilin_synth: L.
Fransferaso: Glycosyltransferaso: Fransmenhagne: Cell wall;
                                                                             "Asperaillus midulans chitin synthase B gene.":
Sibmitted (FER 1997) to the EMBL/GenBank/2083 databases.
Sibmitton in Plays A MATOP FOLE IN CFIL WILL FICKFESTS
OF ANALYTIC ACTIVITY: UDP-N-acctyl D giucosamine ((1))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7: DB 1; Length 916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                916 AA: 102066 MW- CREAAB647FFGA3F7 CRC64;
                                                                                                                                                                         SUBCELLULAR LOCATION: Plasma membrane-bound.
Biosci. Biotechnol. Elochem. 58:1828-1835(1934).
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HMG2 OR YLR450W OR 1.9324.2.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D21269; BAA04807.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 LLIDFIL 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene tamily
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                                                STRAIN-FGSC 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMD2_YEAST
P12684;
                                                               Tatsuno K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. NEUDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
GENERAL BASE (BY SIMILARITY).
GENERAL BASE (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENITAL).
                                                                                                                      MEDLINE-86287298; PubMed-1526336;
Basson M.E., Thorsness M., Rine J.;
"Sarcharomyres cerevisiae contains two functional genes encoding
                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: (E)-mevalonale + CoA + 2 NADP(+) - (S)-+ hydroxy-3-methylqlutaryl-CoA + 2 NADPH.
-!- PATHWAY: CHOLESTEROL HIOSYNTHESIS.
                                                                                                                                                                                                              hydroxys and thy judicity consisting two limitational genes for different hydroxys and thy judicity consisting two limitational genes for different and sci. U.S.A. 83.5563-5567(1986).
-!- FUNCTION: HIS TRANSMEMBRANE GINCOPROTEIN IS INVOIVED IN THE CONTROL OF CHOLESTEROIL HIGSYNTHESIS. IT IS THE RAIE-LIMITING ENZYME OF THE STEROIL BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein, Endopiasmic
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.:
Submitted (MAR-1995) to the EMBL/GenBank/EppH databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1FD9DCD4AC01B15E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD: S000442; HMG2.
InterPro; IPR002203; HMG-CoA_red.
InterPro; IPR002203; HMG-CoA_red.
From: PP00368; HMG-CoA_red; I.
FR.NTS: PR00071; HMG-COA_RED.
FROSITE; PS00066; HMG-COA_REDUCTASE_1: I.
FROSITE; PS0018; HMG_COA_REDUCTASE_2: I.
FROSITE; PS01192; HMG_COA_REDUCTASE_2: I.
FROSITE; PS01192; HMG_COA_REDUCTASE_3: I.
FROSITE; PS01192; HMG_COA_REDUCTASE_3: I.
FROSITE; PS01192; HMG_COA_REDUCTASE_3: I.
FROSITE; PS01192; HMG_COA_REDUCTASE_3: I.
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                                                                                           SEQUENCE OF 772-961 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: M2255; AAA34677.1; -. EMBL: U22382; AAB67527.1; -. PIR: B24317; B24317. PIR: B367244; R40239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523
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1045 AA;
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Caps

3.5%: 3core 7; DB 1; Length 1045; 100.03; Pred, No. 35; ative); Mismatches 0; Indols

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STRAIN-LB555 / PRINGSHEIM;
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|6 LTAFPL 21
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P44177;
                                         Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                  SUBUNITS
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    SYNCH REPAREMENT OF THE PRESENCE OF THE PRESEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Magnesium: ATP-binding.
                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota, Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                       01-NoV-1997 (Pel 35, Last sequence update)
01-MAR-2002 (Pel 41, Last annotation update)
Potential phospholipid transporting Alfase 2 (DC 3.6.3.1).
YNR093W OP YESS7.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Glaucocystophyceae, Cyanophotaccae, Cyanophora.
NYRL_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7, DB 1; Length 1612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           712 712 FHOSPHORYLATION (PROBABLE).
1612 AA: 182617 MW: 09719PPE64256BBC CPC64,
                                                                                                                                                                                                                                                                                                                    Saccharomynetales; Sancharomynetaneae; Saccharomynes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Pel 34, Last sequence update)
01-MAP-2002 (Pel 41, Last annotation update)
Photosystem I reaction center subunit IX (PSI-J).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 AA.
                                                                                                                             PRT; 1612 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%, Fred \dot{M}^{c} '1, tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFam, PF00702, Hydrolase, 1.
PROSITE; PS00154; ATPASE_E1_E2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-FEB-1996 (Rel 43, Created)
                                                                                                                                                                     (5, Pregled)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanophora paradoxa.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N A
                                                                                                                                                                61-NOV-1947 (RP)
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 1.TFYNI.A 74
                   10 HLVKPFA 16
                                                                                                                      ATC4_YEAST
Q12675;
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P48117;
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                                                                               PESTILT 10
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                                                                                                         ATC4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R D., Adams M D., White O., Clayton R.A., Kitkness B.F., Kerlavage A R., Rult C.J., Tomb.U.-F., Dongherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Ffelds C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C A., Spriggs T , Helblom F., Cotton M.D., Utterback TR., Hannam M C., Mayyao D T., Sandek D.M., Rrandon R.C., Grieb L.D., Fritchman J.L., Futtmann J.L., Geoghagen N.S.M., Grebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                     Institute that we strewall v.L., Michalowski C.B., Annarella M., Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Lakowitsch J., Pohnert B.J., Bryant D.A.; Edwisser J.M., Lakowitsch J., Pohnert B.J., Bryant D.A.; the complete semplesty of the cyanelle geneme of Gyangphera paradoxa: the genetic complexity of a primitive plastid "; (In) Schenk H.B.A., Herrmann R., Jeon K.W., Muchler N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                          "Nurleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
Stirewalt V.L., Michalowski C.B., Loeffelbardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MAY HELP IN THE ORGANIZATION OF THE PSAE AND PSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%; Score 6; DB 1; Length 40; 100.0%; Pred. No. 24; tive 0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom: ppon4198; PSI_PsaJ; 1.
Cyanelle, Photosystem I, Photosynthesis: Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM 6 26 POTENTIAL.
SEQUENCE 40 AA: 4481 MW: 798A8CA36A007153 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE PSAJ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=RD / KWZ0 / ATCC 41907;
MEDLINE-95350630; PUPMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Greated)
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InterPro, IPR002615; PSI_Psad.
Pfam; PF01701; PSI_Psad: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, U30821, AAABI183.1, -.
                                                                                                                                                                                                                                                                     STRAIN-LB555 / PRINGSHEIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Conservative
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                                                                                          The European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and lor commercial entities requires a license asterment (See http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch).
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the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 Nov 1995 (Rel. 42, Last sequence update)
16-ocT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease VII small subunit (EC 3.1.11.6) (Exonuclease VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-9549640; PulMed-7542800; MEDLINE-95490640; Eleischmann E.D. Adams M.D., White O., Clayton R.A., Kirkness E.F., Pleischmann E.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenney K., Suffon G., Fitzhugh W., Fields G.A., Gordyne J.D., McKenney K., Suffon G., Fitzhugh W., Fields G.A., Gordyne J.D., McKenney K., Suffon G., Fitzhugh W., Fields G.A., Gordyne J.D., Weidman J.F., Phillips C.A., Springs T., Hedblow F., Cotton M.D., Otterback T.R., Hanna M.C., Navyen D.T., Saudek D.M., Brandon R.C., Springs C.L., Fitzhugh J.L., Fubrann J.L., Geoglagen N.S.M., Smith H.O., Venter J.G.,
                                                                                                                                                                                                                                                                                                        Gaps
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CATALYTIC ACTIVITY: Exonotelenly the clearage is eliber; to 3' of 1' to 5' direction to yield 5'-phosphomonorial and substitutional activities SCHUNITS (BY LARGE AND SMALL SCHUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria: Proteobacteria: qamma subdivision: Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome random sequencing and assembly of Haemophilus
             Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                        DB 1: Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCALION: Cytoplasmic (By similarity).
                                                                                                                                                                                                               Hypothetical protein: Complete proteome.
SEQUENCE 68 AA: 7841 MW: 396F304AABBB7D29 CEC64;
                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 38;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   H4 AA
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                                                                                                                                                                                                                                                                        3.08; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NoV-1995 (Rel. 32, Created)
                                       Science 269:496-512(1995).
                                                                                                                                                                                    EMBL: 032820; AAC23052.3;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus influenzae.
                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
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                           intluentae Ed."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    small subunit).
                                                                                                                                                                                                                                                                                                                                                            4.4 DRULTE 4.8
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                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                 EX75_HAEIN
P43914;
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                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Adams M.D., White D., Clayton R.A., Kirkuess E.F., Reflavage A.R., Bult C.J. Tomb J. F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M., Scott J.D., Shirley R., Luu L.-I., Glodek A., Kelley J.M., Weldman J.F., Philips C.A., Spriggs T., Hedblom E., Cotton M.D., Interback T.F., Hanna M.C., Newgen E.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geochagen N.S.M., Geethm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.D., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, gamma subdivision: Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome random sequencing and assembly of Baemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            ib 1, i.ength 84;
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SUBCELLULAR LOCATION: CYTOPIBSMIC (Hy Similarity).
SIMILARITY: BELONGS IO THE GLUTAREDOXIN FAMILY.
                                                                                                                                                                                                                                                           PITAM: PF02609; Exonuc_VII_S; 1.
Hydrolase; Nuclease; Exoniclease; Complete profeome.
SEQUENCE 84 AA; 9511 MW; 4A3CF6F1855BA72E CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Las: sequence update)
16-00T-2001 (Rel. 40, Las: annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.)%; Pred. m..
                                                                                                                                                                                                                                                                                                                                                                                                                                            3.08, Score 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR1.
                                                                                                                                                                                                                               InterPro, IPRU04761; Exonuc_VII_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002109; Glutaredoxin.
InterPro; IPR000063; Thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95350630; PubMed-7542800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Las: sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-RD / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PRO0160; GLUTAREDOXIN.
                                                                                                                                                               PMRI; 432822; AAC23086.1; -. TIGR; H11437; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMB1, U32829; AAC23182.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.1
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCB1_TaxID-727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 KTEDAP 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRX_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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GLRX_HAEIN
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Weiner J H , Rilous P T , Shaw G M , Lubitz S.P., Frost L , Thomas G H., Colle J.A., Turner R.J.; A novel and ubiquitous system for membrane targeting and serretion of cofactor containing proteins ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-92358234; PubMed-1379743; Daniels D. L., Plunkett G. III, Burland V.D., Blattner F.R.; Paniels D. L., Plunkett G. III, Burland V.D., Blattner F.R.; Anniels D. Escherichia coli genome: DNA sequence of the region Science 257.771-778 (1992).
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97426617; PubMed-9278503;
Higthor F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riloy M., Collado-Vid-s I., Glaser I D., Rode C.K., Maybow G.F.,
Gregor J., Davis N.W., Rirkpatrick H.A., Goodon M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Overlapping functions of components of a bacterial Sec-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-D15:47 FID.933 / AFCC 700927;
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
Perna N T , Plunkert G III, Burland V , Mau B., Glasner J.D.,
Rose D. I, Mayhew G F . Evans P S., Gregor J , Kirkpatrick H A.,
Posfai G., Hackett J, Klink S., Houtin A., Shao Y., Miller L.,
Grottock E J , Davis N W , Lim A , Dimalanta F T , Potamousis K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sargent F., Bogsch E.G., Stanley N.P., Wexler M., Robinson C.
Berks B.C., Palmer T.;
PROSITE; PS00195; GLUTAREDOXIN; 1.

Medica active center. Fleation transpert, Complete protecome. DISULEID 11 14 PEDOX ACTIVE (BY SIMITAPITY) SEQUENCE 87 AA; 9670 MW; 27987P39484899B CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coll K-12 ", Science 277-1453-1474(1997)
                                                                                                                                                               u; Indels
                                                                                                                       3 0%, Shara 6, DR 1; Langth R7
                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Last segmence update)
Gi-MAR-2002 (Re). 41, Last amonation update)
Secrindependent protein translocase protein Lata.
                                                                                                                                      Hest Local Similarity 190.0%; Pred. No. 47;
Matches b; Conservative u; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATA OR MTTAL OR B3836 OF 25358 OF FIS4766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / MC4100,
MEDLINE-98315056; Pubmed-9649434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE-98206471; PubMed-9546395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                          01-Aug-1992 (Pel. 23, Greated)
16-OCT-2001 (Pel. 40, Last seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein export pathway.";
EMBO J. 17:3640-3650(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
STRAIN-ATCC 33694 / HRIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli, and
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                                                                                                                                                                                                                                                                                                                                                           065938; P27856;
                                                                                                                                                                                                  78 AEKLKI AR
                                                                                                                                                                                                                                        21 AFKLKG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
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                                                                                                                                                                                                  STRATH-0157.H7 / FIRD 0509952; MEDGINE-21156231; PubMed-11258736; MEDGINE-21156231; PubMed-11258736; MEDGINE-21156231; PubMed-11258736; Mendan T., Johanno K., Hang C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida F., Takami H., Honda T., Sasakawa C., Oqasawara N., Yasunaqa T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhagic Escherichia coli O157-H7 and genomic rougarison with a laboratory strain K-12."; DNA PES. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1- HUNTLON - PEQUITED FOR COPPET LOCALIZATION OF PRECIPEOR PPOTEINS FRAPING STGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF STAPPING STGNAL PEPTIDES WITH THE TWIN ARGININE TRANSLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTED PROTEINS WITH ROUND COPACTORS THAT PROJUBE FOLLING PRICE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                             Weich R.A , Rlattner F.R., "Canome sequence of enterchagin Escherichia coli 0157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
O
Apodaca I , Anantharaman T S , lin I , Yen G , Schwartz D C.,
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Transport; Protein transport; Translocation; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHECELIHLAR LUCATION: INNER-MEMBRANE BOHND (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%; Score 6, DB 1, Length 89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 21 POTENTIAL.
89 AA; 9664 MW; 4874F393EFFADCIB CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE TATA/E FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 48;
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EMBL; AF067848; AAC19240 1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M87049; AAAA7533 1; ALT_SBO
AEUUU459; AAC76839.1; ALT_INIT.
AEGG5614; AAG59032 1; ALT_INIT.
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Rubert SM. Rosen CA, Harash SC, 2001 483426/52. N-PSEB# AAK62065 Nucleic acids encoding human immune/hematopoietic antiqen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

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ANK54951 to ANK64782 encode the human immune/harmatopoietic antique (1) amino acid sequences given in AAM82170 to AAM9521. (1) have evitostatic activity, and can be used in gene therapy and varcine production. (1) proteins and polymarlectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mulations or deletions in a patient's genome that affect the activity of (1) bediction of (1). Additionally, (1) supplement the patients own production of (1). Additionally, (1) polymoricotides may be used to produce the secretal (1), by inscribing the nucleic acids into a host cell and culturion the cell to express the protein. (1) proteins and polymorleotides may be used to prevent. Characters and cauch metal amentopoletic related diseases, especially calcers and cancel metal asset of harmatopoletic derived cells. ANK64703 to AAK87694 represent human immune/harmatopoletic antique general AAM82169 sequences from the present human immune/harmatopoletic antique general AAM82169.
                                                                                                                                                                                                                                                                                                                                                                             represent sequences used in the exemplification of the present invention.
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responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                    The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antique, BRCAL, binding preparation of the recombinant breast cancer antique, BRCAL, binding proteins BARDI, BL23, BE14, BE14, BE14 or ER445, "" a composition for the detection of a BARDI, BL33, BE24, BE14, BE14 or BE445 nucleic acid sequence, specifically a wild type BARDI composition for the detection of BRCAL, useful to identify a patient having, or at risk of developing cancer. BARDI to identify a patient having, or at oriticaklo antibody, and in the detection and putilication of a BRCAL protein. BARDI, BL23, BE14, BE31 or BE445 can used in the protein. BARDI, BL23, BE14, BE31 or BE445 can used in the oritical activity of the BRCAL-BARDI, BL33, BE2, BE14, BE31 or BE445 to BR445 can used in the oritical activity of the BRCAL-BARDI, BL33, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARDI, al23, BE2, BE14, BE31 or BE445, a specific anti-BARDI antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, immune; hacmatopoietie; immune/hacmatopoietie antigen; cancer, cytostalie, gene therap,, vaccine, metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVYLLISALAALGKVVETTEPHETSPYLEGITISQVIHLEKITISEMGSASQANIKLISLKKFL 60
                                                                                                                                                                                                                                 DNA sequence encoding BAKU1, B123, B12, BE14, BE31 or BE445 - which as breast cancer antigen, BEA1, binding proteins are useful to identify patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100, DB 19, Length 515, Pred. No. 6 6e 99,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/hacmatopoietic antigen SEQ ID NO:16877.
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100.9%, Pred. No ..
1.50 U. Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the AM28 polymegatides are useful as diagnostic reagents. Beliable markers of the BAP28 game are useful in genetic analysis. The present sequence replesents a protein encoded by a first CDNA sequence of the BAP28 game consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATTLAPRVLLPATKKTYKQTEKNWKNHMCPPMSTLQEHIGXMKKFELTSHQSQLTAFFTE 120
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                                                                                                                                                                                                                                                                                                                                New HAP2B polynucleorides and polypoptides avergypressed in prostate cancer cells for diagresing prostate tumors, e.g. by hybridization or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
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Pred. No. 7.7c-188;
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                                                      Harry C.
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the specification. The priner sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynocleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins cheeded by the full-length cDNAs. The primers allow obtaining of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNAs easily without any specialised methods. AAH04166 to AAH14628 and AAH14634 to AAH18742 represent human cDNA segmences. AAB92446 to AAH4689 AAH95893 represent human edid sequences; and AAH13624 to AAH13632 represent cligonucleotides.
                                                                                                                                                                                                                                                                                                       The present invention describes primer sets for synthesising 5602 full length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dl primer and an oilgonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the cingonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5° end
                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5662 tull-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 MKKEELJSHQSQTTAFFLEALDFFAQHSENDLEEVGKLEN, LLD: JVAMVVKLSEVTFRP 161
                                                                             Saite E. Yamamoto J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RARDI: ring protein; BPCAl; breast cancer; risk; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                            Sugiyama f. Wakamatsu A, Nagai K, Otsuki I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 LFFKLFDWAKTEDAPKDRLLTIYNLADCIAEKLKGLFTLF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 109, 188 22:
Pred. No. 4.5e-90;
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                                                                                                                                                                                                                                                                        Claim 8, SEQ ID 11159, 2537pp + CD RoM, English.
                                                                         Hayashi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW54099 standard; Protein; 515 AA
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100.0%; Pro
                                                                           Isogai T, Nishikava T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens BAP28 sequence.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the present invention.
                                      (HELI-) HELIX RES INST
                                                                                                                                   WP1; 2001-318749/34.
                                                                                                                                                                                                                                     full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rest Local Similarity
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GenCorg version 4.5 copyrigh! (c) 1993 - 2000 compagen Ltd

OM protein - protein search, using sw model

July 2, 2062, 16:06:01; Search time 177.59 Seconds (without aliquments) 189.862 Million cell updates/sec Run on:

1 EVYLLSALAALQKVVETLPH.......TPYNLADC!AEKLKGLPTLF 201 US 09 603 665 5_COLY_1754_1954 291 Title. Perfect score.

Sednence:

Scoring table:

Gapop 60.0 , Gapext 60.0

747574 seqs, 111073796 residues Searched: Total number of hits satisfying chosen parameters:

Word size :

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing. Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Protein encoded by	Human protein sequ	Homo sapiens BAP28	Human immunc/hacma	Novel human diagno	B. valgaris NIMI h	Drosophila melanog	Elmeria merosolte	hrosophila melanog	RcsB related gene	Rosh related gene
	10	AABREG29	AAB**272**	AAW54099	AAM89284	ABG15408	AAB27313	ABB63428	AAP13165	ARBESTOOR	AAR36605	AAP 36606
	h DB	44 C.	-	5 19	7 22	8 22	E S	5 22	0 12	13 u	6 14	ķ 14
	Lengt	2144	7. 57	515	7	5	16	195	0.7	C)	21	21
¥C	Owery Match Length DB 1D	P P P	X : 7	49.8	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5
	Score	000	100	100	7	7	7	7	7	7	7	7
	Result No.	7		æ	4	ις:	9	7	œ	6	10	11

Prod of the resB	Human protein sequ	Helicobacter pylor	Novel human diagno	Novel human diagno	Human C.protein co	Arabidopsis thalia	Human olfactory ro	7	Surface antigen pr	#3629 en	Peptide #3574 enco	Nove: haman diagno	Human olfactory re	C.	Human op-11ke poly	Arabidopsis thalta	Novel human diagno	Arabidopsis thalia	Novel human diagno	Human protein sequ	Amino acid sequenc	Human protein sequ	Human polypeptide	ATP-specific succi	Human protein sequ	DNA encoding human	Human polypeptide	Drosophila melanog	PspC alpha helix c	Prēsephila melanog		Enterococis faeca	Buman OPPX OPP2246
AAKiluuu	AAR95232	MITTERA	ABG01568	ABG22802	AAE04555	AAG30094	AAU24523	AAG7 2083	AAR30993	AAM17195	AAM04892	ARGS7639	AAU24685	AAG71719	AAG72489	AAG30093	ABG23767	4401052	ABG10200	AAB92908	AAY49137	AAB92979	AAM39688		AAB93393	AAB70153	AAM41474	ABB59537	AAY43392	ARRETSS	C4	AAIT35116	AAB42482
7	C1	CI CI	C1	C.	C1	21	C1	-1	14	디	음	C1	덤	CI	C1	5	급	2.1	22	C1	20	C1	22	22	Ci	22	C1	C1 C1	3 Ù	(4 (4	27	() ()	21
216	24 t	254	289	292	305	311	311	311	315	320	320	321	323	323	323	327	363	3.F.4	371	417	431	442	463	463	463	463	485	521	589	5.93	604	667	414
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12	13	14	15	16	17	18	13	0.3	7.7	C1 C1	23	54	52	56	2.2	58	62	٧٠	3.1			46	35	36	3.7	38	58	40	4.1	4.2	43	44	ላ ን

ALIGNMENTS

AAB85029 RESULT

AAB85029 standard; Protein, 2144 AA

AAR85029;

06-AMG-2001 (first entry)

Profein encoded by BAP28 cDNA consisting of exons 1 to 45.

BAP28, prostate; tumour, cancer, diagnostic, genetic analysis.

Home sapiens

Location/Qualifiers Key Misc difference 1694

/label= Ser or Asn Misc-difference 1854

/label= Ala or Val Misc-difference 1967

/label - Asp or Asm Mise-difference 2017

/label= Gly or Glu

WOLTH TREEF A.D.

04-JAN-2001.

23-JUN ZOUG; ZOUUMO-IBUI183.

25-JHN-1999; 99HS-0141323. 18-1AN-2000; 2000HS-0175880.

(GEST) GENSET.

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# # E 2
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Ouery Match 15%; Score 7; DB 11; Longth 252; Hest Local Similarity 106.0%; Prod. No. 76; Matches 7; Conservative 0; Mismatches 0; Indels

0; Gaps

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Oy 172 VLALAEK 178 FILLILL Ob 161 VLALAEK 167

Search completed: July 2, 2002, 16:18:32 Job time: 864 sec

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PRELIMINARY,
                                         Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       159 DSSPKVR 165
                                                                                                                                                                                                                                                                                                                                                                                                  11 DSSPKVR 17
                                                                   NCBI_TaxID=487;
                                                                                                               STRA: N=22491
                                                            Bacteria,
                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thesis (2001), Department of Institute of Zoology, Academia Sinica, Taipei, Taiwan.
EMRL, AJ317957: CAC84899.1, ... STAPPHIA29AAC58B CPC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (%ebrafish) (%ebra danio).
Bukaryota, Mutazoa, Chordata; Craniata; Vortebrata; Butelcostomi;
Actinopleryqii, Neopteryqii; Telecstei, Butelcostei; Ostariophysi;
Cypriniformes: Cyprinidae; Danio.
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DBC-2001 (TTEMBLrel. 19, Last annotation update)
ALDERYDE REDUCTSE (FRACMENT).
Cricetulus grisses (FRACMENT).
Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scluroquathi; Muridae; Cricetinae;
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 7, DB 13; Length 232;
100.0%; Pred No. 71;
                                                                                                                                                               Hyndman D.J., Flynn T.G.; "Partial sequence of Chinese hamster aldehyde reductase."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 7; UB 11; Length 228;
00.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                         228 2A; 25450 MW; 90C5625FD810DA93 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLE) 19, Croated)
01-DEC-2001 (TrEMBLE) 19, Last sequence update)
01-DEC-2001 (TrEMBLE) 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prod. mc.
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PROSTTE; PSOUDEJ: ALMONETO_FEDUCTASE_2: 1.
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01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                         HSSP; Fidens, 2005
InterPro, IPR001395; Aldo_ket_red.
                                                                                                                                                                                                                                                               PIAM, PF00248, ald-ket_red: 1
PRINTS, PR00069; ALDKETRDTASE.
                                                                                                                                                                                                               EMBL, AF060820; AAC15750.17
HSSP; P14550; 2ALR
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 7; Conserv
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                            NCB1_Tax1D-10029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 VLALAEK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 VIALAEK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 YKIFLFD 47
                                                                                                                                                                                                                                                              Piam, FF00248,
                                                                                                                 Cricetulus
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RESULT 13

69JPE8

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RX MEDULENCE FROM N.A.

RX MEDULE-LUBSCEO, FubMed 1121781;

RX MEDLINE-LUBSCEO, FubMed 1121781;

RX ALANA T. Shinayawa A. Shibata K., Yoshino M., Ifoh M., Ishii Y.,

RA Arawa T., Shinayawa A., Ebkunishi Y., Kohoo H., Adachi J., Fukuda S.,

RA Arawa K. Izawa M., Nishi K., Kiyosawa H., Koasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Koasukawa T., Saito R.,

RA Adota K., Matsuda H.A., Ashburner M., Hasuba T., Saito R.,

RA Edela K., Matsuda H.A., Ashburner M., Hasubo S., Casavann T.,

RA Kuehl P., Iewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Washner L., Washio T.,

RA Sakai K., Ordor T., Furuno M., Aono H., Baldarchii R., Harsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Pujita M., Cariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Pujita M., Cariboldi M.,

RA Sakaki H., Salto K., Schoundaudh J., Mazzarelli J., Mombaeris P.,

RA Sakaki H., Schoundaudh C., Schoundaudh C., Skamoto N.,

RA Sakaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Willming L.,

RA Hayashizaki Y.,

RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                   MEDIANE-2018748], PubMod-10722605;
Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
                                                                                                                                                                                                                                                                                                                                                                           "Molecular and biological analysis of eight genetic islands that
distinguish nersecria meningitidis from the closely related pathogen
nersseria genorrhowae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                   Proceobacteria; beta subdivision; Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2, Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24830 MW, 52428E97A9A844R7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-50N-2001 (TrEMBLrel. 17, Created)
01-50N-2001 (TrEMBLrel. 17, Last sequence update)
01-bEC-2001 (TrEMBLrel. 19, Last annotation update)
2610201431881R PROTEIN (FRAGMENT).
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 24.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 1.06a; Score 7, DH 2, Local Similarity 100.0%; Pred. No. 72; es 7, Consorvative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1929955; Akrial.
InterPro; IPR001395; Aldo_ket_red.
Pfam; PF00248; aldo_ket_red; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect. Immun. 68.2982-2995(2000).
EMBL, AJ391256. CART1999.1; .
EMPLEDIA Profeso.
SEQUENCE. 238 AA. 24830 MW. 524.
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EMBL; AP000988; BAB67111.;;

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Sekine M., Baba S.-I., Ankai A. Kosuqi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudch Y., Yamazaki J., Kushida N., Oquchi A.,
                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplaniae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Madioliophyta: Madioliophyta: Nesidae, eurosids II; Brassicales: Brassicaceae; Arabidopsis.
                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., Do Clerck K., De Kryser A., Neyt P., Kouze P., Van Den Daele H., Villaroei K., Gielen J., Van Montagu M., Hancrott I., Mewes H.W., Rudd S., Lameke K., Mayer K.E.X.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Cremarchaeota; Sulfelebales, Sulfelebaceae, Sulfelebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oqi
Aoki K. I., Masuda S., Yanaqii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodali strain7.";
DNA Res. 8:123-140(200-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.5%; Score 7; DB 10; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                   0: Indeis
 Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL, Cenhank/Coht. databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMHL/Genhank/2004) database
EMHL/ALJ62451: CARB2761.1;
EMPPONDELICAL protein.
SEQUENCE: 155 AA: 19002 MW, 2140B70BAA98BA2B CR064,
                                                                                                                                                                                                                                    01-0CT 2000 (TERMILE). 15, Last sequence update)
01-0CT-2000 (TERMILE). 15, Last annotation update)
HYPOTHELICAL 19.0 KDA PROTEIN.
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01-DEC:2001 (TrEMBLrel. 19, Last annotation update)
4.5%; Score 7; DB 2;
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               100.0%; Pred. No. 32; ative 0, Mismatches
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                                                                                                                                                                                                                    01-off 2000 (TrEMBLrel, 15, Greated)
                                                                                                                                                                                        PRT
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                                 Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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                                                                                                                                                                                        PRELIMINARY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ST2014.
Sulfolobus tokodaii.
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed-11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AEKLKEN 192
                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D= 4702;
                                                                 29 EKLKGLF 35
                                                                                    20 EKLKGLF 26
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Chery Match
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                                                                                                                                                                                                      09L2V5;
                                                                                                                                                                                    94L2V5
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                               Matches
                                                                                                                                                                 KESOLL
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Arakawa T., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Addohi J., Fokuda S., Arakawa M., Nishi K., Kiyosawa H., Kondo S., Yamadaka I., Salie T., Chazawa M., Nishi K., Kiyosawa H., Kasukawa I., Salie T., Chazawi Y., Osjojecii T., Bencu H., Kasukawa I., Salie P., Radola K., Matsuda H.A., Ashburner M., Balalov S., Casawani T., Radola K., Matsuda H.A., Ashburner M., Balalov S., Casawani T., Radola K., Matsuda H.A., Ashburner M., Balalov S., Casawani T., Radola W., Romina H., Romina H., Washio I., Rasaki K., Okido T., Furuno M., Aono H., Haldarelli K., Harsh G., A. Baka i K., Okido T., Furuno M., Aono H., Haldarelli K., Harsh G., A. Brownstein M.J., Holmon M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Hojunga N., Carninci D., Kamiya M., Lee N.H., Kons P., Marchionni Z., Mashima J., Mazazafelli J., Machaetts F., Nordone P., Ring B., Ringweld M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Weitz C., Whittaker C., Wilming I., Nordone P., Ring B., Klangweld M., Rodiguez I., Sakamoto N., Sasaki H., Toyocaka K., Warg R. H., Weitz C., Whittaker C., Wilming I., Nordone P., Ring B., Klang R., Rawaji H., Kohtsuki S., Nordone V., Warg K. H., Weitz C., Whittaker C., Wilming I., Nordone P., Ring W., Warg R. H., Weitz C., Whittaker C., Wilming I., Nordone P., Romani M., Warg K. H., Weitz C., Whittaker C., Wilming I., Mashima M., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gabs
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Melazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Scivroquathi, Muridae, Mutinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Functional annotation of \epsilon full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:
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                                                                                                                                                                                              Length 167;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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SEGGENCE: 214 AA; 24419 MW; 62A489AC13GCEBE5 CRC64;
                             Hypothetical protein; Complete proteome.
Seguence: 167 AA: 18937 MW; 9058D37EG65FH719 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (IrEMBLrel. 19, East annotation update)
2610201A18RIK PROTEIN.
                                                                                                                                                                                          3.5%; Score 7; DB 17;
100.6%; Pred. No. 52;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPAIN+C57BL/6J; TISSUE-EM3RYO;
MEDLINE-21085660; PubMed+11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001395; Aldo_ket_red.
Pfam; PF00248; aldo_ket_red; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.50.
100.0%; Pre
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EMBL: AK011221; BAB27477.1; -.
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                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
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|123 VLALAEK ||129
                                                                                                                                                                                                                                                                                                                                                    30 KLKGLFT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                  72 KLKGLFT 78
                                                                                                                                                                                              Query Match
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                                                                        STEATN-IFD: 15057;
STRAIN-IFD: 15057;
Suzuki M., Yamaguchi K.;
Suzuki M., Yamaguchi K.;
Puplogacnetic analysis and taxonomic study of marine Cytophaga like "phylogocnetic analysis and taxonomic study of marinemer in nov. with Hacrentibaculum maritimum comb. nov. and Hacrentibaculum ovolyticus comb. nov., and two new species.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-:-CATALYITG ACTIVITY. ATP DEFENDENT BREAKAGE, PASSAGE AND PEJOINING OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GF DOUBLE-STRANDED DNA.
-1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY EMBL; AB048186; BAB33153.1; -.
                                                                                                                                                                              SIMILARITY: HELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                               Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                             481 AA; 53517 MW; 1F3AB57936BC10F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterià; CFB group; Flexibacter group; Chitinophaga
NCBL_TaxID-79329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.50N-2001 (TrEMBLrel. 17, Created)
01.50N-2001 (TrEMBLrel. 17, Last sequence update)
01.50SC-2001 (TrEMBLrel. 19, Last annotation update)
                      Hacteria, CFB group; Flexibacter group; Flexibacter.
NCBL_Tax1D-1004;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 8; DB 2
100.0%; Pred. No. 13;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                    SMART: SM00433, TOP2c; 1,
PROSTER: DS00177; TOPOISOMERASF_11: 1
                                                                                                                                                                                                                                                                                                                                              ATP-binding; Isomerase; Topoisomerase
                                                                                                                                                                                                                                                                                  Pfam; PF01751; Toprim; 1.
PRINTS; PR00418; TP12FAMILY.
ProDom; PD000616; DNA_topoisoII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPPO01241; DNA_topoisoII
                                                                                                                                                                                                             HSSP: P06982; lAJ6.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR003594; HATPase_c.
InterPro; IPR003596; Toprim.
PF00204; DNA_topoisoII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR003594; HATPase_c.
InterPro, IPR002936, Toprim.
pfam; PF00204; DNA_topoiso11; 1.
Plam; PF02518; HATPAse_c; 1.
Plam; PF01751; Toprim: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last. DNA GYRASE B SUBUNIT (FRACMENT).
                                                                                                                                                                                                                                                                       PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chitinophaga pinensis.
                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPOURNCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; PURMAZ; 1A.16.
               Flexibacter sancti
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 SENDPEKC 72
                                                                                                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                   PROSTTE;
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NON_TER
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                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                  F.M.B.L.;
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Gaps
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NCBL_Taxib=666;
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIANE-89123097; PubMed-2644218;
Jacobson M.R., Brigle K.E., Bennett L.T., Setterquist R.A.,
Wilson M.S., Cash V.L., Beynon J., Newton W.E., Dean D.R.;
"Physical and genetic map of the major nil gene cluster from
Azolobacter vinetandil.";
                                                                                                                                                                                                                                        Longth 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Januardon P., Manning P.A.;
Kaewardon P., Manning P.A.;
Submitted (SEP 1997) to the EMBL/GenBank/DDBJ databases.
HMHU. AFUZEGEZ, AAM81983.1, -.
Hypothetical protein.
SKÖUENCE 98 AA, 11215 MW; b15AC1889H6D4FH4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.5%; Score 7; DB 2; Length 72; Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                               481
481 AA; 53681 MW, E845DB5EH79927F2 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azotobacter vinelandil.";
J. Bacteriol, 171:1017-1027(1989).
EMBL, M20568; AAA64721.1: -
SOUBNO. 72 AA, 8004 MW; BCBCA2DBE3035FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 ("FEMBLrel. 05, Created)
01-JAN-1998 (*FEMBLrel. 05, Last sequence update)
01-JAN-1998 (*FEMBLrel. 05, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                        Ouery Match 4.0%; Scote 8, BB 2; Best Local Similarity 100.0%; Pred. No. 13; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 AA.
                  Prodom; PD000616; DNA_topoisoll; 1. SMAk!; SM00433, TOP2c, 1. PROSITE; PS00177; TOPOISOMERASE_II: 1. ATP-binding; Isomerase; Topoisomerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYLOTHETICAL 11.2 KDA PROTEIN.
PRINTS; PRO0418; TPIZFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 ALAEKLK 180
                                                                                                                                                                                                                                                                                                                                              65 SENDPEKC 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azotobacter
                                                                                                                                                                            SEQUENCE
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NON_TER
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                                                                                                                                SEQUENCE FROM N.A.

Voldby J., Virved L., Due M., Gronlund J., Bolmskov U., Teisner B.,
Salomansen J., Hussqaard K., Skjodt K.,
Salomansen J., Hussqaard K., Skjodt K.,
"Cloning, sequence and genomic structure of MHC class II antigens from
the spectacled caiman Calman crocodilus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1909) to the EMBL/GenRank/Order databases of CATALYTIC ACTIVITY: ATP-DEPENDENT RPEAKAGE, PASSAGE AND PETGINING OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum maritimum comb. nov. and Haerentibaculum ovolyticus comb. nov., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-IFO 16041;
Suzuki M., Yamaquchi K.;
"Phylogenetic analysis and taxonomic study of marine Cytophaga like
                                         Herinalpha.
Caiman crocodilus (Speciacled caiman) (Caiman selerops).
Eukaryota: Metazoa, Chordata: Craniata: Vertebrata, Euteleostomi;
Archosauria; Grocodylidae; Alligatorinae; Caiman.
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARHIY: BELONGS TO THE LYPE II FOPOISOMERASE FAMILY.
EMBL.: AB012579; BAB13317.1; .
HSSP: P06982; TAJ6.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 8: DB 7: Length 253;
Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/RenBank/DDBJ databases EMBL: AF256550; AAF99282.1; ...
                                                                                                                                                                                                                                                                  of MAR 230! (FFEMBLEEL, 15, Last sequence appdate)
of DDT 260; (FEMBLEEL, 19, Last annotation update)
MHC "LASS II ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TEMBLIEL 16, Last sequence update) 01-DEC-2001 (TEMBLIEL 19, FAST ABBLIELED update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria: CFB group: Flexibacter group; Flexibacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMAPT: SMOO4.33, TOP2C; 1;
PROSITE: PSO0177; TOP01SOMERASE_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP binding; Isomerase; Topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR 2001 (TrEMBLrel, 16, Greated)
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Profom: PD000618: DNA_topoisoII: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR001241; DNA_topoisoII
InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA CYRASE B SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ptam; PF00204; DNA_topoisoll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002946; Toprim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF02518; HAIPase_c; 1.
                                                                                                                                                                                                                                                       InterPro: IPR003597; 4_cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loprim;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flexibacter japonensis
                                                                                                                                                                                                                                          P01903; 2SEB.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 ALTIVIAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two new species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 ALITVLAL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01751;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9FAX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U9FAX2
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                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-IFO 15056;
Suzuki M., Yamaguchi K.;
"Phylogenetic analysis and taxonomic study of marine Cytophaga like
bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum
maritimum comb. nov. and Haerentibaculum ovolyticus comb. nov., and
two new species.";
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                                                                                                         Caps
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: HELONOS TO THE TYPE II TOPOISOMERASE FAMILY. EMBL: AB032581; BAB1319.1. -. HISBY: P06982; LAJ6. HISBY: P06982; LAJ6. InterPro: IPRO01241; DNA_topoisoII. InterPro: IPRO01394; HATPASE_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                         Length 481;
                                                                                                       U: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1999) to the FMBL/GenRank/NPBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 AA; 53735 MW; 1E4FD8E3F4EEHA30 CRC64;
            481 481 481 481 8707FEA30BDA70B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Hacteria, CFB group, Flexibacter group, Flexibacter
NCHI_TaxID=104663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
UL-MAR-2001 (TrEMBLrel. 15, Last sequence update)
01-DNC-2001 (TrEMBLrel. 15, Last annotation update)
DNA GYRASE B SUBUNIT (FRAGMENT)
                                                                                                                                                                                                                                                                        01-MAR-2001 (TYEMBLTEL. 16, Created)
01-MAR-2001 (TYEMBLTEL. 16, Last sequence update)
01-DEC-2001 (TYEMBLTEL. 19, Last annotation update)
DNA GYRASE B SUBUNIT (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.0%; Score 8; LW 2;
Best Loral Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches
                                                                     4.0%; Score 8; DH 2;
100.0%; Pred. No. 14;
7ative 0; Mismatches
                                                                                                                                                                                                                                              481 AA.
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PROSITE; PS00177; TOP01SOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Isomerase; Topoisomerase.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF02518; HATPase_c; ].
Pfam: pF0751; Toptim: 1.
PRINTS: PR00418: TP12FAMILY.
Prolbom, Pf000616; DNA_topoisoff; ].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1PR002936; Toprim.
                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      Flexibacter filiformis.
                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 SENDPEKC 323
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            NON_TER
SEQUENCE
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NON_TER
 NON_TER
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                                                                                                      Matches
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GenCore version 4.5
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OM protein - protein search, using sw model

July 2, 2002, 16 18 31, Search Lime 96 19 Seconds Run on:

(without alignments)
361.493 Million ceil updates/sec

US-09-603-665-5_COPY_1917_2117 Title:

1 FKLFDWAKTEDAPKDRLLTF......NYIVLLPESIPFLAELMEDE 201 Perfect score: Sequence:

Gapop 60 0 , Gapowt 60.0 Ó1.1GÖ Scoring table:

562222 seqs, 172994929 residues Searched.

Word size :

1509 Total number of hits satisfying chosen parameters:

Maximum DB seq length: 200000000 Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

SPTREMRL_19:* Database :

sp_unclassitied:* sp_invertebrate:* sp_vertebrate:* sp_bacteriap:* sp_organelle:* sp_archea:* sp_bacteria:* sp_archeap:* sp_rodent:* sp_plant:* sp_virus:* sp_mammal:* sp_rvirus: sp_fungi:* sp_human:* sp_phage:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q96es5 homo sapien	09gjn1 caiman croc	Q9fax2 flexibacter	Q9tax0 flexibacter	Ostawé ilexibacter	Q9aq14 chitinophag	Q44537 azotobacter	031026 vibrio chol	Q91zv5 arabidopsis	Q96z15 sulfolobus	09d0p3 mus musculu	070473 cricetulus	Q90wtl brachydanio	Q9jpe8 neisseria m	Q9ct53 mus musculu	Ogedis mus musculu
B ID	4 Q96ES5	7 09G.IN1	2 QFFAX2	2 Q9FAX0	2 COFAWG	2 Q9AQ1.4	2 044537	2 031026	10 09L2V5	17 Q96215	11 Q9D0P3	11 070473	13 Q90Wr1	2 09JPE8	11 Q9CT53	11 Q9CQIS
% Query Match Length DB	349	253	481	481	481	481	72	96	165	167	214	228	232	238	252	252
% Query Match	49.8	4.0	ः •	4.0	4.0	4.0	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5
Score	100	œ	æ	80	œ	90	7	7	7	7	7	7	7	7	7	7
Result.	-	2	m	4	S	9	7	- oc	J	10	11	7.5	13	14	15	16

253 AA.

PRT;

PRELIMINARY;

Q9GJN1 Q9GJN1;

Q9GJN1

01-MAR-2001 (TrEMBLrel. 15, Created)

rhiz nacac caul strep mus mus	094016 mus musculu 094012 mus musculu 0956484 syncehocyst 091892 arabidopsis 09417 brachydanio 092861 staphylococ	400	Q94313 drobophila Q94502 arabidopsis Q952N* streptomyce Q948400 bacillus ha Q961t3 yarrowia 11 Q948b9 vibrio chol
265 16 Q98HM1 285 6 Q9N045 296 16 Q9AAU6 305 2 Q935V5 317 5 P91020 325 11 Q9JII6 325 11 Q9D017	325 11 Q9D016 325 11 Q9D012 325 11 Q9D012 325 16 Q55684 332 10 Q9PK92 333 12 Q9PK92	22224	374 5 Q9V31.3 374 10 Q9C502 391 2 Q1S2B3 393 16 Q9KEQ0 400 16 Q9KSH9 401 17 Q9751.3
<i></i>	アクファファ 東京の自当では あららららら		77777 88887 88888 8888 8888 8888
17 19 22 23 23 23	21444444 41037800	. — М. Ж. М.	७०नथस्य १

ALIGNMENTS

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223 ALMMELVDQLENRLGGEEKFYGEVTKHILFEGTAGESVAMAFDSEWKFINVQTELKTFFSS 282
                                                                                                                                                                                                                                                                                                                                                                                                        102 ALMMPEVPOLENPLGAFEKFOGEPVTKHLIPOIAGESVAMATOSEWKPLNYQILLFKTRDSS 161
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Mammalia; Buthetia; Primetes, Catarrhini, Hominidac; Homo.
                                                                                                                                                                                                                                                                                                                                        49.8%; Score 100; DB 4; Length 349; 100.0%; Pred. No 9.2e-95;
                                                                                                                                                                                                                                                                                                                                                                         Indets
                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/Genhank/TDHJ databases.
EMBL, BC011983; AAH11983.1; -.
SEQUENCE 349 AA, 39921 MW: 3A359597FF7079FR CRC64;
                                                              01-DEC-2001 (TTEMBLIEL. 19, Created)
01-DEC-2001 (TTEMBLIEL. 19, Last sequence update)
01-DEC-2001 (TTEMBLIEL. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ms
+ive 0; Mismatches
                               349 AA
                               PRT;
                                                                                                                                                                                                                           TISSUE-OVARY, AND ADENOCARCINOMA; Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 100; Conservative
                                  PPELIMINARY;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                              NCB1_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                Q96ES5;
                                  Q96ES5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
RESULT
                    096ES5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                            DNA ROS. 3:109-136(1996).
-! FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NGVO PATHWAY OF PURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
Hosoucht I., Matsuno A., Muraki A., Nakazaki N., Natuo K., Okumura S., Shimpo S., Takeuchi C., Wada I., Watanabe A., Yamada M., Yasuda M., Tabata S., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain process. II. Sequence determination of the control cyanobacterium assignment of potential protein-coding regions.";
                                                                                                                                                                                                                CATALYTIC ACTIVITY: GTP + IMP + L-aspartate - GDP + phosphate
                                                                                                                                                                                                                                                                PATHWAY: FIRST COMMITTED STEP IN AMP HIGSYNTHESIS.
SIMILARITY: HELONGS TO THE ADENYLOSUCCINATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom: PROOFIS Ademylaser_synt; 1.
PROSITE: PSOOF14: Ademylaser_synt; 1.
PROSITE: PSOOF14: ADEMYLOSOCCIN_SYN_2: 1.
PROSITE: PSO1266: ADEMYLOSOCCIN_SYN_2: 1.
PROSITE: PSO1266: ADEMYLOSOCCIN_SYN_2: 1.
PROSITE: PSO1266: ADEMYLOSOCCIN_SYN_3: 1.
ACT_SITE: 140 140 HV SHMILARITY.
SEQUENCE 444 AA: 4472 MW: F06900ECF241A4BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goery Match 1.5%; Score 7; DB 1; Length 444; Best Local Similarity 100.0%; Pred. No. 26; Mastches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: [PROG114; Adenylsuce_synt.
Pfam; PF00709; Adenylsuce_synt: ].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: D90905; BAA17413.1; ALT INIT.
                                                                                                                                                                                            NICLECTIBE BIOSYNTHESIS.
                                                                                                                                                                                                                                            adenylosuccinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P12283: 1ADE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 FLAELME 199
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Search completed: July 2, 2002, 16:19:08

Job time: 780 sec

400 FLAELME 406

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PH1214 OR PHBK040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P73290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADSS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB, outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter extracellular binding protein PH1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of control (Ref. 34, Last Sequence update)
10-00T-1990 (Rel. 34, Last Sequence update)
16-00T-2001 (Rel 40, Last annotation update)
18ypothetical 47.0 kDa protein in glnQ-ansR intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato'T., Takeuchi M.;
Submitted (MAY-1016) to the EMBL/GenBank/DDB1 databases.
-: SIMILARITY: BELONGS TO THE IMPB/MUCB/SAMR FAMILY
                                                                                                                                                                             3.5%; Score 7; DB 1; Length 358;
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0824C62U8U8848484 CRC64;
                                                                                                             EB2268FA9A5190A4 FPF64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pirmicutes, Bacillus/Clostridium group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 AA.
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                                                                                                                                                                                                   100.0*, rrod No. 22.
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; E
ilarity 100.0%; Pred. No.
Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00817; 1MS; 1.
Hypothetical protein; Complete proteome
                                                                                                                                                                                               Tried N
                                                                           CARD.
RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                             BIR 1.
BIR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 AA, 47020 MW;
           Apoptosis; Zinc-finger; Repeat
                                                                                                                 40977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D84432; BAA12614.1; -. EMBL; Z99116; CAR14319 1: -.
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InterPro; IPR001126; UMUC.
                                                                                                                                                             Ouery Match
Rest Local Similarity Tus...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168 / JH642;
                                                                                                                 358 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AEKLKGL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-1423;
                                                                           193
                                                                                                                                                                                                                                                                   14 KDRLLTF 20
                                                                                                                                                                                                                                                                                                              5 KDRLLTF 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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                                                                                                                      SECUENCE
                                                                                                 ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                              P54545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YC14_PYRHO
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                                      REPEAT
                                                                             DOMAIN
                                                           REPEAT
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                                                                                                                                                                                                      Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka K., Nakarawa H., Jakamiya M., Ohfirka Y., Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Pobb F T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Pobb F T., Horikoshi K., Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY; BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
                    Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97061201; Pubmed-8905231;
Kaneko T. Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR BINDING PROTEIN PH1214.
N-ACYL DIGLYCERIDE (POTENTIAL).
558D963D816GA7EE CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last aequence update)
16-OCT-2001 (Rel. 40, Last amontation update)
Adenylosuccinate synthetase (RC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000567; SBP bac_1.

pram; Pr01547; SBP_bacterial_1; 1.

PR05IIE; PS00013; PR0KAR_LIROPROTEIN; 1.

PR05IIE; PS01047; SBI_BACTERIAL_1: FALSE_NFG.

Hypothetical protein; Trauspoil; Membrane, Lipoprotein; Signal;

Complete protegome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL ABC TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%; Score 7; DB 1; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             thermophilic archaebacterium, Pyrococcus horikoshii Or3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyanobacteria; Chroococcales: Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macon Similarity 100.0%; Pred. No. 26; Local Similarity Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (Strain PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT,
                                                                                                                                                                                     MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP000005; BAA30314.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 5:55-76(1998).
Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN FAMILY 1.
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                                                                                                                             SEQUENCE FROM N.A.
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                                                       NCBI_TaxID-53953;
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"identification of the Rhizobium meliloti alcohol dehydrogenase gene
(ddhA) and hererologous expression in Alcaligenes cutrophus.";
Biochim. Riophys. Acta 1844:197:203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILIA 1995(9) Dibberd-11181432; Komp C., Abola A.P., Harnett M.J., Fisher R.F., Jones L., Komp C., Abola A.P., Garly Habler F., Bowser L., Capela D., Galkhert F., Gonzy J., Barloy Habler F., Bowser L., Capela D., Galkhert F., Gonzy J., Garloy H., Hora A., Huizar I. Hyman P. W. Rahn P. Kahn M. L. Kalman S., Keatina F.H., Palm C., Peck M.C., Surzycki R., Wells D.H., Yeh K. C., Davis K.W., Federspiel N.A., Long S.K., Surzycki R., Wells D.H., Yeh K. C., Davis K.W., Federspiel N.A., Long S.K., Soquence and predicted functions of the entire Sinorhizobium meliioti psyma megalasmid.":

Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- COFATIOR: ZINC (HY SIMILARITY).
-1- SIMILARITY: HELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY, HIGH, WITH OTHER HACIERIAL ADH'S.
                                                                                                                                                                                                                                                                                                                                                                 DY SIMILARITY.

ACETYLATION (BY SIMILARITY).

11.2 HYDROGEN FOND DONOR (BY SIMILARITY).

46.2.4 MM. A 18075(A5F0F905F2 CR054).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria: Proteobacieria, alpha subdivision; Rhizoblaceae group;
Rhizoblaceae; Sinothizoblum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 49, Last sequence update)
01-MAR 2002 (Rel. 41, Last annotation update)
ACOMOLI dehydrogenese (EC. 1.1.1)
ADHA OR HA0704 OR SMA1296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 20; ive 0; Mismatches
                                                                                                                                                                                                                              PROSITE; PSOUGES ALD KETO_REDUCIASE 2: 1.
PROSITE; PSOUGES ALDCKETO_REDUCIASE 3: 1.
PROSITE: PSOU798; ALDCKETO_REDUCIASE 1: 1.
                                                                                                                               InterPro: IPRU01395; Aldo_kot_rod.
Plam: PF00248; aldo_ket_rod; i.
PRINTS; PR00069; ALGKETPPTASE
                                                                                                                                                                                                                                                                                                                                  exidoreductase: NADP; Acetylation.
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                                                                   EMBL; D10854; BAA01527.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Hest Local Similarity
7: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA:
                                                                                                      ZALR.
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                                                                                               HSSP: P14550;
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MOD_RES
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodaetyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                              3.5%, Score 7, 18 1; heigth 340; 100.0%; Pred. No. 21; tive 0; Mismatches 0: Indels
                                                                                                                                                    SEQUENCE 340 AA; 36235 NW; ClA04B5FEE5095E1 CR064;
                                                                                                             NAD; Plasmid; Complete profeome.
                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTIE: PS01282; BIR_REPEAT_1; 2.
PROSTE: PS50143; BIR_REPEAT_2; 2.
DROSTIE: PS50209; CAPD; 1.
PROSTIE: PS00518; PF.PING_1; FALSE_NEG.
PPOSTIE: PS50089; ZF_RING_2; 1.
                                                                   InterPro: IPR002085: Adh_zn_tamily.
                                                                                                                                                                                                                                                                                                                                                                                                                        Putative inhibitor of apoptosis.
             EMBL, AF031940; AAB87463.1; -. EMHL, AE007258; AAK65362.1; -. HSSP; P00325; IDEH.
                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
                                                                                            PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc; NAD; Pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001841; Znf_ring.
                                                     interPro: IPR002328; ADH_zing.
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HSSP, Q13490; 1ОВН.
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Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00238; BIR; Z. SMART; SM00114; CARD; I. SMART; SM00184; RING; I.
                                                                                                                           40
                                                                                  Piam; PF00107; adh
                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                                                                                                                                                                                                    173 LALAEKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                               203 LALAEKI, 209
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                                                                                                                                         6.3
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062640;
                                                                                                                                                                                               Query Match
                                                                                                                          METAL.
                                                                                                                                          METAL
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-:- CARALYIC ACTIVILY: An alcohol + NADP(+) - an aldehyde + NADPH.

-:- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITAR-89255461; PubMed-2498333; Bohren K.M., Bullock B., Wermuth B., Gabbay K.H.; Fullock B., Wermuth B., Gabbay K.H.; Trefere aldo Keto reductase superfamily rowas and deduced amino acid sequences of human aldolyde and aldose reductases.", J. Biol. Chem. 264:9547-9551(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Interpro; IPPAnna445; MoaA_NIIB_PqqB.
Plan; PFU1444; MoaA_NIIB_PqqB. 1.
PROSTIE; PsOl146; MOAA_NIEB_PQQE; 1.
Molybdenum cofactor blosynthesis; Iron.sulfur; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-ARR-1990 (Pel 14, Tast sequence update)
01-MAR-2002 (Pel 41, Last amortation update)
Alcohol dehydrogenase [NANP+] (B7 1 1 1 2) (Aldehyde reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Lin G., Carson M., Narayana S.V.L.,
DeLucas L. I.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wermuth B., Omar A., Forster A., di Francesco C., Wolf M., von Warthurg J.-P., Bullock B., Gabbay K.H.; Brimary structure of aldebyde reductase from human liver."; prod. Clin. Hist. Res. 232-297-207(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJINESGGATIANU, RubMod 19485210;
Barski O A , Gabbay K H., Rohren K M.;
"Characterization of the buman aldebyde reductase gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, vortobrata, Eutolo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                  DB 1; Length 316;
                                                                                                                                                                                                                                       O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC 1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                             AZBUF 417470 F5BC (PC64)
                                                                                     TEON SULFUR (POTENTIAL).
TRON-SULFUR (POTENTIAL).
TRON-SULFUR (POTENTIAL)
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                                                                                                                                                                                                                    100.0%; Pred. No. 19;
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                                                                                                                                                                                                    3.5%; Score 7;
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                                                                                                                                             CENTAL MW.
EMBL; AP000001; BAA29183.1; -
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Hest Local Similarity Tub...
7; Conservative
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Moore K.M., Flynn T G . E
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKRIAI OR ALDRI OR ALR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                 In AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
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P14550;
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                                                                                                                                                 SEULENCE
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                                                                                             METTAL.
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TISSUE-Kidney, and Liver;
MEDLINE 942744D; PubMed-8500767;
MEDLINE 942744D; PubMed-8500767;
Takabashi M., Fujii J., Pespima T., Suzuki K., Shiba T., Taniquchi N.;
"Identity of a major 3 decayglancesone reducing enzyme with aldehyde reductase in rat liver established by amino acid sequencing and cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniala, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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3.4 AA; 36442 MW; ACSBSDOGSA940FIF CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07T-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase)
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100 0%; Bred w.
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                                                                                                                                                                                                                                                                                                                                                                                              AF036682; AAB92369.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF112485; AAF01260.1; -.
EMBL; AF112484; AAF01260.1; JOINED.
                                                                                                                                                                                                                                                    EMBL; J04794; AAA51711.1; -.
EMBL; AFG36683; AAH92369.1; -.
EMBL; AFG36680; AAB92369.1; JOINED
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PRINTS; PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-2DPAGE; P14550; HUMAN.
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AKRIAI OR ALR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96-NULL-02
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Rest Loral Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 VLALAEK 239
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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MEDLINE-98344137; PubMed-9679194;
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                                                                                                                                                                                                                                                                                                             Pfam: PF00185; GTCace; 1. Pfam: PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5:55-76(1998).
                                                                                                                                                                                                                                                                  HSSP; Q51742; IAIS.
FIGR; AF1255; -.
                               + L-citrulline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 LAEKLKE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LAEKLKE 27
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057854;
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Korfolma K.A., Dodson R.J., Gwinn M., Hickey E.X., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Granam B.E., Kyrpides N.C.,
Fleischmann R.D., Quarkenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Lottus B.,
Peterson S., Reich G.L., McKell L.K., Hadger J. H., Glodek A., Zhou H.,
Overbeck R., Socayne J.D., Weilfanh J.E., McDonald L., Utterback T.,
Cotton M.D., Springs L., Artiach P., Kaine H.P., Sykes S.M.,
Sadow P.W., D'Andrea R.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Eraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                             destric pathogen Helicobacter pylori.";
Miture 497.176 FB0.1999.
-!- CAIALYLE ACTIVITY: 2 delydro 3 deoxy-D octorate 8 phosphate -
-!- CAIALYLE ACTIVITY: 2 delydro 3 deoxy-D octorate 8 phosphate -
-!- Phosphate - phosphoeuolpyruvate - D-arabinose 5-phosphate + H(2)0.
-!- PATHWAY: FRENT TEEP IN LIPOSACCHARAIDE BIOSYNTHESIS.
-!- SUBGELLULAR DOCATION: CYLOplasmic (By similarity).
-!- SUBGELLULAR DOCATION: CYLOplasmic (By similarity).
                                                                            Alm R.A., Lind L.-S.L., Moir D.L., King B.L., Brown E.D., Doig P.C., Smith D.R., Loronan H.D., Guild B.C., delonge H.L., Carmel G., Lummino P.J., Caruso A., Urra'n Nickelsen M., Mills D.M., Lvis C., gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                             Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete genome sequence of the hyperthermophilic, sulphate reducing archaeon Archaeoglobus fulgidus.";
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Fram; PF00793; JAHP_synth_1; 1.
Lippo0194yadcharide biosynthesis: Lyase: Complete proteome.
SEQUENTE 276 AA: 30774 MW: FFF7D879F148D348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 1.5%; Score 7; DB 1; Length 276; Best Lord Similarity 00.0%; Pred, No. 17; Marches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea: Euryarchaeota; Archaeoglobales, Archaeoglobaeeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Re). 36, Last sequence update)
16-OCT-2001 (Re). 40, Last annotation update)
Ornithine carbamoyltransletase (EC 2.1.3.3) (OTCase).
                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license isbasib.oh).
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MEDLINE-98049343; PubMed-9389475;
                                                               MEDLINE-99120557; PubMed-9924682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001440; AAD05587.1;
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                                               SECUENCE FROM N.A.
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              NCB1_Tax1D=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 LKTRDSS 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS PROF entry is ecpyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMH. outstation the European Bioinformatics Institute of are not restrictions on its use by non-profit institutions as lond as its centent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/damounce/or send an email to licensee@lsb.sib.ch).
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- FUNCTION: INVOLVED IN THE BLOSYNTHESIS OF MOLYHDOPTERIN PRECURSOR
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Archaea: Euryarchaeota; Thermococcales; Thermococcareae: Pyrocomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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-!- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MOAA / NIFB / POUE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermophilic archaebacterium, Pyrococcus horikoshii 973.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase, Arginine biosynthesis: Complete proteome.
SEQUENCE 307 AA; 34913 MW; DB043BC5A40ERH5D CRC64;
                                                                                                                                 -t- PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).
-t- SUBCELLULAR LOCATION: Cytoplasmic.
-t- SIMILARITY: BELONGS TO THE AICASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative molybdopterin cofactor synthesis protein A.
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PROSITE: PSOCOGT: CARRAMOYLIBANSFERASE: FALSE_NEG.
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tive 0; Mismatchos
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PIR; A03822; ERADA5
PIR; A22515; A22515.
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 LITVLAL 138
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SEQUENCE FROM N A
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146
30
79
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                                                                                                                                                                                                               COMPLETE GENOME
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δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96026345; Pubmed-756993; Praser C.M., Gorayno R.A., Fraser C.M., Gorayno H.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bull C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchmann B.D., Weidman T.F., Small K.V., Sandusky M., Fuhrmann J.L., Weidman T.F., Sandok D.M., Phillips C.A., Merrick J.M., Tomb J.F., Doughorty H.A., Rott K.F., Hu P.-C., Lucier T.S., Tomb J.F., Doughorty H.A., Hutchison C.A. 111, Venter J.C., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Early E3 18.5 kDa glycopiotein precursor (GP19K).
Human adenovirus type 5.
Viruses, dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: BINDS TO THE 23S RRNA (BY SIMILARITY). SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROFEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillus/Clostridium group, Mollicutes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7; DB 1; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; pFG1281: Fibraschal_19.1.
PROSITE; PSG0651; RIEGSCWAL_19; FALSE_NEG.
Ribbosomal protein; rNM-binding; Complete proteome.
SEGUGENCE 150 AA, 17380 MW; 50A19B6EAA48EBD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AMG-1987 (Rel. 05, Greated)
13-AMG-1987 (Rel. 05, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                     (Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
31 protein L9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 10;
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                                                                                                                                     150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR000244; Ribosomal_L9.
                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                         Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39689; AAC71311.1; -.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                        SHÖUKNCE FROM N.A.
SIRAIN-AFCC 33530 / G-37;
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                         Myccplasma genitalium
                                                                                                                                                                                                                                        RPLI OF PPICA OF MG093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 ALAEKLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ALAEKLIK 69
                          181 ENYIVLL 187
                                                      128 ENYIVIL 134
                                                                                                                                                                                                                                                                                                       NCBI_TaxID-2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01281:
                                                                                                                                                                                                                           50S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MC093;
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                                                                                                                                                                                          01-FEB-1996
                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                         RL9_MYCGE
P47339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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16-OCT-2001 (Rel. 40, Last sequence update)
2-dehydro-2-deaxyphosphosphosorionate aldolase (EC 4.1.2.16) (Phospho-2-dehydro-3-deoxypoctonate aldolase) (3-deoxy-0-manno-actulosonic acid dehydro-3-deoxypoctonate aldolase) (3-deoxy-0-manno-actulosonic acid 8-phosphate synthetase) (KDO 8-P
                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori 1999 (Campylobacter pylori 199).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                           "DNA sequence of the early B3 transcription unit of adenovirus 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLÖNAC. . .) (POTENTIAL).
N-LINKED (GLÖNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i. SUBCELLULAR LOCATION: Type I membrane protein. Findoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLY E3 18.5 KDA GLYCOPROTEIN
                                                                                                                                                       MEDILINE 5130985; PubMed=3882694; Moid W.S.M., Cladaras C., Deutscher S.L., Kapoor O.S.; Wold W.S.M., Cladaras C., Deutscher S.L., Kapoor O.S.; Purification, daracterization, and structural analysis."; J. Biol. Chem. 260:2424-2431(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane, Glycoprotein, Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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EMBL; X03002; CAA26783.1; -.
EMBL; M12406; AAA42492.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.37,
100.0%; Pre
0;
MEDLINE-85092388; PubMed-2981456;
Cladaras C., Wold W.S.M.;
                                                                                                                                                                                                                                                                                                                                                    MEDIINE=92087470, FubMcd 1727603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
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                                                                                 Virology 140:28-43(1985)
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                                                                                                                                                2019 ALMMELYDOLENKLÄGEEKFÜERVTKHILPCLAGESVAMADOSLWKPLNYOLLEKTROSS 2077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
                                                                                                                                  1/12 ALMMPLVDQLENRLGGEEKFQERVIKHLIPGIAQFSVAMADDSIMKPLNYQILLKTRDSS 161
                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Mctazoa: Chordata; Cramiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Cercopitheeidae;
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                                                                                                                                                                                                                                                                                                                                                                               Macaca tascicularis (Trab eating macaque) (Cynomolgus monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolation of full-length cDNA closes from macaque brain cDNA
                                                                            49.8%; Scorv 100; DH 1; Length 2144; 100.0%; Pref. No. 5.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FKLFDWAKTEDAPKDRLLTFYNLADMIAEKLKGLFTLFAGHLVRPFADTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 958;
                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitted (our 2000) to the EMBL/GerBank/DDBJ databases. SIMILARITY: HELONDS TO THE BAP2L FAMILY. SIMILARITY: CONTAINS I HEAT REPIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                     2144 AA: 242355 MW. D668.6EE78D809B7 CRC64;
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                                                                                                                                                                                                    2078 FVWFAALITVLALAFKLKENYIVLLPYSIPFLAELMEDE 2117
                                                                                                                                                                                       162 PKVRFAALITVLALAEKLKENYIVLLPISIPFLAELMELF 201
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/FTId-VAR_010941.
                                                                                                                                                                                                                                                                                                                                         40, Last annotation update)
                        AFT'A VALATAG42
                                                                                                         0: M.smalches
                                                                                                                                                                                                                                                                                                                              40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000357; HEAT_repeat, PROSITE; PS$0077; HEAT_REPEAT; FALSE, NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license tisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB049842; BAB16728.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAT.
                                                                                                                                                                                                                                                                                                               6 off 2001 (Rel. 40, Greated)
                                                                                                     Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                      Protein BAP28 (Fragment).
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecimae, Macaga.
           2017
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Best Local Similarity
                                                                                        Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
          2017
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HISSUE-Brain;
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                                                                                                                                                                                                                                                                                  BP28_MACEA
Q9GM44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matiches 50;
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                                    SHOMENCE
                                                                            Query Match
           VARCANI
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PRI: 141 AA

STANDARD;

CYTS_RAT P19313;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Amino acid sequence of an inducible cysteine proteinase inhibitor (cystatin) from submandibular glands of isopiotenehol treated rats.";
Arch. Blochem. Blophys. 273:245-253(1989).
-1- FUNCTION: THIS PROTEIN STRONGLY INHIBITS PAPAIN & FICIN. PARTIALLY INHIBITS STEW BROWELAIN & BOYINE CATHERSIN C, BUT DOES NOT INHIBIT PORCINE CATHERSIN B OR CLOSTRIPAIN. PAPAIN IS INHIBITED
                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Futeleostomi,
Mammalia, Butheria, Rodentia, Seiurognathi: Muridae, Murinae, Kattus.
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                                                                                                                                                                                                                                                                                                                                                                                           "Structure, organization and regulation of a rat eysteine proteinase inhibitor-encoding gene."; Gene 110:175-180(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- TISSUE SPECIFICITY: FOUND IN SALIVA, TEARS, URINE, AND SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shaw P.A., Cox J.L., Barka T., Naito Y., Carloing and sequencing of cDNA encoding a rat sallyary cysteine proteinase inhibitor inductible by beta-adreneraic adonists."; J. Biol. Chem. 263:18133-13137(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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SECONDARY AREA OF CONTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EH -> QE (IN REF. 3).
. D763290554108266 GR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 10-141 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; IISSUE-Submandibular gland;
MEDLINE-89053983; PubMed-3263967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.
01-NGV-1990 (Rel. 16, Created)
01-FFB-1996 (Rel. 33, Last Sequence update)
01 MAR 2602 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9.9; Mismatches
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BY SIMILARITY.
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Best Local Similarity 100.0%; Pred. No
Matches 7; Conservative 0; Mismat
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                                                                                           Cystatin S precursor (LM protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Submandibular qland;
MEDLINE-89334379; PubMed-2757396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thiol protease inhibitor; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                     MEDILINE-92165056; PubMed-1537554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00287; CYSTATIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M75281; AAA41068.1; ... EMBL; J04206; AAB59703.1; -..
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                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
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PIR; S05252; S05252.
                                                                                                                                                                                                                                                                                                                                                                  Cox J.I., Shaw P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00043; CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 28-132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, 805252, 805252
HSSP, P01038, 1CEW.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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                                                                                                                           CST4 OR CYSS.
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OM protein : protein search, using sw model

July 2, 2692, 16:19-67 ; Search time 30-19 Seconds (without alignments) 257.788 Million cell updates/sec Вип оп:

201 1 FKLFDWAKTEDAPKDPLLTFNYIVLLPESIPFLAELMEDE 201 US-09-603-665-5_COPY_1917_4117 Title: Perfect score:

Scoring table: Sequence:

Gapop 60.0 , Gapext 60.0

105224 seqs, 38719550 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

fotal number of hits satisfying chosen parameters.

Word stze :

359

Post-processing: Listing first 45 summaries

SwissProt_40:*

sect No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STMMARIES

Description	Ogh583 homo sabien						09zn55 helicobacte	G29013 archaeoglob		P14550 homo sapien				P54545 bacillus su			•				-	-			<u>с</u> п	LC.	Q9c8z4 arabidopsis	P44177 haemophilus	•			escheri	simian	P22379 simian immu
GI GI	NAME OCCO	DF ZC IIOMAN	HPZF_MACEA	CYTS_KAT	RL9_AYCGE	E3G;_ADE05	KDSA HELPJ	OTIC, ARCFU	MOA/_PYRHO	ALD) HUMAN	ALDX_RAT	ADHA_REIME	PIAI PIG	YOJEBACSU	YC14_PYRHO	PURA SYNY3	VDHA CHICK	Y190_HELPY	PHR : ARAU	CHS3_EXODE	CHSG_ASPFU	CHSB EMENT	HMD2_YEAST	DDX8 ARATH	ADP1_MYCGA	ATC4_YFAST	BP28 AFA"H	YEO2 HAEIN	RL7_STANU	EX75 HAETE	GLRX_HARLIN	TA TA LECOLI	REV SIVAM	REV_SIVGB
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ALLIGNMENTS

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0; 0; Caps 0; Indels Query Match
Bost Local Similarity 100.0%; Pred. No. 42; Length 325; Matches 7; Conservative 0; Mismatches 0; Indels

Qy 172 VLALAEK 178 ||+|||| | Db 234 VLALAEK 240

Search completed, July 2, 2002, 16:15:41 Job time: 758 sec

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A:Status: preliminary: translated from GB/EMBL/DDBJ
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                                                                                                              Fixfork, H.P. Thaylou, R.A.; Tomb, J.E.; White, O., Nelson, K.E., Kerehum, K.A., Dodson, F.E. Ferschmann, K.D.; Quaekengsb, T. Leo, N.H.; Sutton, G.S.; Gill, S.; Kirkness, E.F. Gilodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.E.; McDonald, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.E.; McDonald, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.E.; McDonald, L.; Swits, T.; Collon, M.D.; Swits, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Switth, H.O.; Woose, T.; Collon, M.D.; Squiper of the hyperthermophilic, sulfate-reducing archaect A: Kererence number: A6925c: MULD:9804934; Ancression: E69406 A: Kererence number: A6925c: MULD:9804934; Ancression: E69406 A: Kererence number: Grand sequence not shown; translation of shown A: Molecule type: BNA A: Kererence in 407 KLE.
A. Status: 1.407 KLE.
A. Status: 1.407 KLE.
A. Status: GR:AE001017: GH:AE000742; NID:q2689340; FILM:AA889987.1; FID:q264932; C:Superfamily: ornithine carbamoyltransferase is partate. Ancress earbamoyltransferase is a partate. Ancress of the Action of the
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HITLS1
modybeteric biosynthesis protein meaA - Fyroceccus herikoshii
C;Species: Pyrocecus horikoshii
C;Species: Pyrocecus horikoshii
C;Sacrission H71241
C;Date: 14-Aug 1998 #sequence_revision 14-Aug-1998 #text_change 24 Cet 2000
C;Accession H71241
R:Kawarabayashi Y; Sawada M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Obtuku, Y.; Fundhashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oquchi DNA Res. 5, 55-76, 1998
A;Aritle: Complete sequence and gene organization of the geneme of a hyper-thermophilic a A;Accession: H71281
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Asmolecule type: DNA
Aspesidues: 1-446.KAW.
Aspesidues: 1-446.KAW.
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Astronomes: strain 043
Astronometal source: strain 043
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C:Species: Caenorhabdifis elegans
C:Date: 15-oct 1999 fsequence_revision 15-oct-1999 flext_change 18-Feb-2000
                                            C:Date: Of Dec 1997 #Sequence_revision O5 Dec 1997 #text_change 18-Jun-1999
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100.0%; Pred. No. 40;
1ve 0; Mismatches 0; Indels
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Altebraham in sequence of C. elegans cosmid C07D8
Altebraham number: 220045
Altebraham 125526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 2;
; Pred. No. 41;
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100.0%; Pre-
Cospecies: Archaeoglobus ulgidus
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Matches 7: Conservative
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                                                                               C:Accession: F69406
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Cjaccession- JN0629; PNJ532
R:Takahashi, M.; Fujii, J.; Teshima, T.; Suzuki, K.; Shiba, T.; Taniguchi, N.
Gene 127, 249-253, 1993
A;Title: Identity of a major 3-deoxyglucosone-reducing enzyme with aldehyde reductase
A;Peference number: JN0629; MUID:93273240
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J. Hiol. Chem. 264, 9547-9551, 1989
A.Titlu: The aidorketo reductase superfamily, clNAs and deduced amino and sequences
A.Reference number: A33851; MULD:89255461
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A,Posiducs: 14 23:35-45:69-77:81-91:135-145:241-249;295-305:309-318 < LAA.
C:Comment: This engine catalyres the NADEH dependent reduction of 3 deoxyqlurosone,a
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A,Molecule type: DNA
A,Residues: 1-317 <NEL>
A,Cross references: EMHL-URA844- PIDN-AAR37476 1- GSPDH-GNU9928; CESP:CO708-6
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CiAccession: 180629; PN0532
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C;Dale: 23:Mar:1990 #sequence_revision 23 Mar:1990 #fext_change 11:Jun 1999
                                                                                                                                                                                                                                                                                                                                                                                                                  Cales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (yaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross=reterences: GB:D10854; NID:q399659; PIDN:BAA01627.1; PID:q399660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.C. COSS-references: CAL-104794; NID:g178480; PIDN:AAA51711.1; PID:g178481
C. Superfamily: aldehyde reductase
C. Keywords: alcohol metabolism; NADP; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                             A, Experimental source: strain Bristol M2, clone 00708
C, Genelies:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Keywords: alcohol metabolism: NADP: oxidoreductase F/269.78 indiag site: NADF (L/s) istatus predicted
                                                                                                                                                                                                                                                                                                                                                   query Match
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DH 1;
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alcohol dehydrogenase (EC 1.1.1.1) - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N:Alternate names: aldehyde reductase
                                                                                                                                                                                                                                                     C; Superfamily: aldehyde reductase
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                                                                                                                                                                                          A:Map position: X
A:Introns: 81/3; 218/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type, mRNA
Residues: 1 325 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 VLALAEK 178
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Pred. No.

100.08;

Best Local Similarity

A; Cross-references. EMBL. AL162351

A; Introns. 99/3; 121/3 A; Note: T20:15:180

A; Map position: 5

1-165 <BEV>

A;Status: preliminary

A; Molecule type: DNA A;Accession: T48212

A; Residues:

0;

Best Local Similarity 100 Matches 7, Consorvative

Query Match

176 AEKLIKEN 182

30 AEKLKEN 36

q

JC7706

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C.Species Callobacter rescentus
C.Jotte. 20-Apr. 2001 #sequence_revision 20 Apr. 2001 #text_change 20-Apr. 2001
C.Jotte. 20-Apr. 2001 #sequence_revision 20 Apr. 2001 #text_change 20-Apr. 2001
C.Jotte. 20-Apr. 2001 #sequence_revision 20 Apr. 2001 #text_change 20-Apr. 2001
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, 1.T.; Nelson, K.E.; Elsen, J.; Heidelberg, B., Lamb, M.T.; Daboy, R.T.; Dodden, R.T.; Durkin, A.S.; Gwinn, M.L.; Halt, D.H.; Kon, J.; Ermolaeva, M.; White, n.; Saltherg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A, tetterice number. A87249, Mülb.2117448, PMID-11259647
                                                                                                                                                                                                                                                                                                                                                             KibelVecchio, V.G., Kapatrai, V., Podkar, P. i. Patra, C. Muher, C. Los, T.; Lyanov, Mazur, M., Goltsman, E.; Sclkov, E.; Flrer, P. H.; Hagius, S.; O'Callaghan, D.; Lot, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002.
A.; Litle: The genome sequence of the facultative intracellular pathogen Brucella melit. A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                           23S ribosomal RNA methyltransferase (BC 2.1.1...) [imported] Procella meditensis (St Cispedas: Brucella meditensis
C,Date, 01 Feb 2001 #sequence_revision n) Peb 2002 #text_change n] Feb 2002
C,Accession: AG3305
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A,Crostinerencus, GH:AE005673, NIE,313421677, PIDH:AAK224R5 1; GSPDH-GND0148
C,Genctics
A,Gene: CC0498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Status: preliminary
A:Notecule type: UNA
A:Red ducs. 1 276 - KUNA
A:Cross-references: GB:AEGOR917, PIDN.AAL51610.1; PID:q17982336; GSPDR-GN00190
A:Cross-references: GB:AEGOR917, FIDN.AAL51610.1; PID:q17982336; GSPDR-GN00190
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   Gaps
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   Indels
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   0, Mismatches
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Matches 7; Conservative
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C;Keywords methyltransferase
         7; Conservative
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Matches 7, Conserva
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240 LFTLFAG 246
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                                                                155 LKTRDSS 161
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                                                                                                                           148 LKTRDSS 154
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C, Accession 12 Feb-1999 #text_rhange 08-oct-1999
C, Accession 12 Feb-1999 #sequence_revision 12-Feb-1999 #text_rhange 08-oct-1999
C, Accession E71987
C, Accession E71987
C, Accession E71987
C, C, Gibson, R., Morbetg, D., Mills, S. P., Jiang, Q.: Taylor, D. R.; Vovis, G. F.; Ives, C., Gibson, R., Morbetg, D., Mills, S. P., Jiang, Q.: Taylor, D. R.; Vovis, G. F.; Articles Genomic sequence comparison of two unrelated isolates of the human gastric path A, Relevence number: A71800; MUD:99120557
A, Accession: E71885
A, Accession: E71885
A, Residucs: 1 276 <ARN>
A, Residucs: 1 276 <ARN>
A, Residucs: 1 276 <ARN>
A, Experimental source: strain J99
C, Genetics:
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Hiochen. Hiophys. Res. Commun. 285, 105-110, 2081
A;Title: Molecular cloning, developmental expression, and hormonal regulation of zebrafi
A;Reference number. JC7706; MIII: 21331298; PMID: 11437379
A;Accession: JC7706.
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C:Species: Helicobacter pylori
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C;Species: Brachydanio rerio (zebra lish)
C;bale, 09 Mivr:2001 #sequence_revision Or-Nivr-root #text_change 27-Nivr-root
C;Accession: JC7706
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C:Comment: This protein is involved in requlation by growth factors.
C:Superlamliy: beta-crystallin
F;20-25/Region: artive proline- and alanine-rich motif #status predicted
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                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone T20L15
                                                                                                                                                                                                                                                                                                                                             3.5%; Score 7; DB 2;
100.0%; Pred No. 24;
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100.0%; Pred: No. 32;
ive 0; Mismatches
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Conservative

Best Local Similarity Matches 7; Conserva

Query Match

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A; Molecule type: mRNA A; Residues: 1-232 <CHE>

3.5%; Score 7;

Query Match

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CiDate: 01-Peb-2002 #sequence_remision 91 Feb 2002 #text_change 01 Fub 2002

C.Accession: AC3385

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Gaps

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O; Indels

Length 151;

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E.Deiveschie, V.G., Kapatral, V., Fedhar, E.J.; Patra, G.; Majer, C.; Los, T.; Ivanov, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Haqius, S.; O'Callanhan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002.
Adritle: The genome sequence of the facultative intracellular pathogen Brucella ment A, Reference number: A03252; PMID:11756688
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R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
Submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                         A; Cross references: CB: AEC08917, PIDN: AAI.52246.1; PID: g17983032; GSFDB: GNO0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Mastadenovirus h5 (human adenovirus 5
C.Species: Mastadenovirus h5 (human adenovirus 5)
A.Note: host Homo sapiens (man)
C.Date: 17-Mar-1987 *sequence_revision 17 Mar-1987 **Hext_change 16 Jul 1999
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C.Date: 20-Apr-2000 #sequence_revision 20 Apr-2000 #:ext_change 20 Apr 2000
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Actors-references: GEM12406; MID:g209911; DIDN:AAA42492.1; PID:g209912
C:Superfamily: adenovirus early E3 18.5% dlycoprotein
C:Keywords: early protein; qlycoprotein; transmembrane protein
E;30,79/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Accession: A03822; A22518
C:Accession: A03822; A22518
R:Cladaras, C.; Wold, W.S.M.
Virology 140, 28-43; 1985
A:TTELE: DNA sequence 75 the early E3 transcription unit of adenovirus
A:TTELE: DNA sequence A94335; MUID:B5092388
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A) Cross references: OB:X03002; BID:958503; PUDA:CAA26283.1; PID:958504
B;Wold, W.S.M.; Cladards, C.; Peutscher, S.L.; Naprot, O.S.
Biol. Obem. 260, 2444-2411, 1988
A;Title: The 19 Kba njyrogedest coded by region E***! ademostrus
A;Reference number: A22515; MUID:85130985
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Prod. No. 22:
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                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-151 <KUR>
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Asilite: Amilio acid sequence of an inducible cysteine proteinase inhibitor (cystatis) fracessions S05262; MJD:89144379
Ashoessides S05262; MJD:89144379
Asholecule type: Protein
Asholecule trophys. Acta 1077, 346-354, 1991
Astille: Isolation of three torms of cystatin from submandibular saliva of isoproterenol
Asholecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C'Accession, C64210
Riffasor, C.M.; Gocdync, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96a26346
A:Reference number: A64200; MUID:96a26346
A:Reference number: and sequence not shown; translation not shown
A:Molecule type: DNA
A:Residual pre: DNA
A:Residual source: STIGRA
A:Experimental source: STIGRA
A:Experimental source: STIGRA
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C;Speries: Mycoplasma qenitalium
C;Date: 17 Nov-1995 #sequence_rovision 17 Nov 1995 #text_change ^7-1002-1999
C:Accession, C64210
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b.1 24/Domain: Signal sequence *status predicted (305)
E.28 44/Zhrodur: cystatin S. status experimental "MATS-
E.29 44/Zhrodur: cystatin S. form RSC 3 status predicted (MATS)
E.30-141/Zhrodur: cystatin homology (CYS)
E.31-14/Zhrodur: cystatin S. form RSC 2 *status predicted (MATS)
E.31-14/Zhrodur: cystatin S. form RSC 2 *status predicted (MATS)
E.32-14/Zhrodur: cystatin S. form RSC 1*status predicted (MATS)
E.32-14/Zhrodur: cystatin S. form RSC 3*status predicted (MATS)
E.34-104,118-138/Disulfide bonds: #status experimental
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C;Supertamily: Escherichia coli ribosomal protein L5
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00.0%; Pred. No. 22;
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dative 0; Mismatch
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Astatrons, 26/4, 114/4
Csuperfamily: cystafin homology
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Gaps

n; Indels

OM protein - protein search, using sw model

Pun on:

July 2, 2002, 16:15:40; Search time 57 09 Seconds

(without alignments)
338.307 Million cell updates/sec

US-09-603-665-5_COPY_1917_2117

NYIVLLPESIPFLAELMEDE 201 Perfect score:

1 FKLFDWAKTEDAPKPPLLTF Sequence:

283138 seqs, 95089334 residues Searched.

Capop 60.0 , Capext 60.0

Scoring table:

Word size :

1011 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post processing: Listing first 45 summaries

pirl.* PIR_71 · * Database ·

pir2:* pir3.* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	V original Value of the Notice	Table 5:	Czstatin s		retrov	5 early E3 18.5K gly	hypoth	beta crystallin B	3-deoxy-d-manno-oc	5 23S ribosomal RNA	l hypothetical prote	s ornithine carbamoy	1 molybdopterin bios	5 hypothetical prote		alcohol			9 alcohol dehydrogen				4 alcohol dehydrogen	7 unknown protein,	9 hypothet.iral_prot.e	9 methionine gamma	5 acetoacetyl-CoA re		3 DNA-damage repair	
ID	A103C2	10000	0/5/30	C64210	AC3385	ERADA 5	T48212	JC7706	E71985	AC3305	A87311	PF9406	1171231	925526	JN0629	A33851	876360	T20644	H95349	069422	JC5964	055534	AE3184	B86457	T36739	G83749	JC7675	C82213	9669H	
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ALIGNMENTS

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RESULT
       S26914
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Ig heavy chain V region (DP-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22 Nov: 1v4 #sequence_revision to Nov: 1v45 #t.ext__nbange 21-tan_2000
C;Accession: \$26914
B;Tomlinson, L.M., Walter, G., Marks, J.D., Llewelyn, M.B.; Winter, G.
A;Tile The reperforment of human garmline V(H) sequences reveals about filty groups on R; Reference number: \$25844
A;Reference number: \$25844
A;Reference number: \$25894
A;Reference prediction of human garmline V(H) sequences reveals about filty groups on R;Reference number: \$2594
A;Reference number: \$25894
A;Reference prediction of human garmline V(H)
A;Reference prediction of human garmline V(H)
A;Reference number: \$25944
A;Reference number: \$25894
A;Reference prediction of human garmline V(H)
A;Reference number: \$25994
A;Reference number: \$25894
A;Reference number: \$25994
A;Reference number: \$259

A;Cross-references: EMBL.212304; NID.332863. FIBN.CAA78174 1, FID.332864 (S. Superfemily: immunoqlobulin V region; immunoqlobulin homology C;Reywords: heterotetramer; immunoqlobulin F;15-98/Domain: immunoqlobulin homology <1MM>

.: :: Gaps .. O 0; Indels Length 98; DB 2; . 15; 3.5%, Score 7, DB 2 100.0%, Pred. No. 15, tive 0; Mismatches Query Match Best Local Similarity 100.0 ...a. 7; Conservative

120 KPQERVT 126 ò

63 KFOERVT 69 qq

RESULT

Ografin S precursor - rat cystatin S precursor - rat C;Species: Raitus norvegicus (Norway rat) C;Pate: 17 Jul 1942 #sequence_revision 17-ful·1942 #text_change 16-ful·1949 C;Accession: JQ1470; A31891; S0\$252; S15132 R;Cox, J.L.; Shaw, P.A.

Gene 110, 175-180, 1992

AJTILIE: Structure, organization and regulation of a rat cysteine proteinase inhibito A;Peference number: JQ1470; MHID:92165056 A;Accession: JQ1470

A;Molecule type: DNA A;Residues: 1-141 ~CTX. A;Cross::references: GB:MZ5281; NID:9294537, PT:N:AAA11068.1, PTD:9294538 P;Shaw, P A; Cox, J L; Harka, T; Naito, V P;Shaw, P A; Cox, J L; Harka, T; Naito, V A; Biol. Chem. 253, LB133-LB137, 1988 A;Title: Cloning and sequencing of CDNA encoding a rat salivary cysteine proteinase i A;Peference number: A31891; MUID:89053983

A; Accession: A31891

A,Molecule type: mRNA A,Rcsiducs, 'ISTDYLYISFEHETLSC',27 141 :SHA:

Arch Ricchem Biophys 273, 245-253, 1989 A, Residues. P, Bedi, G S

Db 10 AEKLKE 15

Scarch completed, July 2, 2002, 16:04:01 Job time: 58 sec

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STATE
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APPLICANT: Rubin, Albert L.; Gordon, Bruce R; Saal, Stuart D.
FITLE OF INVENTION: Methods Useful in Endotoxin Based
FITLE OF INVENTION: Prophylaxis and Therapy
CORRESPONDENCE ADDRESS:
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                                  e. Biskette, 5.25 inch, 450 kb storage
IBM PS/2
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
MEDIUM TYPE: Storage
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Current application Data:
Application number: US/07/928.930A
FILING DATE: 19920812
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FILING DATE: 10-AUGUST-1994
CLASSIFICATION: 514
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REFERENCE/DOCKET NUMBER: E050-211
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08288568
Patent No. 5505218
GENERAL INFORMATION:
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ALTORNEY/AGENT INPORMA TON:
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FILING DATE: 9-AUGUS1-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                    (212) 688-9200
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 848 3884
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 17 amino acids
IYPE: AMINO ACID
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                                                                                                                                                                                                                            NAME: Hangos No 63
REGISTRATION NUMBER
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New York
                                  COMPUTER READABLE FORM:
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                                                                                          OPERATING SYSTEM:
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                                                      MEDIUM LYPE:
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COUNTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Parker, Thomas S.; Levine, Daniel M.;
APPLICANT: Rubin, Albert .; Gordon, Bruce R; Saal, Stuart D.
TITLE OF INVENTION: Methods Useful in Endotoxin Based
TITLE OF INVENTION: Prophylaxis and Therapy
                                                                                                                                                                                                                            C, Indels
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                                                                                                                                                                                      3.0%; Score 6; DB 1; Length 17;
100.0%; Pred. No. 20;
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MEDIUM IYPE: Diskette, 5.25 inch, 360 kb
MEDIUM IYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 20;
tive 0; Mismatches
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SOFTWARE: Wordperlect
CURRENT APPLICATION NOTA:
APPLICATION NOTA:
FILING DATE: June 7, 1955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07/928,930
                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 3, Application US/08187461
; Patent No. 5587366
                                                                                                                                                                          Ouery Match
Best Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DATE: 12-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 688 9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
TELEPHONE: (212) 688-5200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Felle & Lynch
: 805 Third Avenue
New York City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 amino acids
                                                                            17 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS/2
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                                                                                              amino acid
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                                                                                                            TOPOLOGY: linear
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                                                                                                                                US-08-288-568-4
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US-08-487-461-3
                                                                          LENGTH:
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FILING DATE: 19901012

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APPLICANT: Chappell, J.
APPLICANT: Saunders, Court A.
APPLICANT: Cuellar, K.
APPLICANT: Wolf, Fred R.
TITLE OF INVENTION: Process and Composition for Increasing TITLE OF INVENTION: Sterol Accumulation in Higher Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dressler, Goldsmith, Shore, Sutker & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 3.5%; Score 7, DB 1, Length 1045; Hest Local Similarity 100.0%; Pred. No. 87, Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              3.5%; Score 7; DB 1; Length 1045; 100.0%; Pred. No. 87; 1.1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOTTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gamson, Edward P. REGISTRATION NUMBER: 29,381
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TELEPHONE: 312 616-5400
                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
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                                                                                               TELEFAX: 312 616-5460
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1045 amino acids
TYPE: AMINO ACID
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                    Gamson, Edward P.
                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                           312 616-5460
                                                                                                                                                                                  MOLECULE TYPE: protein US-07-596-467-6
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Wolf, Fred R.
Mukharii, Indrani
Mukhariios: A Method and Composition for Increasing
NVENTION: A Method and Composition of Squalene and Specific Sterols in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \Xi . Amore Corp , Patents and Licensing Dept. 200 East Randolph St.
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APPLICANT: Rubin, Albert L.
AITLE OF INVENTION: Methods Usetul in Endoloxin
TITLE OF INVENTION: Prophylaxis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%; Score 7; DB 1; 100.0%; Pred. No. 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19911028
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/613,380
AFILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
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                                                                  Sequence 6, Application US/07783861C Patent No. 5460949
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STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312 856-4972
INFORMATION FOR SEQ ID NO: 6:
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LENGTH: 1045 amino acids
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US-07-783-861C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60680-0703
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicago
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                               US-07-783-861C-6
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RESULT
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New York

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APPLICANT: Lamsa, Michae,
APPLICANT: Hansen, Kim
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                                                                                                                                    New York
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                                                                                   Caps
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                                             Query Match 3.5%; Score 7; DB 4; Length 729; Best Loral Similarity 100.0%; Pred. No. 62; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 7: DB 2: Length 911;
100.0%; Pred. No. 77;
tive 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Fast SEQ for Windows Version 2.0 CURRENI APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENTE/INCTRET NUMBER: 4944,200-US
TELEPOMENTICATION INFORMATION:
TELEPIONE: 212 867-0123
TELEFAX: 212 878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/928,692
                                                                                                                                                                                                                                                                                                                                                                      a Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application 75/08928692
Patent No. 5958727
                                                                                                                                                                                                                                  Sequence 59, Application US/08928692
Patent No. 5958727
                                                                                                                                                                                                                                                                                                                                                                                                                                    405 Lexington Avenue
                                                                                                                                                                                                                                                                                   APPLICANT: Brody, Howard
APPLICANT: Yaver, Decorah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hausen, Kim
TITLE OF INVENTION: Methods to
TITLE OF INVENTION: a Polypept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brody, Howard APPLICANT: Yaver, Deborah S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-SEPT-1947
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
/ MoleCULE TYPE: No. 5958727c
US:08:928-692-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY ZAGENT INFORMATION-
NAME: Lambitis, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 911 amino acids
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Best Local Similarity 100.0
The 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                               175 LAEKLKE 181
                                                                                                                                               448 LAEKLKE 454
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US+08-928-692-59
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US 09 240 196
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STATE:
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5958727disk of No. 5958727th America, Inc
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TITLE OF INVENTION: Methods for Modifying the Production of TITLE OF INVENTION: a Polypeptide NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dressler, Goldsmith, Shore, Sutker & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIILE OF INVENTION: Method and Composition for Increasing IIILE OF INVENTION: Sterol Accumulation in Higher Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
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100.0%; Pred. No. 77;
1ve. 0; Mismatches
                                                                                                                                                                                                                                                    SOUTWARE: FASISE DOS WINDOWS VERSION 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/AD // CTARY.
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APPLICATION NUMBER: US/07/596,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-596-467-6
; Sequence 6, Application US/07596467
; Patent No. 5306862
                                                                                                            405 Lexington Evenue
                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 No.
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chappell, J.
APPLICANT: Saunders, Court. A.
APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 916 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CORPESPONDENCE ADDRESS:
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Best Local Similarity
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Illinois
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APPLICANT: Chappe
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MOLECULE TYPE: protein
Patent No. 6294658
                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 7; DB 2; Length 178; 100.0%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Factors involved in Gene Expression
                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/347,833
CURRENT FILING DATE: 199-07-02
CURRENT FILING DATE: 199-07-02
EARLIER APPLICATION NUMBER: 60/092,415
FARLIER FILING DATE: July 10, 1998
                                                                                                                                                                                                                                                                                  4944.200-US
                                                                                                                                                                               US/08/918,691
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; Patent No. 6294658
                                                                                                                                                                                                                                                 NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 494
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: No. 5958727e
US-08-928-692-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEC 1D NOS: 11
SOFTWARE: Microsoft Office 97
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                              12-SEPT-1997
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        178 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Famodu, Layo O. APPLICANT: Odell, Joan T.
                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                 APPLICATION NUMBER.
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                 FILING DATE: 12 CLASSIFICATION:
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          New York
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| 104 LLLQFIL 110
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                                             USA
                                                            10174
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                                             COUNTRY:
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                             STATE:
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                                                                                                                                                                                                                                                                                                                                        3.5%; Score 7; DB 4; Length 655; 100.0%; Pred. No. 57; Live 0, Mismatches 0; Indels
              APPLICANT: Famodu, Layo O. APPLICANT: Odell, Joan T. TITLE OF INVENTION: Factors Involved in Gene Expression FILE REFERENCE: BB-1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Howson and Howson
Spring House Corporate Cntr., PO Hox 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
                                                                                      CURRENT APPLICATION NUMBER: US/09/347,833 CURRENT FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSTEBBUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,860/038,109
                                                                                                                         EARLIER APPLICATION NUMBER- 60/092,415
FARLIER FILING DATE: JULY 10, 1998
NUMBER OF SEQ ID NOS- 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/230,196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09230196
; Patent No. 6407035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bak, Mary E. 11,215 REGISTRATION NINBER: 31,215 REFERENCE/DOCKET NUMBER: WS: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215-540-9200
                                                                                                                                                                                       SOFTWARE: Microsoft office 97 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 729 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                Query Match 3.5%
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Spring Hous
                                                                                                                                                                                                                                                                      ; ORGANISM: Oryza sativa
US-09-347-833-4
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                   LENGTH: 655
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US-08-928-692-57
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                                                                                                                                                                                                                                                                                                                                           STATE:
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     Gaps
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 0; Indels
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100.0%: Pred. No. 9.8;
                                                                                                                                                                                                                                                           APPLICANT: JESPEKS, Laurent Stephane Anne Therese APPLICANI: WINDER, Gregory Paul III. FILE OF INVENTION: combinetorial approach III.E OF INVENTION: combinetorial approach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Hest Local Similarity 100.0%; Pred. No. 9.5
7: Conservative 0; Mismatches
 0: Mismatches
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FILLING DATE: 15-MAY-1992
ALIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/211,202
FILING DATE: 23 SEP-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NINBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9120377.8 FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9206318.9 FILING DATE: 24-MAR 1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soid-SW/Soid-oid
                                                                                                                                                                    Sequence 140, Application USZUB211202
Patent No. 5565332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPFRATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-4856
INFORMATION FOR SEQ ID NO: 130:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM LYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112-474 5300
                                                                                                                                                                                                                                           BAIER, Michael
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Matches 7: Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                   66 ENDPERC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                         29 ENDPERG 35
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APPLICANT: Lamsa, Michael
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SNOUTHNES: 80
CORRESPONDENCE ADDRESS:
ADDRESSFE. No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
APPLICANT: HOLD FUNIHIKO
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
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100.0%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DAIA:
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Best Local Similarity 100.0%; pred No. 12;
American C. Americania O. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06501,004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/TP93/0663
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
                                                                                                                                                                 NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                Sequence 139, Application HS/28545809A Patent No. 6096878

    Sequence 57, Application US/08928692
    Patent No. 5958727

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/INCKET NUMBER OF TELECOMMUNICATION INFORMATION: TELEPHONE. 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELLEX: 200154
INFORMATION FOR SEQ ID NO: 139:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brody, Howard APPLICANT: Yaver, Deborah S. APPLICANT: Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                       : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 amino acids
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LENGTH: 117 amino acid.
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                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           Boston
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US-08-545-809A-139
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Copyright (c) 1993 - 2000 Compagen Ltd
Gendere version 4.5
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OM protein - protein search, using sw model

July 2, 2002, Thigh-OB : Search time 44 R5 Seconds Run on:

(without alignments)
109.466 Million cell updates/sec

US-09-603-665-5_COPY_1917_2117 Title:

... NYIVILPESTPELAELMEDE 201 1 PKLEDWAKTEDAPKDREFTE. Perfect score:

01.190 Scoring table:

Sednence :

Gapop 60 0 . Gapext 60.0

231628 seqs, 24425594 residues Searched.

9

Word size :

rotal number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000 Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database :

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/cgn2_6/ptodata/2/jaa/6B_comm.pcp:*
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/cgn2_6/ptodata/2/jaa/follis_rimMi.pcp:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

. ca		Query				
	Score	Match	Match Length	DB.	QI	Description
	7	3.5	41	7	US-08-630-915A:79	Sequence 79, Appl
2	7	3.5	86	<u></u>	US-08-211-202-130	_
~	7	3.5	117	~	US-08-545-809A-139	Sequence 139, App
4	7	3.5	178	C a	18-08-978-675	Sequence 57, Appl
Ŋ	7	3.5	42R	7	US-U9 347-833 to	Sequence 6, Appli
9	7	3.5	655	4	US-09-347-833-4	Sequence 4, Appli
7	7	ω .υ	729	4	115-04-2340-146-2	Sequence 2, Appli
30	7	3.5	911	C4	US-08-928-692-59	
6	7	3.5	916	7	08-28a-828-80-SU	Sequence 58, Appi
10	7	3.5	1045	-	US-07-596-467-6	Sequence 6, Appli
11	7	3.5	1045	-	US-07-934-374-6	Sequence 6, Appli
i C	7	κ.	1045		45-07-783-8610-6	Sequence 6, Appli
13	9	3.0	17	٦	US-07-928-930A-3	Sequence 3, Appli
14	Q	3.0	17	-	US-08-288-568-3	Sequence 3, Appli
15	9	3.0	17		US-08-487-461-3	Sequence 3, Appli
16	9	3.0	17	-	US-U8-432-691-3	Sequence 3, Appli
17	9	3.0	17	-	US-08-487-459 3	Sequence 3, Appli
18	ō	3.0	18	-1	US-07-928-930A 1	Sequence 1, Appli
19	ع	3.0	18	~	US-07-920-597-6	Sequence 6, Appli
20	9	3.0	18		US-08-288-568-1	Sequence 1, Appli
21	9	3.0	18		US-08-487-461-1	Sequence 1, Appli
22	9	3.0	18	_	US-08-432-691-1	Sequence 1, Appli
23	9	3.0	18	_	US-08-487-459-1	Sequence 1, Appli
24	œ	3.0	18	3	US-08-940-095-240	
25	9	3.0	18	(m)	-660-	244,
26	Q	3.0	18	33	US 08-940 093-240	240,
27	9	3.0	18	.*;	US-U8-940-Ü93-Ž44	Sequence 244, App

Sequence 240, App	Sequence 244, App	Sequence 240, App	Sequence 244, App	Sequence 240, App	Sequence 244, App	Serponery 9, Appli	Sequence 47, Appl	Sequence 22, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 110, App	Sequence 11, Appl	Sequence 7, Appli	193,	Sequence 193, App	Sequence 19, Appl	Sequence 19, Appl
US-08-940-096-240	US-08-940-096-244	US-09-465-719-240	US-09-465-719-244	115-09-453-605-240	US-09-453-605-244	6-8498-757-80-80	US-09-085-761A-47	US-09-087-455-22	US-09-437-054A-12	US-09-067-782A-4	US-09-247-155-110	PCT-US95-05741-11	US-U8-328-254-7	US-08-482-142-193	US-08-478-572-193	us-09-117-257-19	US-08-945-476-19
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18	18	18	18	1.8	8-	35	103	107	127	131	154	161	180	181	181	181	181
3.0	3.0	3.0	3.0	0.	٥	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0
40	ي	9	ø	(C)	÷	د	9	Q	w	ø	œ	٥	9	9	9	٩	9
38	58	3.0	31	100	33	34	35	36	37	38	39	40	4.1	4.2	43	44	4.5

ALIGNMENTS

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MCCONNELL, SLephen J.
VENTION: POLYPEPTIDES BAVING A FUNCTIONAL
VYENTION: DOMAIN OF INFEREST ANN METHODS OF IDENTIFYING AND
SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Pr'rompatible
OPRRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   ADDRESSEE. Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DS/OR/630,915A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101-174
                              Sequence 79, Application US/08630915A Patent No. 6309820
                                                                                        APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, NO. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,6
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                    COPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER.
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                US-08-630-915A-79
                                                                                                                                                                                                                                                                                                                                            STATE: Ne
                                                                                                                                                   APPLICANT:
APPLICANT:
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RESULT
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3.5%; Score 7; DB 4; Length 41; 100.0%; Pred. No. 4.4; Best Local Similarity Query Match

AAM69827

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                          Human bone marrow expressed probe encoded protein SEQ ID NO: 30133.
                                                                                                                        Human: bone marrow expressed exon; gere expression analysis; probe; microarray: cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4: SEQ ID NO: 30133: 658pp + Sequence Listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.5%; Score 7: DB 22; Length 110; Local Similarity 100.0%; Pred, No. 28; nes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: July 2, 2002, 16:06:04 Job time: 181 sec
AAM69827 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                          03 AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0.234687.
27 SEP-2000; 2000US-0.236359.
04 OCF 2000; 2000CB-0024263.
                                                                                                                                                                                                                                                                 40 JAN-2001; 2001WO-0300668
                                                                                                                                                                                                                                                                                               04-FEB-2000; 2000US 0 80312.
                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000US-0508408
                                                                                                                                                                                                                                                                                                                 2000005-0207456
                                                            06-NOV 2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110 AA;
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                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                    09 AUG-2001.
                                                                                                                                                                                                                                                                                                                 MAY - 2000;
                              AAM69827;
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Matches
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0;

Gaps

0;

0; Indels

3.5%; Score 7; DB 22; Length 110;

Query Match 5.55; Best Local Similarity 100 0%; Prod No 28; Best Local Similarity 100 0%; Mismatches

Sedneuce

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173 LALAEKI. 179

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe. The probes may be used for predicting, measuring and displaying quene expression in samples derived from the human heart via microarrays, by measuring yene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hyperlension, cardiac arrhylmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein #4004 encoded by probe for measuring heart cell gene expression.
measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at ftp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                           Caps
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart, microarray, vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                         DB 22; Length 110;
                                                                                                                                                                                                           0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                             28;
                                                                                                                                                                       3.5%, Score 7, DB 2
100.0%; Pred. No. 28;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ 1D No 23775; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                               ABB22005 standard; Protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  congenital heart disease.
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488899/53.
                                                                                                                                                                                             Hest Local Similarity
Matches 7; Conserv
                                                                                                                         Sequence 110 AA;
                                                                                                                                                                                                                                               173 LALAEKL 179
                                                                                                                                                                                                                                                                               82 lalaekl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-Ang-2000;
21-SEP-2000;
27 SEP-2000;
04-OCY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 - MAY - 2000;
30 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15,
                                                                                                                                                                                                                                                                                                                                                                                                 ABB22005;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                    ABB22005
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The present invention provides a number of single exam murleis acid probes which are derived from genomic sequences expressed in the human train. They can be used to measure gene expression in brain cell samples, which may enable diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                           Human brain expressed single exon picke encoded profein SEQ 1D NO: 29537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sdeo
                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                          AAM57432 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the probes of the invention.
                                                                                                                                                                                                                                                                                                                         2000US-0207456
                                                                                                                                                                                                                                                                                                                                     2000008-0608408
                                                                                                                                                                                                                                                                                                                                                   200008-0632366.
200008-0234687.
                                                                                                                                                                                                                                                                                                                                                                               2000TIS-0236259
                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                           2000034-0024263
                                                                                  05-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                    epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 LALAEKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2C0157275-A2.
                                                                                                                                                                                                Homc sapiens
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27 SEP-2000;
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                                                       AAM57432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brains
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           AAM57432
RESULT
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Conservative
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                                                                                                                                                                                                                         Local Similarity
les 7; Conserv
                                                                                                                                                                                   Sequence 110 AA;
                                                                                                                                                                                                                                                       173 LALAEKL 179
                                                                                                                                                                                                                                                                  WO200157277-A2
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                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 - SED
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د
                                                                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                              Peptide #4107 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for measuring gene expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially addressable set of single exon nucleic acid probes.
                                                        Producting human antibody polypoptide dimer specific for antigen comprises use of chain shuffling using phane expression, useful for reducing anti-globulin responses in humans for increased human characteristics.
                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exem probe; gene expression; breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maim 27; SEQ ID NO 14424: 327pp · sequence listing, English.
                                                                                                                                                                characteristics, preventing anti-globalin response in humans.
                                                                                                                                  which may be used as part of a method of producing chimeric mouse-human antibodies or fragments which have the same binding specificity as a parent Ab but have increased human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast, comprises number of single exem nucleic acid probes
                                                                                                                                                                                                                DB 14; Tength 89;
23;
                                                                                                                                                                                                                                   0; indets
                                                                                                                           The sequence is that of the DP-74 VBl qene heavy chain
                    Jespers LSAT, Winter GF;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                        Prod. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W, Rank DR:
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                                                                                                      Example: Fig 11: 109pp: English.
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(MEDI ) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 JAN 2001; 2001WO USOO662.
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2000ES-0207456.
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                    Baier M. Hoodenboom IRJM,
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                     Query Match
Rest Local Similarity
7: Conserva
                                     WPI: 1993 117534/14.
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                                                                                                                                                                                                                                                                                                                                                                                                            disease; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Wo200157271-A2
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27 SPP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUN - 2000;
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                                                                                                                                                                                    Sequence
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ABB 41456
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nucleic acid probes for measuring gene expression in a sample derived from human breast and HT 474 cells. The method involves contacting the probes with a collection of detectably labelled nowless contacting derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA producted to encode proteins. They are useful for gene discovery, and for expression analysis is useful for assessing the toxicity of chemical agents on earlist the microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
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liver. The single exon nucleic acid probes may be used for predicting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_prt_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   than expressed sequence tag microallays. The method is suitable for rapid production of functional information from genemic sequence. Il
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe of the invention.
Note: The sequence data for this patent did not form part of the
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analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #4174 encoded by human foetal liver single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 110;
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ative 0; Mismatches
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00.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB36668 standard; Peptide: 110 AA.
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200005-0207456.
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2000US 0234687.
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Fang YT, Liu C, Drmanac RT;

2001-514838/56.

N-PSDB; AAI81101

26-FEB-2001; 2001WO-US04927

28-FEB-2000; 2000US-0515126 18:MAY-2000; 2000US-0577409

(HYSE-) HYSEQ INC

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                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
          Peptide #8214 encoded by probe for measuring placental gene expression
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                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for
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                               Probe: microarray, human, placenta; antenatal diagnosis,
                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human placenta .
                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ 1D No 34446; 654pp; English.
                                                                                                                                                                                                                                                                   Rank DR,
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26-MAY-2000; 2000US-0207456
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2000US-0234687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 AA;
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                                             genetic disorder
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                                                                    Homo sapiens.
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27 - SEP - 2000;
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The invention relates to human polynucleotides (AA17941-AA193841) and the encoded proteins (AA0000019-AA014910) that exhibit activity elating to cytokine, cell proliteration or cell differentiation or which may induce
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                                                                                                                                                                                    production of other evickines in other cell populations. The production of other evickines in other cell populations. The polyguclectides and polypeptides have useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytickine like activities, e.g. stem coil growth factor activity, hacmatopolesis regulating
                                                                                                                                                                                                                                                                    activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. Leukaemia, inflammation and immune
                                                                                   Claim 20: SEQ ID NO 15062; 1344pp + Sequence Listing, English.
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chimeric; mouse-human antibodies; antibody; prevention
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91GB-0020377.
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Rost Loral Similarity Tun.
Post Loral 7; Conservative
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15 - MAY-1992;
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Mismatches
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100.0%;
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2000US-0608408.
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2000US-0234687.
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Dest Local Similarity 100.v
See 7, Conservative
  Conservative
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                                                   4 ggeekig 10
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                   filman brain expressed single exon probe encoded protein SEQ ID NO: 33384.
          tetal liver. The present sequence is a poptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pet_sequences.
measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exen nucleic acid probes for analyzing gere expression in human
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microstray; Alzheimer's disease; multiple seleresis; schizophrenia;
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00.0%; Pred, No. 9.7;
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100.0%; Pre-
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2000US-0234687.
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Matches 7: Conservative
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Best Local Similarity
                                                                                        16 AA :
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21-SEP-2000;
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Sales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SdF()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human: bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukacmia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed probe encoded protein SEQ ID No: 34308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U: Indels
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: Pred. No. 9.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                         AAM74002 standard; Proteir; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-0CT-2001 (first entry)
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gyrase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB40457;
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                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   ABB40457
                                                                                                                                                                                                                                                                                                                                                                                                                                         proparation of the recombinant breast cancer anilgen, BRCAL, binding proteins BARDI, B123, BE2, BE14, BE31 or BE445, or a composition for the detection of a BARDI, B123, BE2, BE14, BE31 or BE455 cucleic acid sequence, specifically a wild type HARDI composition for the detection or purification of HRCAL, useful to identify a patient having, or at risk of developing cancer. BARDI can be used in the preparation of an anti-BARDI antibody, and in the detection and purification of a BRCAL forthein BARDI, B123, BE2, BE14, BE31 or BE445 can used in the identification of a binding protein agonist or antagonist that alters the binding of HARDI, H23, H22, BE14, BE31 or BE445 to BRCAL or the binding of HARDI, H23, H22, BE14, BE31 or BE445 to BRCAL or the binding activity of the HRCAL HARDI, B123, BE2, BE14, BE31 or BE445 to BRCAL or the BE11 or BE445, a specific anti-BARDI antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                              DNA sequence encoding BARD1, B123, BR2, BR14, BE31 or BE445 - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification, detection, microbe, gyrase gene, gyrase protein.
                                                                                                                                                                         as breast cancer antiqen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 67; DB 19; Length 515; 100 0%; Pred No 1.7e-61; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        The sequence is that of a protein which can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 n%; Pred ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A gyrase protein of Chitinophaga pinensis.
                                                                                                                                                                                                                Disclusure, Page 287·288, 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY23793 standard; Protein; 220 AA.
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                        97HS-0042985.
                                                  97HS-0042611.
 97WO-US16842
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                                                                          (TEXA ) UNIV TEXAS SYSTEM.
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Matches 67; Conservative
                                     รีวีบุบ-รักษร
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinophage pinensis.
                                                                                                    Bowcock AM;
                                                                                                                            WPI; 1998-230317/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                            515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AELMEDE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 aclmede 488
                                                                                                                                         N-PSDB; AAV24135
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 19-SEP-1997;
                        04 - APR-1997;
                                        30 - SEP - 1 445 ;
                                                  03-APP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                    Baer R,
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measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                     detection of a microbe, using the gyrase gene as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then identified or detected depending on its base sequence. The method can be used to classify and identified anionobe strain rapidly and with high precision. The present sequence represents a gyrase protein.
                                                                                                                                                                                 Identification and detection of a microbe - by detection of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #7963 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                               The specification describes a method for the identification or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 33092; 639pp + sequence listing; English.
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100.0%; Pred No. 4.8
tive 0, Mismatches
(MARI-) MARINE BIGTECHNOLOGY INST CO LTD. (KAIY-) KAIYO BIGTECHNOLOGY KENKYUSHO KK.
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                                                                                                                                                                                                                                                                            Example 3; Page 14-15; 42pp; Japanese.
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2000US-0234687.
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Matches 8, Conservative
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                                                                                           WFT; 1999-422615/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AA;
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                                                                                                                           N-PSDB; AAX86000
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1917 - tMI: HITTIIII | HITTIIII | HITTIIII | HITTIIII | HITTIIII | HITTIIII | HITTIII | HITTIIII | HITTIIIII | HITTIIII |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             New BAP2B polynnelectides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumers, e.g. by hybridization or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AFFDSENDPERMALLQFILIQFILINGLYKLFLFDTQHFLSKERAXALMMPLVDQLFNRLGGBFK 120
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                                                                           Rouqueleret L. Chumakov I. Cohen Akenine A;
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Pred. No. 3.46 199,
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The present invention describes primer sets its synthesising 5602 till-length cubas defined in the specification. Where a primer set completentiess, dals an oligo-dl primer and an oligonociocitde complementary to the completentiates and an oligonociocitde complementary strain of a polynociocitde comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strain of a sequence complementary to the complementary strain of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the first set in the primer sets, can be used in anisense therapy and if gene therapy. The primers are also useful for the primers of the full-length connex. The primers are also useful for the full-length connex. The primers are also useful for the full-length connex. The primers are also useful for the full-length without any specialization of the full-length connex. The primers are also useful for the full-length connex. The primers are also useful for the full-length connex. The primers are also useful for the full-length connex. The primers and and/or diagnosis of the abnormaling of the full-length connex and a con
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                                                                                                                                                                                                                                                                       full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602
                                                                                                               Yamamoto .1;
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                                                                                                            Saito K, Ya
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100.0%; Pred. No. 3.1e-96;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEy ID 11159; 2537pp + CD ROM; English.
                                                                                                         Hayashi K, Sa
I A, Nagai K,
                                                                                                                                   Sugiyama T, Wakamatsu A,
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                                                                                                            Nishikawa T,
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09-JUN-2000; 2000JP-0241899
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                                                    (HELI-) HELIX RES INST.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Etd.

OM protein - protein search, using sw model

July 2, 2002, 16:06:03; Search time 117.59 Seconds (without alignments) 189.862 Million cell updates/sec Run on:

US-69-603-665 5_COPY_1917_2117 201 Title:

1 FKLFDWAKTEDAPKORLITE......NYIVILPESIPFLAELMEDE 201 Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapeat 65.0 Scoring table:

747574 seqs, 111073796 residues Searched:

Q Word size :

Total number of hits satisfying chosen parameters:

729

Minimum is seq length. 9 Maximum DB seq length: 2000000000

Post-processing. Listing first 45 summaries

Database :

1. /SIDSI/gcgdata/hold-yeneseqy-embl/AA1980.DAT:
2. /SIDSI/gcgdata/hold-yeneseqy-embl/AA1981.DAT:
3. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1981.DAT:
4. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1982.DAT:
4. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1983.DAT:
5. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1985.DAT:
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12. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:
13. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:
14. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.NAT:
15. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:
16. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1994.DAT:
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20. /SIDS /SIDSI/geydata/hold-genesey/geneseyp cmb//Aa1997 DAT:*/SIDSI/geydata/hold-genesey/genesegp cmb//Aa1998 DAT:*/SIDSI/geydata/hold-geneseygenesegp cmb//Aa1999 LDAT:*/SIDSI/geydata/hold-geneseyy/genesegp cmb//AA2000 DAT:*/SIDSI/geqdata/hold-genesey/genesegp cmb//AA2001 DAT:* A_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score discribution.

SUMMARIES

	Description	Protein encoded by	Human protein sequ	Homo sapiens BAP28	A gyrase protein o	Peptide #7963 enco	Homan brain expres	Human bone marrow	Peptide #8214 engo	Human ⊳olypeptide	Dp-74 VH1 gene hea	Peptide #4107 enco
	(1)	AAB85029	AAB927 19	AAW54039	AAY 237 +3	ABB404 57	AAM61279	AAM74002	~	AA001170	AAR34271	ABB31456
	gth DB	2144 22	349 22	515 19	220 20	36 22	36 22	36 22	36 22	83 22	89 14	110 22
p	Query Match Length DB			33.3	4.0	3.5	3.5	3.5	3.5	3.5	3.5	3.5
	Score	199	100	67	æ	7	7	7	7	7	7	7
	Result No.		C4	æ	4	S	٩	7	œ	6	10	11

Peptide #4174 enco Protein #4004 enco Hamas brain expres	one mar #4085	Peptide #3991 enco	Human immunoglobul	Mutant Aspergillus	A oryzae P7-14.1	Zea mays protein f		H. Pylori OPF 13go		Buman PNA uncoilin	Human cancer assoc	Human colon cancer	Membrane-bound pro	Human PRC189 (UND)	Drosophila melanog	Homo sapiens BAP15	Amino acid sequenc	Drosophila melanog	R vulgaris NIM1 h	Rice poly (A) bind	Homo sapiens BRCA1	Yeast HMG-CoA redu	Cytadhesin protein	Streptococcus pneu	Streptococcus pneu	Streptococcus pneu	he	Amphipathic helica
ABB36668 ABB22005 AAM57432	AAM17651	AAM10103 AAM05309	AAR66345	AAW37995	AAY 39876	AAC34112	AAW55542	AAW55442	AAB42597	AAG66797	AAB43736	AAG73794	AAY66633	AAB65156	ABB65309	AAW57571	AAY37663	ABB59537	AAB27324	AAE13001	AAW47538	AAR58611	AAP64927	AAY81512	AAU37719	AAU38105	AAW31645	AAW31644
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aea टिटन	15 16	18	19	21	55	23	24	i)	52	27	3.8	58	30	31	32	33	34	35	36	3.7	38	49	40	4.1	42	43	44	4.5

ALIGNMENTS

AAB85029 RESULT

AAB85029 standard; Protein; 2144 AA

AARBSULY;

06-AUG-2001 (first entry)

Protein encoded by BAP28 cDNA consisting of exons 1 to 45.

BAP28; prostate; tumodr; cancer; diagnostic, genetic analysis.

Homo sapiens.

Location/Qualifiers Misc-difference 1694

/label- Ser or Asn

/label- Ala or Val Misc-difference 1854

/label+ Asp or Asn Misc-difference 2017 Misc-difference 1967

W0200100669-A2

04-JAN-2001.

23 nJM-2(npp, 2ppnWo-1Holl83

25-IUN-1999; 99US-0141323. 18-JAN-2000; 2000US-0176880.

(CEST) GENSET.

0; 0; Gaps 0; Indels Ouery Match

8.5%; Score 7: DB 2: Leadth 56;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7: Conservative 0; Mismatches 0; Indels

131 NDCEEVG 137 11141.1 38 NDEEEVG 44 7.7 1.1b

Search completed: July 2, 2002, 16:18:30 Job time: 86.2 sec

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Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces
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Rhabditidae, Peloderinae, Caenolabditis.
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investigating biology. The C. elegans Sequencing Consortium.";
Sejence 282 2012-2018(1998)
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100.0%; Pred. No. 33;
Live 0; Mismatches 0; Indels
                                                                                                                                  Ouery Match 4.0%; Score 8: DB 4; Length 884; Best Local Similarity 100 0%, Pred No. 32, Marches 8, Conservative 0, Mismatches 9, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C. elegans cosmid KUBD10.",
Submitted (APR-1996) to the EMRL/GenBank/DDRT databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GeoRank/DDBJ databases.
EMBL: U55857; AAA98035 2; -.
EMBL: U70855: AAB09160.2; -.
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Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
                       Pfam; PF01805; Surp; 1.
SMART; SM00443; G-patch; 1.
SRQUENCE 884 AA; 100015 MW; 51BBFF371BA132D9 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE=99069614; PubMed-9851916;
    Pfam; PF01585, G patch; 1.
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262 LAALQKVV 209
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PIMS2.
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Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Flavobacterium.
NCBL Tax D-249;
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                                                                            MEDLINE-20547809; PubMed-11094342; Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martin J.F., Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martin J.F., complex multienzyme system encoded by five polykelide synthase ques is involved in the biosynthesis of the 26-membered polyene macrolide pimarroin in Streptomyres matalonsis "; chember Hinl 7-895-905(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evolutionary relationships among archaebacteria, eubacteria, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR 2: Length 9507;
3. 2.4c.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9507 AA; 994228 MW; 57HD80C8AD37E89F CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UN-1903 (TEMBLrel. 17, Last annotation update)
ALANYL-TRNA SYNTHETASE (FRAGMENT).
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0; Mismatches
                                                                                                                                                                                                                                                  EMBL, AJ278573; CAC20321.1; -.
HSSP; P25715; 1MLA.
Interpro: FPPn011227: Acyltransf_domain.
Interpro: IPR000794; Reloacyl:synt.
Interpro; IPR003880; Phosphopant_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS50075, ACP_DOMAIN, 6.
PPOSITE, PS00012, PHOSPHOPANTETHEINE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; Score 8;
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Pfam, PF01411; tRNA-synt_2c; 1.
Aminoacyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP00109; ketoacyl synt; 6.
Pfam: PP02801: ketoacyl synt.c. 6
Pfam: PP00550: pp-hinding: 6
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MFDLINE=99058143; PubMed=9841678;
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00698; Acyl_transf; 6.
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Matches 8; Conservative 0
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EMBL: AF130451; AAD33469.1;
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                                                          SEQUENCE FROM N.A.
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NCBI_TaxID 68242;
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                                                                                                                                                               SERGINE FROM N.A.
STRAIN ATCC 15692 / PAvil;
STRAIN ATCC 15692 / PAvil;
MEDLINE-2044737: pubmed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman E.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Coulter S.N., Folger F.P., Westbrock Madman S., Yuan Y., Brody E.L., Coulter S.N., Folger F.P., Mest D., Larbing K., Lim B.M., Smith K.A., Spender F.H., Weyd S.K.-S., Wu. Z., Paul sen T.T., Reiter J., Saier M.H., Hancock R.E.W., Lory S., Oleon M.V.; Predicte genome sequence of Pseudomonas acruginosa PAOI, an
"The cloAB genes from Pseudomonas aeruginosa code for a novel cyanide-
insensitive terminal oxidase related to the cytochrome bd quinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-0EC-2001 (FFEMELE). 19, East sequence update)
01-0EC 2001 (FFEMELE). 19, Last annotation update)
01-0EC 2001 (FFEMELE). 19, Last annotation update)
FUTATIVE QUINOL WILDASE SUBUNIT I TRANSMEMBRANE PROTEIN.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Frotedadeteria, alpha subdivision; Rhizobiaceae group;
Rhizobiaceae, Shorthizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 AA: 54 )81 MW; F9FADF439B52AC31 CRC64;
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100.0%; Pred. No. 20;
tive 0; Mismatches
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EMBL: AE004810; AAG07.17.1;

InterPro: 1PR002585; Bac_Hbq_Cox.

Uniterpro: PR0554; Hac_Ubq_Cox: 1,

Complete professe, 5/235 MW; 30A
                                                                                                      Mol. Microbiol. 24:574-591(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.".
Nature 406:959-964(2000)
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Best Local Similarity
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Gaps
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Rose E., Feinstein M.B.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa, Nematoda, Chromadorea, Rhabditida: Rhabditoidea:
Rhabditidae; Peloderinae; Zaenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laplante J.M., O'Rourke F., Eu X., Fein A., Olsen A., Feinstein M. "Cloning of buman Ca2+ homceostasis endoplasmic reticulum protein (CHERP): regulated expression of antiseuse cDNA depletes (HERP, inhibits intracellular Ca2+ mobilization and decreases cell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. cleqans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.0%. Score 8; 108.5; Length 725; 100.0%; Pred. No. 27; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBark/UDBJ databases.
EMBL: ACM94703: AAL00865.11 -.
Hypothetical protein.
SEQUENCE: 725 AA: 82788 MW: 18D0466H4C9D0A35 CHC64;
                                                                                      095XA4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                              PRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99069613; PubMed-9351916;
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Interpro; IPR000061; Surp.
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                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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Les 8; Conserv
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Cunningham L., Pitt M., Williams H.D.;
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                                                             Gaps
                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria, Protenbacteria, alpha subdivision, Rhizobiaceae group.
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 8; DB 16; Length 453;
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                                      Length 343,
                                                               6; indels
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 343 AA; 36355 MW; F18ABCEAD31AD499 CRC64;
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01-N:OV-1998 (TrEMBLrel. 08, Last sequence update)
01-D:MC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                 01-0GT-2001 (TFEMBLER) 18, Created)
01-0GT-2001 (TFEMBLE) 18, Last sequence update)
01-0GT-2001 (TFEMBLE) 18, Last annotation update)
001NOL OXIDASE SUBUNIT 1.
                                      DB 2,
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                              453 AA.
                                      4.0%, Score 8, DB 2
100 0%, Pred No 15,
ative 0; Mismatches
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MEDLINE-20519422; PubMed-11064196;
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InterPro; IPR002585: Bac_Ubq.Cox.
Pfam; PF01654; Bac_Ubq_Cox: 1.
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                                        Query Match

Best Local Similarity 100 0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREILIMINARY:
                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                         STRAIN-MAFF303099;
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SEQUENCE 453 AA
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                                                                                                                  255 LLSALAAL 262
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                                                                                         4 1.1.SA1.AAI, 11
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=381;
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   SEQUENCE
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                                                                                                                                                                                           Q98DW1;
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MEDLINE-9703021: PubMed=8896557; Imbert G., Saudou F., Yvert G., Devys D., Trotlier Y., Garnier J.M., Weber G., Mandel J.L., Cancel G., Abbas N., Duerr A., Didlerjean O., Stevanin G., Adid Y., Brice A.; "Cloning of the gene for spinocerebellar ataxia 2 reveals a locus with high sensitivity to expanded CAC/glutamine repeats.", Nat. Genet. 14:285-291(1996).

BMBL, YOR2244, CAAA44591 1:
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                                                                                                                                                                                                                                      Gaps
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Sukaryotas Metazoos Chordatas Craniatas Vertebratas Enteleostomis
Mammalias Eutherias Primates, Gatarrhinis Hominidaes Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.0%; Score 8; DR 4; Length 469; 100.0%; Pred. No. 19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   u; Indels
FEMS. Microbiol. Lett. 192:205-210(2000).

EMBL, AF084032; AAC34673.1; -
InterPro; TPP002584; Bac_Thq_Cox.

Pfam; PF01564; Bac_Thq_Cox; 1

SEQUENCE 465 AA; 51445 MW; SOWERDEJFSA770410 PM764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 469 AA; 52531 MW; 690E29873AFD5BEE CRC64;
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19, Last annotation update)
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01-JUL-1997 (TrEMBLICEL. 04, Last sequence update)
01-DEC-2001 (TrEMBLICEL. 19, Last annotation update
                                                                                                                                                                                4.0%, Score 8, DB 2;
100.0%; Pred. No. 19;
tive 0; Mismalches
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STRAIN-ATCC 15692 / PA∩1;
MEDLINE-97323403; PubMed*9179851;
                                                                                                                                                             Guery Match
Best Local Similarity 100.00
8; Conservative
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Tremblie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
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Q94PH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                              White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haff D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffatt K.S., Oth H., Gang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Kettchum K.A., Nelson K.E., Salzberg S., Smith B.C., Venter T.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
Sukaryota Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Amphibia; Matrachia; Anura; Neobatrachia; Kanoidea: Ranidae; Rana.
NCHLIAXID-58174;
                                                                                                                               Barteria: Thermus/Definedaces group. Define occaies, Definedacus.
NCBL_iax(D-1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 8; DB 16; Length 123; 100.0%; Pred. No. 6.1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 8; DB 8; Length 300;
170.0%; Pred No. 13;
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MAY-2000 (TriMHLITE : 13, Last sequence update) MAR-2001 (TriMHLITE : 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-080-2001 (TrEMBLIGEL 19, Last sequence update) 01-080-2001 (TrEMBLIGEL 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
                                                                                                                                                                                                                                                        MEDLINE-20046896; PubMed 10567266;
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130.0%; Pr⊷
0,
                             01-MAR-2001 (ITEMHLIE 16, LA
HYPOTHETICAL 12.7 KDA PROTEIN.
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Mol. Ecol. 10:1499-1513(2061).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA: 12733 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571 1577(1999).
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                                                                                                         Deinococcus radiodurans.
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Best Local Similarity
Matches 8; Conserva:
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Best Local Similarity
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SEQUENCE
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210 LLSALAML 217

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RESULT

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MEDLINE-21306528, FubMed-11412371;
Bos D.H., Sites J.W. Jr.;
"Phylogewaraphy and conservation genetics of the Columbia Spotted Frod
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Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coclinolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBU; AL359949; CAB95810.1;
InterPro: IPR002197; HTH_Fis.
SMART; SM00421; HTH_LUXR: 1.
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                                                                                                                                            Eukaryota, Metazoa, Chordala, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anora: Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%, Score 8; DB 8; Length 300; 100.0%; Pred. No. 13; tive 0; Mismatches 0; Indels
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Submitted (JUN-2000) to the EMBL/Cenhark/UDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN A3(2):
Oliver K., Harris D.;
Submitted (JTH-2000) '-- the FMML/GLERFE,TEG JATEGASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AA; 33606 MW; 562A26BB7DHF5CA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-001-2000 (TrEMBLIEL, 15, Created)
01-001-2000 (TrEMBLIEL, 15, Last sequence update)
01-JUN-2001 (TrEMBLIEL, 17, Last annotation update)
                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
300 AA
PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
MEDLINE=97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                        (Rana luterventris).;
Mol. Ecol. 10:1499-1513(2001)
EMBL, AV016649; AAK54396.1
EMBL: AY016652; AAK54399.1
EMBL: AY016654; AAK54401.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                       CYTOCHROME B (FRAGMENT).
Rana luteiventris.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches 8; Conserv
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NON_TER 1
NON_TER 300
                                                                                                                            Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                   094PH4;
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OM protein - protein search, using sw model

July 2, 2002, 16-18-28 ; Swargh time 96 19 Seconds Run on:

(without alignments)
361.493 Million cell updates/sec

US-09-603-665-5_COPY_1754_1954

1 EVYLLISALAALQKVVETLIPH.....TFYNLADCIAEKLKGLETLF 201 Title: Perfect scote.

Sequence:

Scoring table:

Gapop 60.0 , Gapext 60.0

Selli seqs, 172394919 residens Searched.

9

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Total number of hits satisfying chosen parameters:

2002

Post-processing: Listing first 45 summaries

SPTREMBL_19:* Database :

sp_unclassified:* sp_human:* sp_invertebrate:* sp_mammal:* sp_vertebrate:* sp_organelle:* sp_phage:* sp_archea:*
sp_bacteria:*
sp_fung1:* sp_rvirus.* sp_rodent:* sp_plant:* sp_virus:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_archeap:

SUMMARIES

Dosoription	v96es5 homo sapien	Q9rxu9 deinococcus	Q950f5 rana luteiv	094ph4 rana luteiv	Q9k3yl streptomyce	Q98dwl rhizobium l	ORGORO rhodobacter	u99492 homo sapien	007440 pseudomonas	Q92s67 rhizobium m	<u>∩</u> 95xa4 rarnorhabdi	000302 homo sapien	Q21325 caenorhabdi	Q9ewal streptomyce	Q9x617 flavobacter	Ç9x618 cyt∪phaga a
3 E	L UYBESS	бихиф 91	3 Q950F5	3 Q94PH4	2 Q9K3Y1	16 098DW1	2 585680	1 099492	16 007440	16 092867	5 Q95XA4	1 0000102	5 021325	2 Q9EWA1	2 Q9X617	2 <u>0</u> 9x618
% Ouery Match Length DB	349 4	123	3008	300	343	453	465	469 4	488	493	725	884	895	9507	26	57
% Query Match	8.54	4.0	4.0	4.0	4.0	4.0	0.4	₹	4.0	4.0	4.0	0.4	4.0	4.0	3.5	3.5
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ឧយយយយ កំបស់កំបស់	പയയയയ പ്രസ്സ്സ്		သမ္မာတ္မင္း သိုင္းသည္ေတြကို	യയയയ വേടുമുന്ന	សសមមម សសមមម សសមមម
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# AL. I GNMENTS

162 MKKEELTSHÖSGLTAPPLEALDPRAQHSENDLEEVGKTENCI DCLVAMVVKLSEVTFRP 161 0; Gaps 49 8%; Score 100; DB 4; Length 349; Indels Pred. No. 1.2e-91; Mismatches 0: 100.0%; Pred. w. Ouery Match
Best Local Similarity 100.0
Matches 100; Conservative

6

01-MAY-2000 (TrEMBLrel, 13, Created) PRT; PRELIMINARY; Q9PXII9 Q9RXU9; RESULT 2 Q9RXU9 AC AC

123 AA

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O
                                                                                                                                                                                                                            Additional Boundary Management S., Artiquenave E., Gouzy J., Mangemot S., Aniat M., Hillault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunace S., Demanqe N., Gaspin C., Lavie M., Noisan A., Roberl C., Saurir W., Schiek T., Siquier P., Thebault F., Whalen M., Wincker P., Levy M., Merissenhach J., Houcher C.A., Girnome Sequence C.A., Girlon M., Borner C.A., Sibhit H., Schiek T., Sibhit ted (DEC 2001) to the EMBL/Greskerk/Publ databases.

I FUNTION: MAY BE INVOLVED IN SYNTHESIS OF N.
ANERYLFEIDEOXYGALACIOSE, A CHANDENEN OF EXOFILYSACHARIDE EPS I WHICH FUNCIONS AS A VIPULENE FATOR (By SIRIJATIVE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAFALYIE ATIVITY: UDP-N-acetyl-D-glucosamine - UDP-N-acetyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: EXOPOLYSACCHARIDE EPS I SYNTHESIS.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE UDP-N ACETYLGLOPOSAMINE 2-EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of the eps gene cluster of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-00T 1996 (Rel. 44, Greated)
Ol MAK 2002 (Rel. 41, Jast Sequence update)
Ol MAK-2002 (Rel. 41, Jast annotation update)
Probable UDP accepy(qlucosamine 2-epimerase (RC 5.1.3.14) (UDP-
                  Probable UDP'N acetylqincosamine 2 epimerase (EC 5.1.3.14) (HDP
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Barteria: Proteobarteria: Deta subdizision: Ralstonia group:
                                                                                                                Bacteria: Profeobacteria: beta subdivision, Balstonia group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lenath 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Shortening 175 AA: 40959 MW: A9BEH435602B2AH0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipopolysammharide Ninsynthesis, Tsumerase, Plasmid;
                                                                             Ralstonia solanacearum (Pseudomonas solanacearum).
MAR 2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Matches 7: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%; Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AL646082; CAD18168.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 96059643; PubMed-7476194;
                                                        EPSC OR RSP1017 OR RS02355.
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                                                                                                 Piasmid megaplasmid.
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                                                                                                                                                        N'BI TaxID- (05;
                                                                                                                                                                                                                      SIRA:N-CM:1000;
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P52641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-AW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                              UDP N deetyl D
                                                                                                                                                                     -i- PATHWAY: EXOPOLYSACCHARIDE EPS I SYNTHESIS.
-i- SUBCELLULAR LOCATION: Syloplasmic.
-i- SIMILARITY: BELANGS TO THE UDP-N ACETYLGLUC SAMINE 2 EPIMEMASE
                                                           FUNCTION: MAY BE INVOLVED IN SYNTHESIS OF N
ACETYLTRIDEOXYGALACTOSE, A COMPONENT OF EXOPOLYSACCHARIDE EPS
WHICH PUNCTIONS AS A VIRULENCE FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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solanacearum and its transcriptional regulation at a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%; Score 7; DH 1; Length 375; 100.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipopolysaccharide biosynthesis; Isomerase.
SEQUENCE 375 AA: 40944 HW; B07B54DAC90F7889 CRC64;
                                                                                                                           CATALYTIC ACTIVITY: UDP:N acetyl D glucosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Hest Local Similarity 100.0%; Pred. No. 20:
T. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July 2, 2002, 16:19:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U17898; AAA91626.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003331; Epimerase_2.
                                      Microbiol, 16:977-989(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02350; Epimerase_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 FLATTEA 105
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                    promoter.
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Matches
PIAP_PIG
                                                          SOLD STANKING STANKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modited and this statement is not removed Usage by and for commercial entities requires a license agreement (See http.//www.isb·sib.ch/announcc/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           Randin I -0', chohert J.-M., Haertle I.; "Molecular cloning of oliactory receptor-like mRNAs expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBSCELLUTAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: EXPRESSED IN THE TONGUE.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED PECEPTORS
                                                                                                                                                                                                                              Eukaryola; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LINKED (GLONAC. ..) (POTENTIAL).
ECE506FBBC962A82 CRC64;
                                                                                                                                                                 Olfactory receptor 802 (Olfactory receptor like protein JCC2).
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InterPro; IPR000276; GPCR_Rhadpsn.
PFIME; PF00001; 7tm_1; 1,
PRINE; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
G-PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLUIAP (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                    16-0CT-2001 (Rel. 40, Last annotation update)
                                                                 311 AA
                                                                                                      [b-ccr-2001 (Rel. 40, Created)
16-ccr-2001 (Rel. 40, Last sequence update)
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                                                                 STANDARD;
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139
158
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195
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272
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                   OBD2_HUMAN
Q9G2M6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                       Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                          MEDLINE-98162622; PubMed-9501011;
Stahlik C , da Martin P , Binder R P , Lipp J.;
"Cytokine induced expression of porcine inhibitor of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,5%; Score 7; DH 1; Length 35%;
100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                            EB2268FA9A6190A4 CRC64;
                    062640;
15-DEC-1998 (Rel. 37, Created)
1-DEC-1998 (Rel. 37, Last sequence update)
16-cvrp-zöül (Gel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. w..
358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPOSITE; PSGAGOG, CAPD; 1.
PROSITE; PSGO518; ZE_RING_1, FALSE_NEG.
PROSITE; PS50089; ZE_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIR 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01282; BIR_REPEAT_1; 2. PROSITE; PS50143; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARD.
                                                                                               Putative inhibitor of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis, Zinc-finger, Repeat.
REPEAT 4 70 P. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U79142; AAC39171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00097; Z1-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01315; CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPPOO1370; RIR
  S'FANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00238; BIR; 2.
SM00114; CARD; 1.
SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00653; BIR; 2.
Pfam; PF00619; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q13490; 1QBH.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KDRLL/IF 183
                                                                                                                                         Sus scrofa (Piq).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KDRLLTF 11
                                                                                                                                                                                                 NCBI_TaxID-9823;
                                                                                                                                                                                                                                                             TISSUE-Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPC1_RALSO
P58600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
PIAP_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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0; Gaps

0; Indels

100.0%; Pred. w...

Best Local Similarity 100.0 Matches 7; Conservative

Ouery Match

207 TLATTLA 213

59 TLATTLA 65

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or send an email to license eisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08.776;
15.0PC-1998 (Rel. 37, Itast sequence update)
15.0EC-1998 (Rel. 37, Last sequence update)
16-0C1-2001 (Rel. 40, Last annotation update)
Purine nucleoside phosphorylase (ET 2.4.2.1) (Inosine phosphorylase)
                                                                                                                                                                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                     Length 217;
                                                                                                                                                                                                                                                                                                                                   e, indels
                                                                                                                      High Arolits : Hypothetical protein: Transmembranes Complete proteome.
                                                                                                                                                                                                                                                       9E148F0F726777E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spirochaetales: Spirochaetageae; Treponema
                                                                                                                                                                                                                                                                                                  DB 1;
5. 17;
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                                                                                                                                                                                                                                                                                                               Pred. No. 17;
                                                                                                                                                                                                                      POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                     2 (847 MW;
                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                           EMISL: AE001094: AAB91:64.1;
                                                                                                                                                                                                                                                                                                     1,54
                                                                                                                                                                                                                                                                                                                                   Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                       94
131
174
216
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               4 LISAIAA ID
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or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCIENCE 281-375 SHR(1998)
-: FUNCTION: CLEAVAGE OF GIANDSINE OR INDSINE TO RESPECTIVE BASES AND
                                                                                                                                                                                                                                                                                                          Fraser C.M., Norris S.L., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzherg S., Perteron T., Khalak H., Richardson D., Howell J.K., Chidamharam M., Hiterback T., McMondald L., Artiach P., Bowman C., Colton M.D., Fulis C., Garland S., Hatch H., Horst R., Roborts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT HOMOBEXAMER (BY SIMILARITY).
SIMILARITY RELOAGS TO THE PUPZHOP FAMILY I OF PHOSPHORYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i. CAJALYTIC ACTIVITY: Purine nucleoside + phosphate - purine +
alpha D-ribose 1-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGAR | PROSPHATE MOLECULES (BY SIMILARILY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spirochete.";
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AE001245; AAC45702.1: -.

P09743; 1A69.

TP0734:

MEDI, LNE-98332770; PubM-d-9665876;

SECUENCE FROM N.A.

STRAIN-NICHOLS;

N'B1_1ax1D=160;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires atacement is not remered. Usage by and for commercial of send an email to license agreement (see http://www.isb-sib.ch/announce/of send an email to license@isb sib.ch).
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                                                                                                                                                                                                                                                                                                                  Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CAIALYTIC ACTIVITY: Hydrolysis of DNA containing thus-opened N7 mmethylydunine residues, releasing 2,6-diamino 4 hydroxy-5 (N methyl)lormanidopyrimide.
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam L.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: THIS ENZYME PAY A SIGNIFICANT FOLE IN PROCESSES IEADING TO RECOVERY FROM MUTAGENESIS AND/OR CELL DEATH BY ALKYLAFING AGENTS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                              ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, camma subdivision, Pastenrellaecae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 oct 2001 (kel. 40, last sequence update)
01-MAR 2002 (kel. 41, last annotation update)
Formamidopyrimidine-DNA qlycosylase (EC 3.2.2.2) (Tapy DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 7; EB 1; Length, 270; 100.0%; Pred. No. 21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Length 233;
                                                                                                                                                                                                                                                                                                           0; Indels
InterPro; IPR000845; PNP_UDP.
Plam; PP01048; PNP_UDP_1; 1.
PPOSTIE; PS01232; PNP_UDP_1; 1.
Transferase, Slycosyltrans Perase; Complete proteome.
SROURNCE 233 AA; 25318 MW; D1A9448787444A23 CR044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30612 MA: B44C3BDFDD968734 CRC64;
                                                                                                                                                                                                                                        3.5% Score 7; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA
                                                                                                                                                                                                                                                                        Pred. No. 18;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE FPG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AE006155; AAK03229.1; 'quyco.
Interpro; IPR000191; Fapy_DNA_qlyco.
Interpro; IPR00214; Fapy_DNAglyco_Tn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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PROSITE; PS01242; FPG; 1.
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                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                    7; Conservative
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nes 7; Conservative
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                                                                                                                                                                                                                                                                        Best Local Similarity
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Archaeoglobus fulgidus.
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                                                                                                                                                                                                                                                                                                                           56
168
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                                                                                           REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus.
                          SYNTHESIS.
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030065;
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DNA_BIND
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb·sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, RCSB IS A MEMHER OF THE TWO COMPONENT RECULATORY SYSTEM, RCSB/RCSC, WHICH REGULATES THE EXPERSION OF GENERS INVOLVED IN COLANIC ACID CAPSULE SYNTHESIS. RCSB ACTS AS THE EFFECTOR. ALDITIONAL CONTROL IS PROVIDED BY THE DEPENDENCE ON THE ALTERNATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kyan E., Sun H., Florca L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
-i- FUNCTION: ALSO STIMULATES FISZ EXPRESSION. THIS SUGGEST THAT RCSB IS A REGULATOR IMPLICATED IN THE REGULATION OF MORE THAN ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                             CELLULAR FUNCTION (BY SIMILARITY).
!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                        Sensory transduction; Phosphorylation, Transcription regulation;
DNA-binding; Activator; Complete proteome.
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H-T-H MOTIF (BY SIMILARITY).
; D35CE2AH2P1DCOE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 7; DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                  -! SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                    PESPONSE PEGHLATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P58663;
01-MAR-2002 (Rel. 41, Greated)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 17;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capsular synthesis regulator component B.
                                                                                                                                                                                                                                                                                                                              PROSITE, PS00622; HTH_LUXE_FAMILY: 1
PROSITE, PS50110; RESPONSE_REGULATORY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-LT2 / SGSC1412 / ALCC 705720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                            EMBL: A600683; BAA19163.1; -.
EMBL: AL627274; -.
EMBC: PROFIC: IPRO00792; HTHL LuxR.
InterPro; IPRO01789; Response_reg.
                                                                                                                                                                                                                                                                            Pfam, PFGU072, response_reg, l. PRINTS, PRODO38, HTHLUXR.
SMART; SMO0421; HTHLUXR: l.
                                                                                                                                                                                                                                                                                                                                                                                                                         23728 MW;
                                                                                                                                                                                                 EMBL; X87830; CAA61094.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                 Pfam; PF00196; GerE; 1.
                                                                                                                                                                                                                                                                                                                                                                                     1.24
                                                                                                                                                                                                                                                                                                                                                                                                                         216 AA;
                                                                                                                                                                                                                                                                                                                    SMART; SMOG448; KEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                        REGULATORS.
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DNA_BIND
SEQUENCE
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SIGMA FACTOR, RPON, FOR THE SYNTHESTS OF BOSB. ROSA AND ROSB FORMA COMPLEX TO PROMOTE TRANSCRIPTION OF THE GENES FOR CAPSULE
                                                                                                                                    FUNCTION: ALSO STIMULATES FTSZ EXPRESSION. THIS SUGGEST THAT ROSB
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                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                            IS A RECOLATOR IMPLICATED IN THE REGULATION OF MORE THAN ONE CELLULAR FUNCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     StyGene: 8G27277; rcsB.
PROSITE; PSGGGZ2; HTH_LUXP_FAMILY; 1
PROSITE; PSGGGZ2; HTH_LUXP_FAMILY; 1.
PROSITE; PSGGILD; PHOSPHORY; 1.
SCHSOTY; transduction; Phosphorylation; Transcription regulation;
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H-T-H MOTIF (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%, Score 7, DB 1, Length 216,
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16-00f-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE008801; AAL21171.1; -.
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"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                   MEDEINE-21074935; PubMed-11296551;
Berna N.T., Plunkett G. III. Burthand V., Man B., Glasner J.D.,
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fostai G., Hackett J., Klink S., Houtin A., Shao Y., Miller L.,
Arotheck E.J., Davis h.W., Gim A., Dimalanta E.F., Potamousis K.,
Apodara J., Anantharama F.S., Lin J., Yen G., Schwartz D.G.,
Welch R.A., Blattner F.R.,
                                                                                                  Itoh T., Aiba H., Babi T., Fujita K., Hayashi K., Inada T., Roboo K., Kasai H., Kimura S., Kilakawa M., Kiraqawa M., Kisaqawa M., Kisaqawa M., Kadawa K., Makino K., Makin T., Mizaburhi K., Mori H., Moremira K., Nakado S., Nakamura Y., Oshima I., Saito N., Sampel G., Seki Y., Sivasundaram S., Iaqami H., Iakeda J., Takamuro K., Wadana C., Yamamorto Y., Horinchi T.; A. 460 kb DNA sequence of the Escherichia coli K-12 qenome corresponding to the 40.1-50.0 min region on the linkage map.";
Davis N.W. Kirkpatrick H.A., Obedon M.A., Poso D.J.,
                          "The complete genome sequence of Escherichia col: K-12.";
                                                                                                                                                                                                                                        STRAIN 0157:87 / EDL9 4 / ACC 700927;
                                                                                    MEDILINE-97251458; Pabhod-9097040;
                                       Science 277:1453 1474 [1997]
                                                                                                                                                                                                    4:479 492(1956).
                                                                                                                                                                                                                                                                                                                                                          Nature 409:529 533(2001).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                               SECUENCE FROM N.A.
             Mau B., Shao Y.;
                                                                                                                                                                                                    DNA Ress.
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SIRAN-CISTAN PRODUCTION OF SUBSTREET STREET STREET

- DNA RES. #11-22(2001).
  -1- FUNCTIONS RECENT S A MEMBER OF THE TWO-COMPONENT BESULATORY SYSTEM.
  FROM TIONS RECENT S A MEMBER OF THE TWO-COMPONENT BESULATORY SYSTEM.
  FROM FROM CONTROL SERVICES THE EXPRESSION OF GENES INVOLVED IN
  COLANIC ACTO CARGINE SYNTHESIS. FROM A THE ALIBENDENCE ON THE ALIBENATE
  SIGMA PACTOR. REPORT THE SYNTHESIS OF BESIS AND POSR POPM
  A COMPLEX TO PROMOTE TRANSCRIPTION OF THE GENES FOR CARSHIE SYNTHESIS
  - FUNCTION: ALSO STIMULATES FTSZ EXPRESSION. THIS SUGGEST THAT ROSH IS A REGULATOR IMPLICATED IN THE REGULATION OF MORE THAN ONE CELEULAR FUNCTION.
    - SIMILABILY RELONGS TO THE LUXB MURA FAMILY OF TEANSOFIPTIONAL PERMINATORS

SIMILARITY: CONTAINS | RESPONSE REGULATORY DOMAIN.

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Ecocone, EG10821, resB.
InterPro, 198000792, HFH_LuxR.
InterPro, 198001789; Response_reg.
                L11272; AAA24596.1;
AEUGU 410; AAC75277.1;
                                                                                     AE005453; AAG57352.1;
AE002560; BAB36529.1;
M28242: AAA24504.1;
                                                  D90850; BAA16000.1;
D90851; BAA16008.1;
                                                                                                                          JV0068: BVECCB
EMBL;
                                                    E.W.E.
                                                                    EMHIL
                                                                                                        EMBL;
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J., Churcher C., Mungall K.L., Bentley S.E., Holden M.T.G., Setaibia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R., Dowd L., White N., Farrar J., Fertwell T., Hamlin N., Hacke A., Hich T.H., Holroyd S., Javels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaota P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE A COMPONENT PERMITTION OF THE ACCORDONENT RECULATIONY SYSTEM, 1- FUNCTION RESEARCH AS A MEMBER OF THE TWO-COMPONENT RECULATIONS RESEARCH RECULATES THE EXPRESSION OF CENES INVOLVED IN COLANIC ACID CAPSULE SYNTHESIS. RCSB ACTS AS THE EFFECTOR. ADDITIONAL CONTROL IS PROVIDED BY THE DEPENDENCE ON THE ALTERNATE SIGMA FACTOR, RPON, FOR THE SYNTHESIS OF RCSB. RCSA AND RCSB FORM A COMPLEX TO PROMOTE TRANSCRIPTION OF THE GENES FOR CAUSULE SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Villogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.; *Characterization of the resA and resH genes from Salmonella typh:
resB through tviA is involved in regulation of Vi antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (TIB.",
                                                                                     PROSITE: PS00622: HTH_LUXK_FAMILY: 1.
PROSITE: PS50110: RESPONSE_RECULATIONY: 1.
Sensory transduction: Phosyhorylation: Transcription regulation;
DNA-binding: Activator; Complete Froteche.

DNA-binding: Activator; Complete Froteche.

RESPONSE REGULATORY:
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                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIF (BY SIMILARITY).
: A7RDIMDARDAF9689 CRC64;
                                                                                                                                                                                                                                                                           3.5%: Score 7; DB 1; Length 216; 100.0%; Pred. No. 17; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FER-1997) to the EMML/Genkank, EDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rcl. 35, Last sequence update)
01-MAR-2002 (Rcl. 41, Last annotation update)
Capsular synthesis regulator component B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-21534947; PubMed-11677608;
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                   Pfam; PF00072; response_rej; l.
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                                                                                                                                                                                                                      21h AA; ZANZO WW;
                                     PRINTS; PR00038; HTHLUXR.
SMAPT; SM00421; HTH_LUXR; 1.
SMART; SM00448; REC; 1.
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                                                                                                                                                                                                                                                                                            Local Similarity 100.
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                   187
Pfam; PF00196; GerE; L.
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056127;
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DNA_BIND
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                                                                                                                                                                                                                                                                            Query Match
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This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Hielnformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its order it is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license exterment (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; PP02652, Lactatc_perm; l.
Hypothetical protein, Transport, Transmembrane, Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts D., Allen E., Araujo R., Aparicio A., Chung F., Davis K., Duncan M., Rederspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
                          -:- FUNCTION: MAY PLAY A ROLE IN L-LACTATE TRANSPORT.
-:- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-:- SIMILARITY: BELONGS TO THE LLDP FAMILY OF TRANSPORTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, qamma subdivision, Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K 12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ivength 563,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E3B0983059B19B08 CRC64;
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16-67T-2061 (Rel. 40, Last annotation update)
Hypothetical protein ybaw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; Score 8, DB 1
100.0%; Pred. No. 3.9
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003804; Lactate_perm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59761 MW;
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                                                                                                                                                                                                                                                                                                                                                                 EMBL; 234043, CABOBOC2.1, ...
EMBL; 271928; CAA96486.1; -.
EMBL; 299121; CAB15424.1; -.
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of rosB and rosC from Escherichia coll 99.839.812 and examination of the role of the ros regulatory system in expression of group I capsular polysaccharides."; Unacteriol, 175:5384-5394(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed 9278503;
Blattere F.R., Plunket G. III, Bloch C.A., Perna N.T., Burland V., Filey M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "McsB and RcsC: a two-component regulator of capsule synthesis in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
Low E., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jayaratne P., Keenleyside W.J., Maclachlan P.R., Dodgson C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                SEQUENCE FROM N.A
STRAIN-KIZ / Wallo;
Hatada F., Chmori H., Qido Y., Tsuji M., Fukuda K.;
Submitted (OCT-1996) to the FMRI/GenRank,AndRI databases.
                                                                                                                                                                                                                                                                                                                                                                                          EBB3539149A37383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-2020 (Rel. 41, Last annotation update)
Capsular synthesis regulator component B.
PCSH OR P2217 OP X3476 OP PCS1106
                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 7; DB 1;
100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                       EcoConc; EG13251, ybaw.
Interpro; IPP040365; 4HBcoA_thioestrse.
Piam; PF03061: 4HBT; 1.
                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93374832; PubMed=8366025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDI.INE-90130299; PubMed-2404948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172:659-669(1990).
                                                                                                                                                                                                                                                                     EMBL; AE000150; AAC73546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          15088 MW;
                                                                                                                                                                                                                                                                                       EMBL; U82664; AAB40199.1; -. FMRI; IM2943; RAA11647 1; -.
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Best Local Similarity 100.0
7; Conservative
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                                                                                                                                                                                                                                                                                                   Osada N., Hida M., Kusuda J., Tanuma R., Tseki K., Hirai M., Terao K.,
Suzuki Y., Surano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                        1 EVYLLSALAALQKVVETI PHFISPYFFAH SQVIHLFRITSFMCSASQANIPLTSL KO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maraca Lascicularis (Crab eating macaque) (Cynomolqus monkey).
Eukaryota, Metazca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria: Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                             49.8%; Score 100; DH 1; Length 2144; 100.0%; Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; Score 63; DH 1; Length 958; 1500.0%; Pred. No. 1.7e-55;
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                                                                                                                                                                                                                 0; Indels
                                                                           2144 AA: .42455 MW: D66816EE78D8C9B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT 2000) to the EMBL/GenPank/DPR databases *! SIMILARITY: BELONDS TO THE HAP28 FAMILY. *! SIMILARITY: ONDAINS 1 HEAT REPEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT 920 956 HEAT.
SEQUENCE 958 AA; 108644 MW; 108095036230EB31 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1814 ATTEAPRVELPAIKKTYKQIEKNWKNHMGPFMSILQEHIG 1853
                                                                                                                                                                                                                                                                                                                                                                                 61 ATTLAPRVILPAIKKTYKQIFKNWKNIIMOPFMSIIQEHIG 100
/FTIG-VAR_010941.
                                                 /FTId-VAR_010942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 oct 2001 (Rel. 40, Created)
16-oct 2001 (Rel. 40, Last sequence update)
16 oct 2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 AA
                                                                                                                                                                                                                 0; Mismatches
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PROSLIE: PS50077; HEAL_KEPFAL; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to licensegish sib.ch).
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                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein BAP28 (Fragment).
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                          2017 2013
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O9GM44;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by now profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www isb-sib-ch/announce, or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence analysis of the genome of the barterium My oplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Firmicutes, Raci.lus/Clostridium group; Mollicutes;
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N-ACYL DIGLYCERIDE (POTENTIAL).
AD2PCB2R826R1E9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Himmelreich R., Hilbert H. Plagens H., Pirkl E., Li H.-C.,
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100.0%; Pred. No. 4.7;
live 0; Mismatches 0; Indels
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                                                                                                                                                                           16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MPNO97 precursor (ROZ_orf541)
MNNO97 OR MPD67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000007; AAB95705.1; -.
Hypothetical protein, Lipoprotein; Membrane; Signal;
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SIMILAPITY: BFLONGS TO THE MC185 / MG260 FAMILY.
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16-OCT-2001 (Rel. 40, Last annotation update)
                                                 541 AA
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
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SEQUENCE 541 AA; 59153 NW;
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P71067:
                                             YA97_MYCPN
P75595;
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GenCore version 4.5
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fully 2, 2002, 16 19.06 , Search time to 19 seconds (without alignments) 257.788 Million ceil updates/sec Run en

US-09-603-665-5_COPY_1754_1954 Title: Periect score:

201 1 EVYLLSALAALQKVVETLPH Sequence:

TFYNLADCIAEKIKGLFTUF 201

105224 seqs, 38719550 residues Searched:

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Scoring table:

Word size :

Total number of hits satisfying chosen parameters.

463

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		o <del>x</del>			SOMMENTES	
Result		Query				
ડ્ર	Score	Match	Match Length	DB.	10	Description
-	100	49.8	2144	_	BP28_HUMAN	Q9h583 homo sapien
C	63	31.3	958	-	BP28_MACFA	_
3	æ	4٠	541	٦	YA97_MYCPN	_
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ц,	į.	3.5	132	٠.	Y BAW_PCOLI	P77712 escherichia
9	7	3.5	216	_	RCSH_BCOLL	F14374 escherichia
7	7	3.5	216	_	RCSB_SALT1	Q56127 salmoneila
œ	7	3.5	216	-	RCSB_SALTY	P58663 salmonella
6	7	in m	217		Y172_ARCFU	030065 archaeoglob
10	7	3.5	233	~4	DEOD_TREPA	o83716 treponema p
11	7	3.5	270	-	PPC_PASMU	P57910 pasteurella
12	۲۰	3.5	311	_	QBD2_HUMAN	
13	7	3,5	358	_	PIAP_PIG	-
14	7	3.5	375	٦	EPC1_RALSO	P58600 ralstonia s
15	7	3.5	375	П	EPC1_RALSO	P52641 ralstonia s
16	7	3.5	385	-	YB01_MYCTU	_
17	7	3.5	414		YOUH_BACSU	
18	1	3.5	440	-	T788_HURBU	OS1728 borrelia bu
19	7	3.5	476	_	MM10_RAT	P07152 rattus norv
0.7	**	33	478	-	NRFA_ECOLI	
21	7	3.5	484	П	AMYA_ASPNG	-
.C3	7	ω, 	537	_	CYDA_AZOVI	
53	7	3.5	550	-	MP10_XENLA	P30308 xenopus lae
24	7	3.5	550		MP 1.1_XENLA	P30309 xenopus lac
12.5	۲,	3.5	572	۲-	MP13_XENLA	P30311 xenopus lae
97	7	3.5	579	٦	HMDH_MAIZE	•
27	7	3.5	599	-	MPI2_XENLA	.,
38	7	3.5	709	-	OATB_HUMAN	044956 homo sapien
29	7	3.5	794	~	YH52_MYCPN	
30	7	3.5	883	-	CAPP_ECOLI	P00864 escherichia
3.3	7	3.5	096	_	L.136_CABEL	-
35	7	€1 ~	SCEET	-4	XAE6_SCHPO	
33	7	3.5	1434	-	PTC1_MOUSE	Q61115 mus musculu

090693 qallus qall	Q13635 homo sapien	O9tu23 bos taurus	O15078 homo sapien	Q12675 saccharomyc	P41188 buchnera ap	P48117 cyanophora	P34521 caencrhabdi	Pi8951 xenopus lae	P38952 xenopus lae	P44177 haemophilus	P05443 rhodopseudo
PTC1_CHICK	PTC1_HUMAN	Y373_BOVIN	Y373_HUMAN	ATC4_YEAST	RL7_BUCAP	PSAJ_CYAPA	YM45_CAEEL	XEN2_XENLA	XEN3_XIINLA	YEO2 HAEIN	YAT1_RHORL
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# ALLIGNMENTS

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	Z Y	Nishikawa	DEN .	, X	Sugar		Shira	ori A., Sudo H.,	
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EMPL: AX667160; CAC25476.1; EMBL; AL136105; CAC15948.1; EMBL; AX60121; BAA91564.1; A Interpret; PRSG0121; BAS91564.1; PPOSITE; PSSG0177; HEAT PEPEAT PEPEAT PEPEAT PEPEAT PEPEAT PEPEAT PEPEAT 11694.1694 VARIANT 1854.1854	Ü			1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1	
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A;Accession: A44909 A;Status: preliminary

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A; Wolecule Type: DNA
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A; Hetcerner number: A64720; Mulb: 97426617
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A; Melecule Lype: DNA
A; Restrimental source. Strain K 12, Substrain MG1655
A; Melecule Lype: DNA
A; Restrimental source. Strain K 12, Substrain MG1655
A; Melecule Lype: DNA
A; Respectives: GRAPEO Control of the two component regulatory system to the strain of the strain transcription requiation; two component regulatory protein comA; response regulator homology
C; Menerion: acts as the receiver of effector of the two component regulation; two ciseners of the strain transcription regulatory protein comA; response regulator protein comA; response regulatory protein
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Search completed: July 2, 2002, 16:15:39 Job time: 756 sec Gaps

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C. Accession: F68839

K. Kunst, F.; Gasawara, N.; Mozzer, I.; Alberthni, A.M.; Alloni, G.; Azevedo, V.; Herrick and C.; Bron, S.; Broullet, S.; Bluschi, C.V.; Caldwell, H.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabert, C.; Perrian, Nature 390, 249-256, 1997

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Cista 30-Jun-1991 **Sequence_revision 30-Jun-1991 **Lext_change 16-Jul-1999
Cista 170 Kish, A44909; G64991
Ristout, V.; Gottesman, S.
J. Hacteriol, 172, 659-669, 1990
J. Hacteriol, 172, 659-669, 1990
A;Reference number: JV0068; MUID:9499
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A.Experimental Source, Strain KI2
R.Gervais, F.G.; Phoenix, P., Drapeau, G.R.
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A.Title: The rest gene, a positive regulator of colonic acid biosynthesis in Escheric A.Reference number: A44909; MUID:92283751
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A;Cross-references: CB:299109; 28:AL009126; AED;q2634260; PERN:7AB12946.E; PEE.q26334
A;Experimental source: strain 158
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C;Species: Bacillus subtilis
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 20 Jun 2000
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N/Alternate names: regulator of capsule synthesis B component
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C;Superfamily: conserved hypothetical protein yit!
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A:Reterence number: A7245); MUID:99310339
A:Arcession: E724603
A:Status: preliminary
A:Molecule: Type: DNA
A:Residues: 1-142 *KAW*
A:Residues: 1-142 *KAW*
A:Coss references: DiBA:AP000061; NID:q5104821; PIDN:BAA80283.1; PID:d3044069; PID:g510
A:Expension: Strain K1
C:Generics:
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E.Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jettries, A.C.; Nelson, K.E.; Eisen, J.B.

E.Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jettries, A.C.; Nelson, K.E.; Eisen, J.B.

E.T.; H.; 910, H.; Vanarhovan, J.; 311, J.; Garlate, O.; Fleischmann, R.D.; Dougherty, B.A.; T.; H.; 910, H.; Vanarhovan, J.; 311, J.; Garlate, V.; Masignani, V.; Pitza, M.; Sortence 2H7, Hevellefs, 200

A.Aduthors: Grandly, G.; Smith, H.Ö.; Fraser, C.M.; Moxon, F.P.; Pappuoli, R.; Vanarather complete genome sequence on Neisseria merioditidis serogroup B strain MCSB.

A. Accession: GBL00

A. Accession: GBL00

A. Status: proliminary

A. Molecule Type: BNA

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C;Species: Neisseria meningitidis
C;Date: il-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 19 Jan 2001
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A:Gene: NMH1284
G:Superfamily: Neisseria meningitidis hypothetical protein NMA1454
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C.Superlamily: Neisseria meninaltidis hypothetical profein NMA1494
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R/Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin.no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A;Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
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A;Residues: 1132 -REGONTSO: CR:D00096; NID:g1786639; PIDN:AAC73546.1; PID:g17866
A;Experimental source: strain K-12, substrain M31655
                                                                ybaw protein - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12.58p-1997 #sequence_revision 17 Sep 1997 #text_change 24-Nov-1999
C;Date: 12.58p-1997 #sequence_revision 17 Sep 1997 #text_change 24-Nov-1999
C;Accession: C6477 Bunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Pitle: The complete genome sequence of Escherichia coli K-12.
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O
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C;Species: Aeropyrum pernix
C;bate: 26 Aug 1999 #se-qu-mee_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: P72603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: C64774
A;Status: nucleic acid sequence not shown; translation not shown
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100 0%, Pred. No. 27;
tive 0; Mismatches 0; Indels
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C,Superfamily: 15.5K protein (tolAB operon 5' region)
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C,Superfamily: 15.5K protein (tolAB operon 5' region)
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Best Local Similarity Tun.
Tr. Conservative
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A; Molecule type: DNA
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Cispecies: Ball-2001 Escherichia coii altore coi assawata, N.; Vasunaga, T.; Nuhara, S.; Shiba, T.; Hatio, K.; Vokoyama, K.; Han, C.B.
DNA Ros. B., 11-22, 2001
A.; Natara, N.; Vasunaga, T.; Nuhara, S.; Shiba, T.; Hattori, M.; Shinaqawa, H.
A.; Reletence number, A90629, MUID-21156231, PMID-11258796
A.; Reletence number, A90629, MUID-21156231, PMID-11258796
A.; Reletence number, A90629, MUID-21156231, PMID-11258796
A.; Reletence relations
A.; Reletence conduct cype: DNA
A.; Residuce: 1-132 - HAV
A.; Reletence coi altain ols7:H7, substrain RIMD 0509652
Cispections.
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C.Species: 15-0-+-1999 #sequence revision 15-0et-1999 #fext_change 15-0et-1999
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                                                                                                     4.0%; Score 8; DB 2; Length 875; milarity 100.0%; rred. No. 15; Conservative 0; Mismatches 0; Indels
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R;Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid K08D10.
A;Reference number: Z20616
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C,Superfamily: 15.5k protein (to!AB operon 5' region)
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A/Status, preliminary; translated from GB/EMBL/DDBJ
A; Introns: 97/3; 172/3; 837/2; 875/2
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A;Residues: 1-935 <GEI>
                                                                                                                                                                 Local Similarity
es 8; Conserv
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A: Notice: \$1Y0492

A; Genetic code: SGC3

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100.0%;
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C:Superfamily: L:Tactate permease
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Matches 8; Conservative
Query Match
Best Local Similarity
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                                                             Matches
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Mol. Microbiol. 24, 579-591, 1997
AZTILLE: The cloak genes from Pseudomonas aeruginosa code for a novel cyanide-insensitiv
A:Peterssion: 147273
A:Secusion: 147273
A:Status: preliminary: translated from GH/EMHL/DDBJ
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A.Residues: 1-488 ACTUN.
A.Cross retetences: EMBLY10528: NICHQ2089053; FIDNHOAA71555 1; PIDHQ2208964
A.Experimental source strain PANI, substrain PANA649
R.Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P., Hickey, M.G.; Br
adman, S.; Ynan, Y., Hrody, F.E., Coulter, S.N., Fulger, K.P., Kas, A., Laibig, K., Lin,
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Nucleir Arids Ros. 24, 4429-4445, 1994
Ariller Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A.Retorence number: 874827; MUID:97105885
A.Arcession: 873883
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A:Cross-reterences: EMBL:AE000007; GB:U00089; NID:q167:704; PIDN:AAB95705.1; PID:q167:37d
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
ArTitle: Complete genome sequence of Eseud-monas aeruainosa PAGL, an opportunistic pathol Artitle: Complete genome sequence number: ARZ-950, MOID:204-97-87
Arecession: 088155
Arsterus: preliminary
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C:Species: Mycoplasma paesmoniae
A:Varioty: AICC 29342
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                                                                                          Caps
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                                     Length 467;
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Cyspecies: Psendomenus asperimosa
                                   4.0%; Score 8; DB 2;
h00.0%; Prod. No. 8.3;
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log.0%; Pred. No. 8.6;
ive 0: Mismatches
                                                          100.0%; Prod. No. 8.3
tive U: Mismatches
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  grery Match
Bost Local Similarity 100.0
Ans 8: Conservative
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A:Residoes: 1 488 seto:
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C. Accession: A2.00.1.37 Segmental Electron of the C. Accession: A2.00.1.
C. Accession: A2.00.1.37 Segmental Electron of the C. Accession: A2.00.38
E. Kunst, F., Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alfoni, G.; Accedo, V.; Herrick, Brilleh, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 240-256, 1997
Nature 390, 250-2506, 1997
Nature 390, 250-2
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Apprenmental source: Strain 163
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submitted to the BMHL Data Library, September 1996
A.Bescription: The sequence of C. elegans cosmid KOBFIL.
A.Reterence number, 220723
A.Accession: T3002
A.Status: prefiminary; translated from GB/EMHL/DDHJ
A.Molecule type: DWE.
A.Fesidus: 1-875 cMIR>
A.Fesidus: 1-875 cMIR>
A.Cross-reterences: EMBL:U70855; PIDN:AAB09160.1: GSEDB:GN00922; GESF:KGBFIL.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A70038
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-lactate permease homolog yvIH - Bacillus subtilis
C.Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #:ext_::Lange 20 Jun 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C)Species: Gaenorhabdilis elegans
C)Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #:ext_change 15-Oct-1999
                                                                                                                          Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cabs
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Length 541;
                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0); Inde is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain Bristol N2; clone K08Fll C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 8; LB 2;
100.0%; Pred, No. 9.9;
Score 8; DB 2;
Pred. No. 9.5;
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                                                                                                        0; Mismatches
      Score 8;
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GenCore version 4 5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search using sw model

July 2, 2002, 16:15:38; Search time 57:09 Seconds Run on:

(without alignments) 338.307 Million cell updates/sec

US-09-603-665-5_COPY_1754_1954

TFYNLADCIAEKLKGLFTLF 201 1 EVYLLSALAALQKVVETLPH Perfect score:

001.10 Scoring table: Sequence:

Gapop 60 0 , Gapext 60

283138 seqs, 96089334 residues Searched:

9

Word Size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing. Listing first 45 summaries

PIR_71.* 1: pir1:* pir2:* pir3:* Database :

pir4:*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

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-	æ	4.0	123	C١	B75546	hypothetical prote
C+	Œ	·	16.7	C.	ACCS46	Ξ
٣.	80	4.0	488	C1	1.47273	cyanide insensitiv
4	80	4.0	541	2	873383	probable lipoprote
S	æ	4.0	563	~	A70038	
9	89	4.0	875	~	T30023	hypothetical prote
7	ထ	4.0	935	C1	T29390	hypothetical prote
90	7	3.5	132	7	A90691	hypothetical prote
5	7	3.5	132	7	C64774	ybaW protein - Esc
10	7	3.5	132	C I	E85541	hypothetical prote
11	7	3.5	132	೧೩	E72603	hypothetical prote
12	7	3.5	146	.71	HB1840	hypothet.real profe
13	7	3.5	146	(1	C81100	hypothetical prote
14	7	3.5	209	C4	F69839	conserved hypothet
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16	7	3.5	216	C4	D85861	hypothetical prote
17	7	3.5	216	۲,	AC0790	requiator of capsu
18	7	ر م	216	c.	P91017	rolanic arid biosy
19	7	3.5	217	C)	069271	hypothetical prote
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e ca	7	3.5	151	<b>C</b> 1	1187692	conserved hypothet
24	7	3.5	254	C 4	E64716	conserved hypothet
G)	7	3.5	276	C a	1.08859	hypothetical prote
95	Ļ	3.5	282	C1	A99205	hypothetical prote
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c4.dlcarboxylate-b	hypothetical prote	probable qlycesylt	apoptosis inhibito	alcohol dehydrogen	hypothetical profe	hypothetical profe	probable UDF-N-ace	acetoacetyl-CoA re	cytochrome P450 -	DNA-damage repair	hypothetical prote	hypothetical prote	coaserved hypothet	cytochrome d (bd-t	Chr diacylglycerol
698326	AG2956	вэ6008	JC5964	AE3184	\$19740	C70897	577637	JC7675	R75261	H69963	D84556	AI1906	C70198	F83759	A82337
324 2	324 2	347 2	58 2	72 2	376 2	85 2	<b>3</b> 96	97 2	2 60	414 1	17 2	427 2	440 3	443 2	146 2
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7	7	7	7	7	7	7	7	7	7	7		7	7	7	7

## ALIGNMENTS

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RESULT
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hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-Der_1999 #sequence_revision 03-Der-1999 #text_change 31-Mar-2000

C.Accession: 875546

K.White, C. Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D.: Dodson, R.J. M. Vanathevan, J.J.; Lam, P. Merbenald, E., Etterbark, T., Zalewski, C.; S. Smith, H. O.; Wanathevan, J.J.; Fraser, C.M.
S. Smith, H. O.; Vonter, J.C.; Fraser, C.M.
A.Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A.Fierence comber, A75250, MUTH, 29036896

A.Accession: B75546
A.Status: proliminary
A.Molecule Uype: DNA
A.Molecule Uype: DNA
A.Rosidues: 1 123 AMBIZ
A.Cross-references at B.AEGOLNRS, GB AEGOGIA, NID G645787M, Film AAROYBOLI; PID:q645
A.Experimental source, strain R1

C; Genetics:

A; Gene: DK0207

A; Map position: 1

Cabs .. Ç Length 123; global jū DB 2; Oucry Match 4.0%, Score 8, DB 2 Host Lucal Similarity (05.0%, Pred. No. 2.4 Matches 8, Conservation 0, Mismatches

4 LLSALAAL 11

Db

probable terminal exidase chain I [imported] - Salmonella enterica subsp. enterica se

C.Species: Salmone la entorica subspicingly. C.Species subspicingly. C.Species las also been called Salmone la typhical subspicingly. C.Species las also been called Salmone la typhical subspicingly. C.Species last subspicingly. C.Species last subspicingly. C.Species. Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Parry, S., Mouley, S., O'Gaora, P., Cannin, A., Davis, P., Davies, R.M., Skelton, J., Stevens, A. Authors: Parry, C., Quall, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, A. Alauthors: Parry, C., Quall, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, A. Anchorsina: AB0502; PMID:11677608
A. Anchorsina: Danger of a multiple disq resistant salmonella enterica se A. Anchorsina: pretiminary
A. Molecule type: DNA
A. Molecule type: D

0;

 Matches
 6;
 Conservative
 0;
 Mismatches
 0;
 Indels
 0;
 Gaps

 QY
 57 AKTEDA
 62
 11111
 11
 11
 10
 90 AKTEDA
 95

Scarch completed. July 2, 2002, 16-16-46 Job time: 823 sec

Caps

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: OTHER INPORMATION: Xaa equals any of the naturally occurring Leamino acids US-10-106-698-5708
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0: indets
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.0%; Score 6; DB 6; Length 92; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mishatches 0: indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPERFNOE/FOCKET NUMBER: UALE-03356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COKRESPONDENCE ALDRESS:
ADDRESSER: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/085,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/023,171
FILING DATE: 17-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                    PRIOR APPLICATION NUMBER: US 60/163,280 PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAMF: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Not Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-023-171-47; Sequence 47, Application US/10023171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weiner, Joel H. Turner, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEG ID NO: 47
  PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                     NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 KIEDAP 63
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23 KTEDAP 28
                                                                                                                   SEQ 1D NO 5708
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                                                                                                                                             LENCTH: 92
                                                                                                                                                                      TYPE: PRT
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               APPLICANT: Chen, Sel-Yi
APPLICANT: Liu, Chenchia
APPLICANT: Liu, Chenchia
APPLICANT: Liu, Chenchia
APPLICANT: Liu, Chenchia
APPLICANT: Luriber, Lean
IIILE OF INVENTION: Commosilions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0241
CHEREN APPLICATION UNGER: US/10/002 444A
CHEREN APPLICATION UNGER: US/10/002 444A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILLS OF INVENTIONS FOLOR and Folor Sameer Associated Polynocieotides and Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: FM328:11N
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6, DB 6, Length 73, Pred. No. 1.1e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 6; DB 6; Length 85;
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100.0%; Pred. no. -
ve 0; Mismatches
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CORRENT ARELITATION NUMBER - US/10/106,698
CURRENT FILING DATE: 2002-03/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: 95/10/137, 337 CURRENT FILLING DAIF: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCI/US00/26524
                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 69/242,698
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 277
SOFTWARE: Patentin version 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILLING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5708, Application US/10106698
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBEE: 60/180,628
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/758,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 730, Application US/10137337
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NUMBER OF SEQ ID NOS: 812
SOFTWARE: Patentin Vel. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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Sun, Yonqming
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US 10 137-337 730
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                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similārity
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US-10-106-698-5708
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US-10-137-337-730
                                                                                                                                                                                                                                                                                       SEC ID NO 241
LENGIH: 73
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ORCANISM: Saccharomyces cerevisiae

7 UK-ANISM. CACC. US-60-360-039-1836

: Sequence 1628, Application US/50350039; GENERAL INFORMATION:

0.8-60-360-0.39-1628

KESULT

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APPLICANT: Cao, Yongwei

APPLICANT:

APPLICANT:

Chen, Xianfeng Göldman, Barry S.

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APPLICAMT: ALEXANDROY, NICKOLAİ et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THRREBY
FILE REPRENCE: 2750-1068P
CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT APPLICATION NUMBER: 2000-07-21
SUMMER OF SEQ ID NOS: 9448
SOFTWARE: PAIPORIT VOFRION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE. DEX-0241
CUPPENT APPLICATION NUMBER: US/10/002,344A
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 50/242,998
PRIOR FILING DATE: 2000-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Ceres Seq. ID 1376826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 240, Application US/10002344A
US-09-620-3938-550
; Sequence 550, Application US/09620393B
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08:
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APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 277
                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..57
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US-10-002-344A-240
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Best Local Similarity
                                                GENERAL INFORMATION:
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42 DRLLTF 47
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LENGTH: 73
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LENGTH: 57
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TITLE OF INVENTION: POLYNOCLEOTIDE ENCORING MOVER HUMAN G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: SPLICE VARIANTS THEREOF
FILE REPERBACE: D0262 PSP
CURRENT APPLICATION NUMBER: US/60/386,336
CURRENT APPLICATION NUMBER: US/60/380,336
SOUPPHY FILLOR NOS: 465
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinkle, Gregory J.

APPLICANT: State, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PROJUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/60/360,039

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
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                                                                                             Query Match 3.5%; Score 7; DB 7; Length 1045; Best Loral Similarity 100.0%; Prod No. 1.19+02; Matches 7; Conservative 0; Mismatches 0, Indels
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Matches 6; Conservative 0; Mismatches
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; Sequence 395, Application US/60380336 ; GENERAL INFORMATION:

US-60-380-336-395

RESULT

ORGANISM: Homo sapiens

TYPE: PRT

SEQ ID NO 395

US-60-380-336-395

Query Match

21 EEVCKT 26 

q

RESULT 10

) ORGANISM; Saccharomyces cerevisiae US-60-360-039-1628

SEQ ID NO 1628

1612

TYPE: PRT ORGANISM:

Best Local Similarity 100 | Matches 7; Conservative

Query Match

68 LTFYNLA 74

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1045
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                                                                                                                                                                                                                            APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Bart, Ellzabeth A.
FITHE OF INVENTION: Diterpone-Producing Unicellular Organism
FITHE REFERENCE: PU2080US1/10025547
CURRENT FILLN: DATE: US/10/041,018
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLE OF INVENTION: Diterpene-Producing Unicellular Organism FILE REFERENCE: P02080USL/10025547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 7; DB 6; Length 1045; 100:0%; Pred; No. 1.1e+02; ive 0; Mismatches 0; Indels
                    Indels
Prod No 1.10.02;
Mismatches 0:
                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 809, Application US/10041018
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Selichi P.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // Sequence 264, Application US/10041018
// GENERAL INFORMATION:
                                                                                                                                                                                          Sequence 218, Application 68/10041018
GENERAL INFORMATION:
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; ORGANISM: Saccharomyces cerevisiae
US-10-041-018-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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100 08:
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SOFTWARE: Patentin version 3.1
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Best Local Similarity 190.6
The Conservative
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                7; Conservative
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Matches 7; Conserv
Best Lonal Similarity
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                                                      91 HLVKITA 97
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US-10-041 018 218
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APPLICANT: Chen, Xianteng
APPLICANT: Chen, Xianteng
APPLICANT: Gridman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C
TITLE OF INVENTION: EXPRESSION OF MICROHIAI DROTFINS IN DIANTS FOR PROPICING OF
TITLE OF INVENTION: PARTY WITH IMPROVED PROPERTIES
FILE PEPERPRICE: 34-10(5/2052)A
CUPPENT APPLICATION NUMBER- 115/60/360,039
CUPPENT APPLICATION NUMBER- 115/60/360,039
SUMMER OF SEQ ID NOS: 47374
SEQ ID NO 1836
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APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diferpene-Producing Unicellular Organism FILE REPERENCE: P020B0USI/10C25547
CURRENT APPLICATION NUMBER: 15/10/041,018
CURRENT FILING DATE: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.5%, Score 7; DH 6; Length 1045; Best Local Similarity 109.03; Pred. No. 1.1e{\cdot}02; Maiches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hart, Elizabeth A. TITLE OF INVENTION: Diterpend Producing Unicellular Organism FILE REPERENCE: POZUBUUS1/10025547
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.1.1e-02;
... 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/041,018 CURRENT FILLING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: US 60/259880
                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/259880 PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1836, Application HS/60360039; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 336, Application US/10041018
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ©FGANISM· Saccharomyces cerevisiae
US-10-041-018-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Matsuda, Selichi F.T.
                                                                                                                                                                                                   NUMBER OF SEG ID NOS: 413
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE, Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.9 Matches 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 HLVKPFA 16
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Copyright (c) 1993 · 2000 Compugen Ltd.
GenCore version 4 5
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OM protein - protein search, using sw model

July 2, 2002, 16:16:45; Search time 59 99 Seconds Run on:

(without alignments) 338.459 Million cell updates/sec

US-09-603-665-5_COPY_1867_2067

CIAQFSVAMADDSLWKPLNY 201 201 1 LTAFFLEALDFRAQHSENDL Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

307805 seqs, 101015595 residues Searched.

Word size :

254 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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No.	Score	Match	Length	E :		Description
	7		876	۲.	TIS-09-540-209B-7121	Sequence 7121, Ap
2	7	3.5	1045	9	199	199.
æ	7	3.5	1045	ع	US-10-041-018-218	218,
4	7	3.5	1045	ي	115-10-041-018-264	264,
5	7	3.5	1045	9	US-10-041-018-309	309,
ထ	7	3.5	1045	9	US-10-041-018-336	336,
7	7	3.5	1045	7	US-60-360-034-1836	1836
8	7	3.5	1612	7	118-60-360-039-1628	-
ş	ō.	3.0	9	7	US-60-380-336-395	395, 7
10	ų.	Ů K	57	Ľ:	US-09-620-3938-550	550,
11	9	3.0	73	ي	US-10-002-344A-240	240,
्ट	40	5.0	7.4	J	US 10-002-344A 241	241
13	9	3.0	85	œ	US-10-137-337-730	730.
14	9	3.0	92	w	US-10 106-698 9708	5708,
15	9	3.0	103	ç	US-10-023-171-47	47. A
16	ع	٠	103	æ	US-10-155-881-21465	
17	9	3.0	106	LC.	US-09-573-6558-460	
18	9	3.0	109	ur:	US-09-882-227 546	546,
19	÷	3.0	115	\$	US-10-041-018-211	211,
20	e	C **	115	œ	TS-10-041-018-351	351,
21	9	3.0	125	Ŋ	US-09-667-170A-59	26' 1
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£ 7	w	3.0	140	Ş	US-10-155 881 32557	Sequence 32557, A
24	٩	3.0	141	9	US-10-117-087-4	4
25	9	3.0	141	9	US-10-117-087-6	Sequence 6, Appli
y.*	Œ	<del>ر.</del>	169	7	US-60-365-384 255	C.1

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	ALIGNMENTS					
Sequence 7304, Ap	US-60-360-039-7304	/	50 50 30	3.0	۵	<b>4.</b>
Sequence 17388, ,	1	7	251		ا ب	44
Sequence 4546, A	US 60-360-039-4546	~	245	3.0	ا و	43
Sequence 9608, Ap	US-60-360-039-9608	7	244	3.0	9	۲. در د
	US-09-540 209B-6757	S)	236	9.0	۰ ي	4.
Sequence 5603, Ap	.60-360	7	231	9.0 8	ص	<b>4</b>
	US-10-155-881-22838	ç	558	3	٧	30
Sequence 32503,	US:10-155-881 32609	٧	C1 C1	3.0	Œ	æ.
Seguence 32580, A		ø	C1 C1	3.0	9	37
	155 881	w		3.0	9	36
	-881-	9	222	3.0	9	35
Sequence 105, App	HS-10-160-162-105	2	177	3.0	9	34
Sequence 410, App	US-09-882-227-410	רע	022	3.0	٥	33
sequence 5001, Ap	US+60+466 039+5a01		714	5.10	ټ	3.5
	US-10-155-881-10291	9	211	3.0	9	31
	US-09-573-6558-969	ľ	211	3.0	9	30
	US-60-365-384-579	7	202	3.0	φ	58
Sequence 62, Appl	23 VUU9-266 60-81	Ľ	50°	⊂ ,~.	Œ	8.3
Sequence 20767,	115-10-155-881-20767	œ	174	C ~	œ	27

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APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOF DIAGNOSTICS AND THERAPEUTICS
FILE EPEPERNCE 2709 1001-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
LENGIH, 876
LENGIH, 876
                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 876; 92;
                                                                                                                                                                                                                                                            ORGANISM: B.fragilis
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       US-09-540-209B-7121
                                                                                                                                                                                                                                          TYPE: PRT
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0; 0; Indels Query Match 3.5%; Score 7; DB 5 Best Local Similarity 100.0%; Pred. No. 92; Matches 7, Conservative 9; Mismatches

0

18 NOLEEVG 24 οy Db

RESULT 2 US-10-041-018-199

Sequence 199, Application US/10041018
GENERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
FILLE REFERENCE: ACUSUUSI/10025547
CHRPENT APPLICATION NUMBER: US/10/041,018
PPLIM APPLICATION NUMBER: US bu/259880
PRIOR FILLOS DAUE: 2001-01-05

NUMBER OF SEQ ID NOS: 413 SOFTWARE, Patchtin version 3.1 SOFTWARE, Pat SEQ ID NO 199

ORCANISM: Saccharomyces cerevisiae 1045 TYPE: PRT LENGTH:

US-10-041-018-199

Query Match

3.5%, Score /, DB 6; Length 1045;

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OY Db

Scarch completed, July 2, 2002, 16:03:59 Job time: 56 sec

Patentin Ver. 2.0

1447

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Patent No. 620010.
GENERAL INDEMATION:
APPLICANT: Genmill, Robert W.
APPLICANT: Drabkin, Harry A.
ITIE OF INVENTION: TRCB, A GENE RELAIED TO THE HEDGEHOG RETEDIOR, PATCHED
ITIE OF INVENTION: TRCB, A GENE RELAIED TO THE HEDGEHOG RETEDIOR, PATCHED
                                                                                                                                                            CURRENT APPLICATION NUMBER: 15/09/268,140 CURRENT FILING LATE: 2000-08-12 PRIOR APPLICATION NUMBER: 105.60/7077,723 PRIOR FILLING DATE: 1998-03-12
US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                               SOFTWARE: 1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                      4.5%; Score 7: DB 3: Longth 1447; 100.0%; Pred, No. 1.9e-02; 11Ve 0: Mismatches 6: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: SCOIL, MAIHEW P
APPLICANT: GEOBEICH, LISA V
APPLICANT: JOHNSON, FONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: VINCOUT, MAIT YOW F.
REGISTRATION NUMBER: 36709
REFERENCE/NOTRE! NUMBER: SUV-003,06
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20-ост 1997
вк. 530
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PCFOSSMS-180S
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/OB954668
Patent No. 6172200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley, Hoad & Eliot STREET: one Post office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NOT 19. SEQUENCE CHARACTERISTICS: LENGTH: 1447 amino acids
                 (NFORMALION FOR SEQ 1D NOT 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
                                                                                                                                                                                                                      4.5% Curry Match 4.5% Best Local Similarity (00.0° Matches 7: Conservative
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1FLEFAX: 415 398 3249
                                                                             TYPE: amino acid
STRANDEDNESS: sing e
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US OB 656 055 19
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MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER.
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Best Local Similarity
Thosa 2: Conserva
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STRANDEDNESS: sin
                                                                                                                      Linear
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THE BOARD OF TEUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY
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                                                                                                    3.5% Score 7; DB 4: Length 1447; 100.0%; Pred. No. 1.9e+02; trive 0; Mismatches 0; indels
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Four Embarcaderc Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.40 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               Sequence 19, Application PC/TUS9513233
GENERAL INFORMATION:
APPLICANT: THE DOARD OF TEUSTEES OF IEH LELAND SITTLE OF INVENTION: Patched Genes and their Use NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT/US95/13243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: a60190-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-0CI-1990
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TELEPHONE: 415-398-3249
                                                                                                                        Best Local Similarity 100.0
Matches 7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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; TYPE: PRT
, OKGANISM. Homo sapiens
US-09-268-140-5
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                                                                                                                                                                                                                             936 ASUANIR 942
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                                                                                                      Query Match
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Pred. No. 1.9e+02;
3.5%; Score 7; DB 4; Length 1434; 100.0%; Prod No. 1 90.02; tive 0; Mismatches 0; indeis
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Pour Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1 0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Patched Genes and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match ..., Best Local Similarity 100.0%; Pred No. 1.90 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US95/13233
06-0CT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a60190-1
                                                                                                                                                                                                            Sequence 10, Application PC/TUS9513233 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPHRATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5837538
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
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REGISTRATION NUMBER: 20
                                        7; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                           STREET: Four Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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    Query Match
Best Local Similarity
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                                                                              46 ASQANIR 52
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                                            Matches
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Pred. No. 1.9e+02;
0; Mismatches 0; Indels
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Four Embarcadoro Center, Suite 3400
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APPLICATION NUMBER: US/08/656.055
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patched Genes and their Use
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3.5%; Score 7; DB 2;
Best Local Similarity 100.0%; Prod. No. 1.96
Matches 7; Conservative 0; Mismatches
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REGISTRATION NUMHER: 20015
PEFFENCYTON FOR THREE 460190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                               UMBER: US/08/540,406
06-OCT-1995
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                                                                                                                                                                                                                                            NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/JOCKET NUMBER: a601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1889
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-
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APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1447 amino acids
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                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                   FILING DATE: 06 CLASSIFICATION:
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COUNTRY:
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0, Mismatches 6; Indels
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                                                                                                                                                                        ADDRESSEE: Flohr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadeto Center, Suite 3400
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STREET: Four Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.6, Version #1.30 CURRENT APPLICATION DATA:
                                       APPLICANT: SCOII, MATHEW P
APPLICANT: GoodRICH, LISA V
APPLICANT: JOHNSON, MONALD I.
TITLE OF INVENTION: Patched Genes and their Use
CORRESPONDENCES: 19
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APPLICANT: GOODBRIGH, LISA V
APPLICANT: JOHNSON, RINAGE, U
LITLE OF INVENTION: PATCHED Genes and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/540,406
FILING DAIR: 06 OUT-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPPRATING SYSTEM: PC-DOS/MS ENS
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Patent No. 6027882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rowland, Bertram I
RELISTRATION NUMBER: 20015
REFERENCE/INSTRI NOMBER: 4501
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-781-1989
TELECAX: 415-488-3249
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LENGTH: 1434 amino acids
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                       GENERAL INFORMATION:
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: Patent No. 5847548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW F
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, ROMALD 1,
TITLE OF INVENTION: Patched Genes and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOUCKET NUMBER: SUV-001.05
TELECOMMUNICATION INVESTATION:
TELEMENTON: 617-832-1000
FELLEMAX: 617-832-7000
                                                                                                                        REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-338 3.249
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,668
FILLIG DATE: 20-0ct-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08954568 Patent No. 6172200
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
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One Post Office Square
                                                                                                          20015
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                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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                                                                                          NAME: Rowland, Bertram REGISTRATION NUMBER: 20
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                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    922 ASOANIR 928
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                                                      FILLING DATE:
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DEVELOPMENTAL STAGE: merozoite

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737 ALQKVVE 743
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                                                                                                                                                                            APPLICANT:
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                                                                    US-08-967-104-2
                                                                                                                                         APPLICANT:
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APPLICANT: SUGIMOTO, MASAKAZU
APPLICANT: SUZUKI, TOMOKO
APPLICANT: SUZUKI, TOMOKO
APPLICANT: MATSUI, HILOSHI
APPLICANT: IZUI, KALSUKA
TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: IT'S GENE, AND PRODUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    UBLON, SPIVAK, MCCLELLAND, MAIER, & NEUSTADT,
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Best Local Similarity 105.0%, Fred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                         3.5%; Score 7; DB 3; Length 315;
                                                                                            0; Indels
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1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER 115/(04/59%, 36%)
                                                                             pred No 48:
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-784-0 PCT
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APPLICATION NUMBER: JP 5-209775
FILING DATE: 24-806-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: JP 5-209776
24-AUG-1993
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05-JHL-1994
                                                                                                                                                                                                                                                Sequence 2. Application US/08596366 Patent No. 5876983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
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                                                   Ouery Match
Best Local Similarity 100 0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-596-366-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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US-08-596-366-2
         US-08-770-035-1
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Gaps
                                                                                                                               TITLE OF INVENTION: MUTANT PHOSPHOENOLPYRUVATE CARROXYLASE, TITLE OF INVENTION: ITS GENE, AND PRODUCTION METHOD OF AMINO ACLD NUMBER OF SEQUENCES: 12
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                                                                                                                                                                           NUMBER OF SECTENCES: 12
COPPERSONDENCE ADDRESS:
ADDRESSER: OFLOW, MCCLELLAND, MAIER, & NEUSTADT,
ADDRESSER: P.C.
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100.0%; Pred. No. 1.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PU-DOS/MS-DOS
SOFTWARE: Falentin Release #1 0, Version #1 30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-784-0 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/967,104
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24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 6-153876 FILLING DATE: 05-JUL-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TP 5-209776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 10, Application US/08540406
Sequence 2, Application US/UB967104
Patent No. 5919694
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,618
                                                    SUGIMOTO, Masakazu
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                                                                            SUZUKI, Tomoko
MATSUI, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 413-2220
TELERX: 248655 ORAT HR
INFORMATION FOR SEQ 10 NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Best Local Similarity 100.0
                                                                                                                    1201, Katsura
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                        GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
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URRENT APPLICATION DATA:
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APPLICANT: Pasamontes, Lois
ITLE OF INVENTION: Checidiosis Vaccines
CORRESPONDENCES: 15
                                                                                                                                                                                                                                              IMBER: US/07/729,099
199107:2
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OFFRESPONDENCE ADDRESS
ADDRESSEE: Hottmann-La Roche Inc. STREED: 340 Kingsland Street
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FILING DATE: 09-JUN-1994
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340 Kingsland Street
                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: THM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-1808/MS-1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Eimeria tenella
DEVELOPMENTAL STAGE: merozoite
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/LOCKET NUMBER: H514
TELECOMMUNICATION INFORMATION:
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Patent No. 5688513
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ALTORNEY/AGENI INFORMATION:
NAME: Roseman, Catherine P
REGISTRATION MIMBERS 34,240
                                                                                                                                                                                                                                                                                                                                                                                                    | ECLEPHONE: (201) 235-6208
| ELEFAX: (201) 235-3500
| INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILLING DATE: 09-JUN-1
CLASSIFICATION: 424
PRICH APPLICATION DATA:
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                                                                              New Jersey
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STATE: New Je
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                                                                                              COUNTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Passamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/03/770,035
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                                                                                                                                                                                                                                                                                         ORGANISM: Eimeria tenella
DEVELOPMENTAL STAGE: merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/7.39,099
              NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
THIJERAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08770035 Patent No. 6008342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roseman, Catherine R
                                                                                           TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
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Hest Local Similarity 100.0v
Hest Local Similarity 100.0v
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                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NIMBER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
U.S.
                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LLSALAA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 LLSALAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07110
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                                                                                                                                                                                                                                                                                                                               US-08-257-392-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-770-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE
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ORGANISM: Elmeria tenella

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GenCore version 4.5
Copyright (q) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

109.466 Million ceil updates/sec  $\rm Tr_{1}\rm Ty=2$  , 2002, 16-84-57 ; Search time 44-85 Seconds (without alignments) Run on

US-09-603-665-5_COPY_1754_1954

TEYNLADGIAEKLKGLFTLF 201 1 EVYLLSALAALQKVVETLPH..... Perfect score:

Sednence:

Gapop 60 0 , Gapoxt 60 0 01,160 Scoring table:

231628 seqs, 24425594 residues Searched:

9

Word size

fotal number of hits satisfying chosen parameters:

181

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database :

3: /cgn2_6/ptodata/2/iaa/6A_COMH.pcp:*
4: /cgn2_6/ptodata/2/iaa/6B_COMH.pcp:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMH.pcp.*
6: /cgn2_6/ptodata/2/iaa/backLiles1.pcp:* 1: /eqn2_6/Ptodata/2/jaa/54_COMB.pep:* 2: /eqn2_6/Ptodata/2/jaa/5b_COMB.pep:* 3: /egn2_6/ptodata/2/jaa/6A_COMB.pep:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a

#### SUMMARIES

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NO.	Score	Match	Length	DH	≘	Description
	00	4.0	829	. 4	US-09-413-814 105	Sequence 105, App
2	7	ις. (*)	3]5	-	пs-07-729-099-1	Sequence 1, Appli
٣	7	3.5	315	-	US-08-257-392-1	Sequence 1, Appli
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5	7	3.5	883	r^v	5.998-385-80 SN	Sequence 2, Appli
Ş	7	۳.	883	<b>(4</b>	US 08 967-104 2	cų
7	7	3.5	1434	~	US-08-540-406-10	10,
œ	7	3.5	1434	~	US-08-656-055-10	10,
6	7	3.5	1434	4	US-08-954-668-10	10,
10	7	3.5	1434	S	PCT-US95-13233-10	10,
11	7	3.5	1447	~	US-08-540-406-19	19,
12	7	3.5	1447	~	US-08-656-055-19	
13	7	3.5	1447	7	US-08-954-668-19	19,
14	7	3.5	1447	7	US-09-268-140-5	5, 7
15	7	3.5	1447	S	PCT-US95-13233-19	Sequence 19, Appl
16	9	3.0	12	~	US-08-578-674-10	Sequence 10, Appl
17	9	3.0	12	4	US-09-498-346-10	Sequence 10, Appl
18	9	3 0	5.5	~	HS-09-082-2798-1043	1043
19	9	3.0	29	4	US-09-315-304B-1043	Sequence 1043, Ap
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53	9	3.0	3.4	-	US 08 178 477B 28	Sequence 28, Appl
24	ع	C ~	3.5	-	US-08-252-9668-9	Sequence 9, Appli
25	9	3.0	37	٣.	US-08-578-674-6	Sequence 6, Appli
2h	٢	÷	4.3	4	115-114-448-448-5	Sequence 6, Appli
27	¥	~	4.3	.~	118-08-578-674-7	Sequence 7, Appli

Sequence 7, Appl	Sequence 17, App	Sequence 17, App	16,	16,	3, 1	Sequence 4, Appl	٠.	Sequence 3, Appl	-	r.	150	Sequence 4, Appl	Sequence 3, Appl	4	્રં	2,	323
115-09-498-346-7	US-08-578-674-17	US-09-498-346-17	US-08-578-674-16	US-U9-498-346-16	US-08-578-674-3	US-U8-578-674-4	115.08 578 674 5	US-09-498-346-3	US: U9 498-346-4	175-09-498-346-5	US-U8-839-709-3	175-08-839-709-4	115-00-204-859-4	118-64 264 859 A	US OB 578 674 2	US-09-498 346-2	US-08-965-762-32
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# ALIGNMENTS

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APPLICANT: Reyer, Stein
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Brandt, Petra
APPLICANT: Gluberty, Brian A
APPLICANT: Goldberty, Brian A
APPLICANT: Goldberty, Brian A
APPLICANT: Glodberty, Brian A
APPLICANT: Holle, Gerhand
APPLICANT: Reichenbach, Hans
APPLICANT: APPLICANTON NUMBER: US/07/413,814
CUBRENT FILLS DATE: 1999-10-97
                                                                                                                                              APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: DE 198 45 493.2
                                     ; sequence LU5, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION;
                                                                                                                                                                                APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILLING DATE: 1998-10-09
NUMBER OF SEQ ID NOS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , TYPE. PRT
, ORGANISM. Serangium cellulosum
US-09-413-814-105
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US-09-413-814-105
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Caps 0; Length 829; 0; indels 4.0%; Score 8; DE 4; 100.0%; Pred. No. 13; ative 0; Mismatches Query Match Best Local Similarity 100.0 Matches 8; Conservative

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309 LLSALAAL 316 4 LLSALAAL 11 qq á

Sequence L. Application HS/07/29009 : Patent No. 5403581 GENERAL INFORMATION: RESULT 2 HS-07-729-099-1

APPLICANT: Binger, Mary-Helen APPLICANT: Pasamontes, Luis TITLE OF INVENTION: Coccidiosis Vaccines NUMBER OF SEQUENCES: 15

17-			

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PCT-US02-09671-1124

FCT-US02-09671-1124

SCGUEGCC 1124, Application PC/TUS0209671

SCGUEGCC 1124, Application PC/TUS0209671

CENERAL INFORMATION:

TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01

CURRENT APPLICATION NUMBER: PCT/US02/09671

CURRENT APPLICATION NUMBER: 60/292,844

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: 60/336,370

PRIOR APPLICATION NUMBER: 60/336,370

PRIOR APPLICATION NUMBER: 60/336,380

PRIOR APPLICATION NUMBER: 60/336,380

PRIOR APPLICATION NUMBER: 60/336,985

PRIOR APPLICATION NUMBER: 60/336,985

PRIOR ELLING DATE: 2001-12-04

SOFTWARE: FASTED IO NOS: 2041

SCOFTWARE: FASTED IO WINDOR: 2041

SED ID NO 1124

LENGTH: 406

TYPE: PAT

ONCHANISM: HOME SAPIENS
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Ouery Match

1.5%; Score 7; DB 1; Length 406;

Hest Local Similarity 100.0%; Prod. No. 1.55+02;

Matches 7; Conservative 0; Mismatches 0; Indels

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Db 364 KKEGEEE 370

Search completed: July 2, 2002, 16:16.44

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                                                                                                                                                                                                                                                                                                                                       APPLICANT: ZyCOS INC.
IITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191 026W01
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: 3-170502/09671
CUPPENT FILING DATH: 2002-0-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILINS EATE: 2001-03-28
PRIOR PRILING FALE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR APPLICATION NUMBER: 60/310,801
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1125
                                                                                                                                                                                                                                                        ; Sequence 1125, Application PC/LUS0209671; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PILING DATE: 2001-08-08
PRIOR PAPLICATION NUMBER: 60,326,370
PRIOR PILING DATE: 2001-10-0.
PRIOR APPLICATION NUMBER: 60,336,780
PRIOR PILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60,358,985
PRIOR PILING DATE: 2001-12-04
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: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM, Homo sapiens
PCT-US02-09671-1125
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ORGANISM: Homo sapiens
                                                                          364 KKEGEEE 370
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63 KKECEEE 69
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CURRENT FILING LATE: 2002-04-28

PRIOR ABPLICATION NUMBER: B0/229, 495

PRIOR ABPLICATION NUMBER: 60/292, 544

PRIOR FILING DATE: 2001 03-28

PRIOR FILING DATE: 2001 05-21

PRIOR PULING DATE: 2001 06-21

PRIOR PILING DATE: 2001 08-08

PRIOR PILING DATE: 2001 08-08

PRIOR APPLICATION NUMBER: 60/356

PRIOR APPLICATION NUMBER: 60/356

PRIOR APPLICATION NUMBER: 60/356

PRIOR APPLICATION NUMBER: 60/358, 985

PRIOR APPLICATION NUMBER: 60/358, 985

PRIOR APPLICATION NUMBER: 50/358, 985

PRIOR FILING DATE: 2002-02-20

NUMBER: PSEQ ID NOS-241
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Best Local Similarity 100:0%, Pred. No. 1.4
Matches 7; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001.05.21
PRIOR FILING DATE: 2001.05.21
PRIOR PRILING DATE: 2001.08
PRIOR FILING TATE: 2001.08
PRIOR FILING TATE: 2001.08
PRIOR FILING TATE: 2001.10 01
PRIOR PRILING TOTE: 2001.10 01
PRIOR PRILING TOTE: 2001.10 01
PRIOR APPLICATION NUMBER: 60/346,780
PRIOR APPLICATION NUMBER: 60/368
PRIOR APPLICATION NUMBER
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                                                                                                                                                                             TITLE OF INVENTION: FRANSLATIONAL PROFITING FILE REFERENCE: 08191 025WG1
                                                                   Sequence 1123, Application Pt/TUS0209671 GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                                              Zyeos Inc.
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Wed Jul 3 12:05:17 2002

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APPLICANT: Slater, Steven C. TITLE OF INVESTIGATION EXPRESSION OF TITLE OF INVENTION: EXPRESSION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERENCE: 38-10(52052)A
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FRIGG APPLICATION NUMBER: 60/287,151, 60/296,516, 60/291,217, 60/314,752,
60/389,217, 60/343,718, 60/343,903

FRIGG FILING DATE: 2001-04-27, 2091 05-11; 2001-05-15, 2001-08-24,
2001-10-12, 2001-10-19, 2001-11-62,
NUMBER OF SEQ IN NOS: 28
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                                                                                                                                                                                                                                                                                3.5%; Score 7; DH 7; Length 316; 100.0%; Prcd. No. 1.2e+02; tive 0; Mismatches 0; Indels
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PCT-US02-13329-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/US02/13329 CHPRENT FILING DATE: 2002-04-25
                                                                          CURRENT APPLICATION NUMBER (18/60/346),039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SRQ ID NOS: 47374
SEQ ID NO 2220
LENGTH: 316
                                                                                                                                                                                                          ORGANISM: Schizusaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 8, Application PC/TUS0213329
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WARREN, Bridget A.
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Best Local Similarity luv.v
Enc 7; Conservative
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Best Local Similarity
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                                                               POLYPEPTIDES, CELLS, AND METHODS THERROF CAPABLE
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                                                                                                                                                                                                                                                                                                                                                                                                               3.5%; Score 7; DH 5; Length 138; 100.0%; Pred, No. 55; tive 0; Mismatches 0; Indels
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                                             APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MOLULALING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER 11S/03/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 10675
                                                                                                                                                                                                                                                                                             ; LOCATION: 1.138
; OTHER INFORMATION: Ceres Seq. 1D no. 1017068
US-09-935-625-10675
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches
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LOCATION: 1..158
OTHER INFORMATION: Ceres Seq. ID 1393051
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APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Berry S.
APPLICANT: Hinkle, Gregory J.
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Best Local Similarity 100...
Local 7; Conservative
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LOCATION: 1, 158
        Sequence 10675, Appl. GENERAL INFORMATION:
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APPLICAMES AND MANAGEMENT ALEXANDROV, NICKOLAI et al.
APPLICAMES ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIU
TITLE OF INVENTION: THREHEY
FILE REPERENCE: 2750-1068P
CURRENT APPLICATION NUMBER: LS/09/620,393B
CURRENT APPLICATION NUMBER: LS/00-07-21
SUMBER OF SEQ ID NOS: 9948
SOFTWARE: PALENTIN VERSION 3.0
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: Patentin version 3.0
SEQ ID NO 6606
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION. Xaa is ary amino acid
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US-09-620-3938-6607
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US-09-620-393R-6606
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: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
                      Sequence 6607, Application US/09620393B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana
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Dest Local Similarity 100.0
Matches 7; Conservative
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LOCATION: 1.105
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LOCATION: 1..105
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US-09-620-393B-6606
  US-09-620-393R-6607
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LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: N. ALEXANDROV et al.
IITHE OF INVENTIONS POLYNOCHESTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
IITHE OF INVENTIONS MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
COURRENT APPLICATION NUMBER- US.00,043,625
CURRENT FILLNO IATE: 2001-08-24
NUMBER OF SEO ID NOS: 33136
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                                                                                  Length 603;
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                                                                                Query Match 4.0%; Score 8; DB 5; Best Local Similarity 100.0%; Pred. No. 25; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
4.0%/ Score 8: DB 5.

Hest Local Similarity 100.0%, Fred. No. 25.

Matches 8: Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCATION: 1, 606
DOCHER INFORMATION: Cercs Seq. 1D no. 3086967
IIS 09-935-625-9918
THER INFORMATION: Cores Seq. II no. 3086968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 8; DB 7.
100.0%; Pred. No. 27;
19ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/482,898
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 1344
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.)
                                                                                                                                                                                                                                                                    Sequence 332, Application US/60482898 GENURAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thalland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guery Match
Hest Local Similarity 100,555
Fest Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hudson, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 KKKEGEEE 574
                                                                                                                                                                  62 KKKENESE 49
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                                                                                                                                                                                          Z KKKEGEEE 9
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    13:09-945-625-9919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ 1D NO 9918
LENGTH: 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
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GenCore version 4.5
c) 1993 - 2000 Fungagen Ltd
                     Copyright (+) 1993
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OM protein – protein search, using sw model

July 2, 2002, 16:03:03 ; Search time 59 99 Seconds

(without alignments) 338.459 Million cell updates/sec

US-09-603-665-5_00FY_1594_1794

Pertect score:

ISPYLEGILSQVIHLEKIIS 201 1 LLPTETFIPVIRGLVGNPLP Segmente

Gapop 60.0 , Gapext 60.0 01.10 Scoring table:

307805 seqs, lolol5595 residues Searched:

Word size :

1858 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Pending_Patents_AA_New:*

1. /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

2. /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3. /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

1. /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:* /cgn2_6/ptodata/1/paa/US16_NEW_COMB_pep:* /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	-0.44-20635 Sequence 20635	325-9919 Sequence	25-9918 Sequence	398-332 Sequence 332,	07 Sequence	6606,	Sequence	US-09-620-3948-6605 Sequence 6605,		Sequence	1123 Sequence	11:28 Seducine	-1125 Sequence 1	806-510 Sequence 510,	124 Sequence	1126 Sequence 1126,	1127 Sequence 1127,	606	2123 Sequence	209B-9330 Sequence 9330,		-6558 786 Sequence	018-261 Sequence 261,	6112	649	00000
<u>a</u>	P+0-048-09-511	60-SH	511	09-SN	60-SN	-60-80			7. T	PCT US02-13329	- L2960 - 2080 - Jud	PCT-US02-09671	FCT-US02-09671	US-10-102	PCT-US02-09671-1	[ (360 - 2080 - 1.5d	1.4360 - 0.367 - 0.3671	115-60-360-	60 SH	ns-	TIS-09-513	US 09-573	ns.	-SN	FCT - US02 - 09944	0.00 000 000
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ORGANISM. Arabidopsis thaliana

TYPE: PRT FEATORE:

peptide 1.503

NAME/KEY:

Sequence 5568, Ap Sequence 3534, Ap			8534,	Sequence 8534, Ap		Sequence 4112, Ap		Sequence 53, Appl	Sequence 48, Appl	Seglence: 5:16. Ap	1898,	9573,	231. 4	Sequence 7926. Ap	9610.		12014
US-60:350 039:5568 PCT-US02 13142:3534	US-10-128 714 3534	US-60-360-039-3832	PCT-US02-13142-8534	US-10-128-714-8534	118-60-360-1144-23646	US-60 360 039-4112	US-6U-460-039-4660	115-10-033-741-53	US-10-033-662-48	08-10-105-5dd 511k	US-99-520-393B-1898	HS-10-155-881-9573	US-10-002-344A-231	98 09-548-2098 7976	US-10-155-881-9610	US-10-157-031-156	US 10-155-881 12014
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CUPPENT APPLICATION
CHEREND APPLICATION
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20635
LENGTH: 543
TYPE: ...
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GENERAL INFORMATION: DELYNDER ALL INFORMATION: CELES, AND METHODS THEREOF CAFA
TITLE OF INVENTION: POLYNOTLES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAFA
TITLE OF INVENTION: POLYNOTLES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAFA
TITLE OF INVENTION: 2750-1481P
CURRENT PELLOR LOAD: 250-1481P
CURRENT FILING DATE: 2001 08 24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NOS: 33136
SEQ ID NOS: 33136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 543;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 8; DB 7
100.0%; Fred. No. 22;
tive 0, Mismatches
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US-60-360-039-20635
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Matches 8, Conserva
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DM 26; Length 460; 0; Indels

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Xenorhabdus sp. Genome Sequences And Uses Thereof
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4.0%; Score 8; DR 26
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                              Achorhabdus sp. 38-21(51847)A CURRENT APPLICATION NUMBER: US/60/215,161 CURRENT FILING DATE: 200-(6-30 NUMBER OF SEQ ID NOS: 8409 10 NO 7795
    Huesing, Joseph E.
Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July 2, 2002, 16:14:37
                                    APPLICANT: Krasomil-Osterfeld, I
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sercel
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: 38-21(5184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Xenorhabdus sp. US-60-215-161-7795
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                                                                                                         Sequence 548), Application US/39543681A
GENERAL INFORMATION
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CURRENT APPLICATION NUMBER: 05/09/897,516
CURRENT FILING DATE: 20.01-06.29
PRIOR APPLICATION NUMBER: 05 60/215, 161
PRIOR FILING DATE: 2000 06-30
NUMBER OF SEQ ID NOS: 8409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 8; DB 22; Length 460;
100.0%; Pred, No. 51;
tive 0; Mismatches 0; Indels
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APPLICANT Goldman, Balry S.
APPLICANT Hinkle, Gregory J.
APPLICANT Bresling, Joseph E.
APPLICANT Krasomil Osterfeld, Karina C.
APPLICANT Malvar, Thomas M.
APPLICANT Stater, Steven S.
APPLICANI Spiridonov, Sergei
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// GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANI: Coldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Profeus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0°
Matches 8; Conservative
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; ORGANISM: Xenorhabdus sp.:
US 09-897-516-7795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obery Match
Best Local Similarity
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103 LIAFFLEA 110
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US 60 215 161 7795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 457
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Gaps

0,

Indels

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Pred. No. 46;

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100.0%; Pred. w..
        Best Local Similarity 100.0
Matches 8; Conservative
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APPLICANT: Hinkle, (
TITLE OF INVENTION:
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                                                                                                           46 LTAFFIJRA 53
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                                                                                                                                                                     RESULT 11
IIS-04-847-516-5029
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FILLE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,038A
CURRENT PILING DAFE: 2000-01-27
PRICK FILING DAFE: 1999-01-29
NUMBER OF SEQ 1D NOS: 14342
SEQ 1D NO 7912
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kasai, Hiroaki
APPLICANT: Hamada, Tohro
TITLE OF INVENTION: METHOD FUR IDENTIFICATION AND DEFECTION OF MICROCKGANISMS
TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR
FILE REFERENCE: 12817-0040011
CURRENT APPLICATION NUMBER: US/09/823,829
CURRENT PILLING DATE: 2001-03-30
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                                                                                                                                                 Guery Match 4.0\% , Score 8, DB 22; icngth 220; Best Local Similarity 100 0%; Pred. No. 26; Matches 8; Conservative 6, Mismatches 0; Indels
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Best Local Similarity 100.0%; Fred. No. 26;
Matches 8; Conservative 0; Mismatches
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PRIOR FLING DATE. 1937-12 12
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 2.0
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GENERAL INFORMATION:
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ORGANISM: Klebsiella pneumoniae
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US-09-823-829-6
                                                       TYPE: PRT ORGANISM: Chitinophaga pinensis
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamamoto, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura,
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                   SEQ ID NO 6
LENGTH: 220
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APPLICANT:
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4.0%; Score 8, DB 18, Length 411;

Query Match

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Xenothabdus sp. Genome Sequences And Uses Thereof
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                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Krasomil-Oscherfeld, Karina C.
APPLICANT: Krasomil-Oscherfeld, Karina C.
APPLICANT: Stater, Steven C.
APPLICANT: Spiridonov, Serven C.
APPLICANT: Spiridonov, Servei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof FILE REPREMENTE: 38-15184718
CURRENT APPLICATION NUMBER: US/09/R97,516
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4.0%; Score 8; DB 26; Length 445;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels
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Pred. No. 49;
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V 100.0%; Pred. No. 47.
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APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5029
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; Sequence 5029, Application US/09897516
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Hinkle, Gregory J.
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Best Local Similarity 100.0
Matches 8; Conservative
                                                  APPLICANT: Corbin, David R.
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; OPGANISM· Xenorhabdus sp.
US-60-215-161-5029
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OTHER INFORMATION: potential membrane-spanning segment, lopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: A N.VEL BAP28 GENE AND PROTEIN
FILE OF INVENTION: A N.VEL BAP28 GENE AND PROTEIN
CURRENT APPLICATION NUMBER: US.CO.7141-323
CURRENT FILING DATE: 1999-06-25
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100.0%; Pred. no.
..a 0: Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
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PRIOR APPLICATION NUMBER: PCT/US01/04941
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PRIOR APPLICATION NUMBER: PCIZUS01Z08656
                                                                     PRIOR APPLICATION NUMBER: US 09/519,705 BRIOR APPLICATION NUMBER: US 09/519,705 BRIOR PILLING DATE: 2000-04-07
                                                              PRIOR APPLICATION NUMBER: PULTBESLY 34 123
PRIOR FILING DATE: 2001 02-26
                  PRIOR APPLICATION NUMBER: US 09/577.409
PRIOR FILING DATE: 2000-05-18
                                                                                                                             PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/574.454
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/540.217
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                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/552,929
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PRIOR APPLICATION NUMBER: US 09/770,160
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: GENERAL INFORMATION:
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SOFTWARE: pt_FL_genes Version 6.0
SEQ 1D No 167
                                                                                                                                                                                                                                                                 2000-03-31
2000-02-28
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SEC ID NO 4
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  PRIOR FILLING DATE:
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TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROSHGANISMS USIN TITLE OF INVENTION: GENE AS AN INDICATOR
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 937..957
OTHER INFORMATION: potential membrane spanning segment, TopPred Program
                           LOCATION: 861..881
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
                                                                                                                                             1.0CATION: 884..904 Ottential membrane-spanning segment, TopPred Program
                                                                                                                                                                                                                                                                                        OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, loppred Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1725..1745
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane spannina segment, TopPred Program
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PRIOR APPLICATION NUMBER: US 09/208,688
PRIOR FILING DATE: 1998-12-10
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; Sequence 6, Application US/09823823
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 2.0
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APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Hamoda, Tohru
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NAME/KEY: TRANSMEM
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Best Local S
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COUNTRY
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                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions and Methods Comprising TITLE OF INVENTION: BARDI and Other BRCAL Hinding Proteins NUMBER OF SPOURNES: 115 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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    61 DAPKDRIJJEFYNIADCIAEKLKGIFTLFACHLVKPFADTL 100
                      298 DAPKDKLLTFYNLADGIAEKLKGLFTLFAGHLVKPFADTL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hest Local Similarity 100.0%; Pred. No. 7.8
Matches 100; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                    Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   Sequence 52, Application US/60042611 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: P-41.07
REFERENCE/DOOKET NUMBER: 0TS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 52:
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                                                                                                                                                                                            APPLICANT: Bowcock, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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LENGTH: 515 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                           77210
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US-66-042-611-52
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238 ITAFFLEALDFRAOHSENDLEEVGKTENCIIDCLVAMVVKLSEVTFRPLFFKLFDWAKTE 297
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                                                                TBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1 0, Version #1.30
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live 0, Mismatches
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/60/339,453
                                                                                                                                                                                                                                                                                              PEFEPENCE/POCKET NUMBER: TTSD:499PZ3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: JUND-04-27
PRIOR APPLICATION NUMBER POTJUSULJUSBUD
PRIOR FILLUD DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILLING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILLING DATE: 2000-02-03
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PRIOR APPLICATION NUMBER: US 09/552,317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR PILLING DATE: 2000-12-22
PRIOP APPLICATION NUMBER- HS 09/491.404
                                                                                                                                                                                     Concurrently Herewith
                                                                                                                                                             APPLICATION NUMBER: US/60/042,985
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                                                                                                                                                                                                                                                                               P-41,071
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INFORMATION FOR SEQ 1D NO: 52:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                ATTOPNEY/AGENT INFORMATION:
                      COMPUTER READABLE FORM MEDIUM TYPE: Floppy disk
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amino acid
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APPLICANT: Weng, Geshi
APPLICANT: Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 100, Conservative
                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         NAME: Hibler, David W. REGISTRATION NUMBER: P
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Wang, Jian-Rui
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                                                                                         OPERATING SYSTEM:
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Best Local Similarity
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77210
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US-60-042-985-52
                                                                     COMPITTER
                                                                                                                     SOFTWARE:
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1867 LTAFFLEALDFRAGHSENDFERVGKTENTILMLVAMVVKLSEVTFRPLFFKLFDWAKTE 1926 61 DAPKORIJTEYNIJADÇI AEKLIKGI ETILEAGHLUKPEADTLIXQUN I SKITDEAFEDSENDPE 120 Compositions and Methods Comprising HARDL and Other BRCAL Binding Proteins

Sequence 52, Application US/03936487 GENERAL INFORMATION:

RESULT 3 US-08-936-487-52

APPLICANT: BOWCOCK, Anne M. APPLICANT: Bacr, Richard

2047 PCIAQESVAMADESLWKFLNY 2067

181 PCIAGESVAMADDSI.WKPI.NY 201

ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433

Houston

USA Texas

COUNTRY:

CORRESPONDENCE ADDRESS:

NUMBER OF SECUENCES: TITLE OF INVENTION:

TITLE OF INVENTION:

130

121 KOCLILQFILNOLYKIFLFDTJHFISKERAXALAMPLVDQLENRLGGEEKFQERVTKHLI 180

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APPLICANT: BOAQUECISTE, LYGIE
APPLICANT: Choumakov, Ilya
IIILE OF INVENTION: A NCWEL BAP28 GENE AND PROTEIN.
FILE REPRENCE: 67.082.FRO
CURRENT APPLICATION NUMBER: US/60/176,880
CURRENT PILING DAIE: 2000-01-18
EARLIER APPLICATION NUMBER: US/60/141,824
EARLIER FILING DAIE: 2000-01-18
EARLIER FILING DAIE: 109-0-0-25
NUMBER OF ESQ ID NOS: 12
                                                                                   OTHER INFORMATION: Xaa-Gly or Glu
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                      "THER INFORMATION: Xaa-Asp or Asp
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                                          VARIANT
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LOCATION:
LOCATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,487 Concurrent y Herewith

CLASSIFICATION: 435 PRICE APPLICATION DATA:

FILING DATE:

OPERATING SYSTEM: PC-DOS/MS-DOS

IBM PC compat ble

Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER:

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238 LTAFFLEALDFPAQUSENDLEEVSKTENCTIDCLVAAVVKLSEVTFFLEFKLFDWAKTE 297
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APPLICATION NUMBER: US 60/025,296
FILING DATE: 20 SEP-1996
FRIOR APPLICATION DATA:
                                                                     APPLICATION NUMBER: US 60/042,611
FILING DATE: 03-APR-1997
                                                                                                                                                                                                                                    REGISTRATION NUMBER: P-41,071
REFERENCE/DOCKET NUMBER: UTSD:499
                                                                                                                                             US 6.0/042,985
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                               FILING DATE: 04-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           515 amino acids
                                                                                                                                                                                                                Hibler, David W.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                512/474-7577
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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0; Indels 0; Gaps

Length 2144;

Score 199; DB 26; Fred. No. 2e-197; U: Mismatches

91.08:

Owery Match

Hest Local Similar:ty 130.0%; Matches 201: Conservative U

1 LIAPPLFALDERAQHSENDLEEV: KTENOTIDOT VAMOVKI SEVTEPPI HPKLEDWAKTE KO  27 (2)

# Gentore version 4.5 Copyright (c) 1993 · 2000 Compugen atd.

OM protein - protein search, using sw model

July 2, 2004, 16.14.35 , Search time 505 3 Seconds (Without alignments) 146.012 Million cell updates/sec Run Gh.

Title: Perfect score:

CIAQESVAMADDSLWKPINY 201 US-09-603-565-5_COPY_1867_2067 201 1 LTAFFLEALDFRAGHSENGL Sequence.

01.100 Scoring table: 350zzb3 seqs, 351980561 residues Searched.

Gapup 60.0 , Gapext 60.0

Word size :

1663 Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database

Pending_Paleuls_AA_Main:*  1.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	 	5, Ap	4. Ap	52, A	52, A	52, A	167,	3. An
	Description	Sequence 5, Appli	Sergiabilities	Sequence	Sequence	Seguence	Sequence	Sequence
	91	TS-00-603-665-5	11S-60-176-880-4	US-08-936-487-52	US-60-042-611-52	US-60-042-985-52	118-60-419-453-167	115-60-141-323-3
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NAME/KEY: VARIANT

Sequence 6, Appli Sequence 7, Appli Sequence 5029, Ap Sequence 6481, Ap Sequence 7795, Ap Sequence 7795, Ap Sequence 7148, Ap Sequence 7148, Ap Sequence 7148, Ap Sequence 452, Ap Sequence 452, Ap Sequence 452, Ap Sequence 7189, Appli Sequence 7189, Appli Sequence 7189, Appli Sequence 7189, Appli Sequence 7189, Appli Sequence 7189, Appli Sequence 174, Appli Sequence 174, Appli Sequence 3, Appli Sequence 3, Appli Sequence 174, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 174, Appli Sequence 3, Appli Sequenc	748. A 524. A 4141. A 194. A 100. Ap 57. A 13298. I 11461. I 11461.
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# ALIGNMENTS

ESULT 1 S-09-603-665-5	Sequence 5, Application US/09603665	GENERAL INFORMATION:		APPLICANT: Chumakov, Ilya	APPLICANT Cohen-Akenine, Annick	TITLE OF INVENTION: A NOVEL BAP28 GENE AND PROTEIN	PILE PEFFENCE: GENSET 063AUS	CHRPENT APPLICATION NUMBER: HS/09/603,665	CHPPENT FILING DATE: 2000-06-23	PPIOP APPLICATION NUMBER: US 60/141,323	PRIOR FILING DATE: 1999-06-25	PRIOR APPLICATION NUMBER: US 60/176,880	PRIOR FILING DATE: 2000-01-18	NUMBER OF SEQ ID NOS: 63	SOFTWARE: Patent.pm	SEQ ID NO 5	DENGTH: 2144	TYPE: PRT	ORGANISM: Homo sapiens	FEATURE:	NAME/KEY: VARIANT	LOCATION: 1694	OTHER INFORMATION: Xad Set or Ash	NAME/KEY, VAPIANT	LOCATION 1854	OTHER INFORMATION: Xaa-Ala or Val	
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RA Variotz Holand 1.-A., Voss H., Wohiand J., Cossart P.;
El Promparative denomics of Listeria species.";
El Science 24849-8642(2001).
ER EMBL ALSHARBS PASS(644.1: -...)
ER CASSILIST LINULSO: -...
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EN COMPLETE PROTOCOME.
SQ SEQUENCE 180 AA; 20757 MW; 96382A1A7332FP22 CRC64;
ENST Local Similarity 100.0%; Pred. No. 71;
ENTER CASSILIST ENTER PROTOCOME. -...
ENTER CASSILIST ENTER CASSILIST ENTER ```

Search completed: July 2, 2002, 15:42:19 Tob time: 457 sec

129 DGGKIPKD 146

SECTIENCE FROM N.A.

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Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yushisawa T., Taraka T., Kadoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
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Mammalia; Eutheria; Rodentia; Seiurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-EMBRYO, AND MAINLY HEAD;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Nadai K., Sugano S., Takahashi-Fujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara P., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Wakamatsu A., Nakamura Y., Nagabari K., Masuho Y., Oshima A.;
Submitted (MAY-2001) to the EMBL/GenHank/DDBJ databases.
EMBL: AK027275; BAB55011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Horikawa H , Jin-no K., Takahashi M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%; Scote 8; 58-17; Length 167;
100.0%; Pred No 67;
                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic crenarchaeon, Sulfolobus Lokodaii strain?",
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01-DEC-2001 (IEEMBLICEL 19, Last annolation update)
CDNA FLIJ4369 FIS, CLONE HEMBALOODIA, HIGHLY STWHIAR TO
ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Indels
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EMBL: APOUVBEL: BABESELL: -
EMBL: APOUVBEL: DITCLED COMPLETE PROTECUME.

SEQUENCE: 167 AA. 19252 MW. 2CICAGDAEL202FA3 GRC64;
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01-DEC-2001 (TEMBLICE: 19, Last annotation update)
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Matches 8; Conservative 6; Mismatches
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   Kawarabayasi Y , Hino Y
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MEDILINE-21085660; PubMed-1121785;
RA ATARAWAT Y. Shindara K., Yoshino M., itoh M., ishii y., Rawai J., Shindagawa A., Shidata K., Yoshino M., itoh M., ishii y., RA ATARAWAT Y., Hara A., Firkunishi y., Romon H. Adarhi J., Firkunishi y., Ra Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Radcia K., Matsuka H., Ashburnar M., Bahilo S., Casawani T., Washi R., Mochiwa H., Ra Schimi D., Lowis S., Matsuo Y., Nikaido I., Pissie G., Quarkenbush J., Rachimi M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakaka K., Okido T., Pulli D., Bolunga M., Carninci P., de Bonaldo M.F., R., Balake J., Bolfelli D., Bolunga M., Carninci P., de Bonaldo M.F., Romsieli M. J., Bull C., Fletcher C., Fujita M., Gariboldi M., R. Alzonselli M., Marchionni L., Mashima J., Mazzarolli J., Mombaerts P., Nordose P., Marchionni L., Mashima J., Mazzarolli J., Mombaerts P., Nordose P., Eing K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masshia Y., Kawaji H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Masshia Y., Kawaji H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilki K., Schoenbach V., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
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01-DBC-2001 (TrEMBLIEL 19, Last Sequence update)
01-DBC-2001 (TrEMBLIEL 19, Last annotation update)
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Bacillus/Staphylococcus group; Listeria.
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Matches 8; Conservative 0, Mismatches
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MGD; MGT:1993119; 4930587A11Rik.
InterPro. IPPR061806, Pas.trnsfrmng.
InterPro. IPPR061806, Pas.trnsfrmng.
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             STRAIN-C57BL/6J; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK016359; BAB30204.1; -.
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PRINTS; PPOO128; SARIGTBBP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00177; ARF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 NVEETVVK 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_Tax1D+1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPOUENCE
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Hypothetical protein. SROUENCE 159 AA; 17732 MW; FFA5D6503F3CFCF7 CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Viridiplantae: Streptophyta, Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: endicotyledons: core endicots: Rosidae;
eurosids [1] Brassicales: Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps
                                                                                                                                       Sdet
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Labata S., Mewes H.W., Rudd S., Lemeke K., Mayer K.F.X.;
Submitted (AUG-2008) to the EMRGAS chank, Jones databases
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                                                                                                 DB 6; Length 144;
n 59;
                                                                                                                                     0: Indels
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Submitted (AUG-2000) to the EMBL/CenBack/DDBJ databases
EMBL; AL391143; CAC01741.1;
                                          V · I.
B 7DSF3R1DA2F0842F CRC64;
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01-071-2000 (TERMILE). 15, East sequence update)
01-071-2000 (TERMILE). 15, East annotation update)
                                                                                                                                                                                                                                                                                                       01 MAY 2000 (TrEMBLrel. 14, Created)
01 MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-3HN 2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 159 AA.
                                                                                                      0.4%; Score 8; DB 6
100.0%; Pred No 59;
tive 0; Mismatches
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                                                          SEQUENCE 144 AA; 16177 MW;
             SMARL: SMOUGAU: CSF2; 1.
PROSITE: PSOUZOE: GM_CSE; 1.
VARIANT 60
Probom; PD007449; JM (SF; 1.
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                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                     Local Similarity
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                                                                                                     Query Match
Best Local Si
Matches 8;
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                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Ribotypes and virulence gene polymorphisms suggest three distinct
Listeria monocytogenes lineages with differences in pathogenic
potential.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiedmann M., Bruce J.L., Keating C., Johnson A.E., McDonough P.L.,
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      Length 159;
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                                                                 0; Indebs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JON-2000) to the EMBL/GenHank/DDHJ databases.
EMBL, AF281893; AAF82597.1; -.
NON_TER
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165 AA: 18272 PW; COEFE78CLEA860F1 CRC64;
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Last aunotation update)
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01-DEC-2001 (TrEMBLTel. 19, Last sequence update)
01-DEC-2001 (TrEMBLTel. 19, Last annotation update)
HYPOTHETICAL PROTEIN ST0311.
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Bacillus/Staphylococcus group, Listeria.
   0.4%: Score 8; DB 10;
                                   Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                            165 AA
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                100.0%; Pred. wv.
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01-0CT-2000 (TrEMBLEEL 15
01-0CT-2000 (TYEMBLEEL 15
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes.
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PubMed-11572479;
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                                   Hest Local Similarity
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                                                                                                                        312 KPESLGKK 319
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                                                                                                                                                                                   9 KPESLGKK 16
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SEQUENCE
Query Match
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RESULT
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NCBI_TaxID=53953;
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                                                                                                                                                                                                                                                                                                                                                                   Moffat K.S., Qin H., Jiang L., Pamphile W., Grosby M., Shen M., Vandathevan J., Lam P., McDonald L., Hiterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Mctchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                        MEDLINE-20036896; Pubmed-10567266;
White O., Bisen J.A., Heidelberg J.F., Hickey R.K., Peterson J.D.,
Podson R.J., Haff D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
                                                                                                                                                       Macteria; Thermus/Deinococcus group, Deinococcales, Deinococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1";
Science 286.1571-1577(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 4%; Score 8; DB 16; Length 123;
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SEQUENCE 123 AA, 12733 MW, 389368703081C CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last Sequence update)
01-AUG-1900 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 14.2 KDA PPOTEIN PHI983.
01-MAY-2000 (TTEMBLIEL 13, Created)
01-MAY-2000 (TTEMBLIEL 13, Last sequence update)
01-MAR-2001 (TEMBLIEL 16, Last annotation update)
HYPOTHERICAL 12.7 KDA PROTEIN.
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Hypothetical profein; Complete proteome.
SEQUENCE 123 AA, 14212 MW; 177190E13
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                                                                                                                                   Deinococcus radiodurans.
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nes 8; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUTENCE FROM N.A.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                      NCB1_faxID-1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGE; DR0207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                       STRAIN-RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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MEDELINI-993103349, Pubbwed-10382966,
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-T., Ankal A., Kosuqi H.,
Jin-no K., Takahashi M., Sekine M., Baba S.-T., Nakazawa H.,
Pakaniya A., Fikui S., Punahashi Y., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Acki K.-T., Kutora K.,
Nauran N., Naura N., Oguchi A., Kakinchi H.,
Nakanura V., Naura N., Kikuchi H.,
Nomplete genome sequence of an aerobic hyper thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hutchinson K.L. Villinger F., Miranda M.E., Ksiazek T.G., paters C.T., Pollin P.E.; Miranda M.E., Ksiazek T.G., paters C.T., Pollin P.E.; materials of cytokines in the sera of cynomolgus macaques naturally infected with Ebola (Reston)...; submitted (AUC-2000) to the FMH./SenBank/hork, databases EMBL; AV00376; AAG16626.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metažoa, Chordata, Čraniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopilhecidae,
                                                                                                                                                                         Archaea, Cremarchaeota, Desulfuropiccales, Desulfurococaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 8; DB 17; Length 123; loo 0%; Pred No 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AA; 13142 MW; 8FC1D7FE307F403C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01 DEC-2001 (TremBirel, 19, Last annotation update) GRANULOCYTE-MACROPHAGE COLONY-STIMULATING PACTOR.
                                                          01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
123AA LONG HYPOTHETICAL CYTIDINE DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01 MAR-2001 (TrEMBLrel. 16, Last sequence update)
01 DEC-2001 (TrEMBLrel. 19, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00383; dCMP_cyt_deam; 1.
PPGSITE; PSOUGGES; CYT_DCMP_DEAMINASES; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AA.
  123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   crenarchaeon, Aeropyrum pernix Kl.";
                                            01-NOV-1999 (TrEMBLIEGI, 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002125; dCMP_cyt_deam.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; APOQOODO; RAAROO23 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04141; 2GMF.
InterPro; IPR000773; GM_CSF.
Pfam; PF01109; GM_CSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00693; GMCSFACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopitheeisae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Pes. 6:83-101(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P13652; 1CTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LSQLLPMA 115
                                                                                                                                                                                                                                                               SEQUENCE PROM N A
                                                                                                                                                                                                                   NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9544;
                                                                                                                                                         Aeropyrum pernix.
                                                                                                                                                                                                                                                                                         STRAIN=K1;
                                                                                                                                                                                                   Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                               APE1038.
                       Q9YD74;
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09YD74
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09GL44
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Adams M.D., Celonker S.E., Holf R.A., Evers C.A., Gocayne J.D., Adams M.D., Celonker S.E., Holf R.A., Evers C.A., Gocayne J.D., Adams M.D., Celonker S.E., Holf R.A., Evers C.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Stiffen G.G., Worlman J.R., Yandell M.D., Zhang Q., Chen L.X., Brindon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G., An Brindon R.C., Addyin D., Helt G., Nelson C.R., Miklos G.L.G., An M.H., Doyle G., Harder E.G., Helt G., Nelson C.R., Miklos G.L.G., A Atill J.E., Addyani A., An H.-J., Addrews Pfannkoch C., Haldwin D., Anil J.E., Addyani A., Barnalle B., Bhandari D., Bolshakov S., Rotkova D., Bottelan M.R., Bouck J., Brekstein P., Brottier P., Rotkova D., Bottelan M.R., Bouck J., Brekstein P., Brottier P., An Cherty J.M., Cawley S., Dahlke C., Davenport L.H., Davies P., Acherty J.M., Cawley S., Dahlke C., Davenport L.H., Davies P., Acherty J.M., Cawley S., Danke Z., Mays A.D., Bow J., Dove J., Bow 
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O
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Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                Bukaryota: Fungi: Basidicmyosta: Hymenemycetes: Homobasidiomycetes:
Agaricales: Coprinaceae; Coprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olesnicky N.S., Brown A.J., Dowell S.J., Casselton L.A.;
A constitutively active G-protein-coupled receptor causes mating
sell-compatibility in the mushroom Coprinus.";
EMBO J. 18:2756-2764(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mating Specificities in the Mushroom Coprinus virerus 7;
Genetics 154:1115-112-(2000).
EMHL: AF146522; AAD27448.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6452 MW; 96A35EH28H530605 CRC64;
                                                                                                                            01 New-1999 (Tremblice, 12, Created)
01 New-1999 (Tremblice, 12, Last sequence update)
01 DBC-2001 (Tremblice), 19, Last annotation update)
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01 MAY-2000 (TIEMBLEEL, 13, Last sequence update)
01 MAY-2000 (TEMBLEEL, 13, Last annotation update)
0211462 PROTEIN.
                                                       5.9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20221720, PabMed-1976757,
Halsall J.R., Milner M.J., Casselton L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                             01 DEC:2001 (Tremblre), 19, Last annot B42 MAIING PHEROMONE PRECURSOR PHB2.2.
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                                                                                                                                                                                                                                                                                                                                              Coprinus cinereus (inky cap funqus).
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                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE-99262413: PubMcd-10329622;
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100.0%; Pre-
0;
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                                                       PRELIMINARY;
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U9W467
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RA Glodek A., Gong E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.T., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Howgann C.,
Adiali M., Kalush F., Kapin G.H., Ke Z., Kennison J.A., Kerthum K.A.,
RA Kimmel H.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lau X., Mattel B., McIntosn T.C., McPood M.P., McPherson D.,
RA Mount S.M., Moy M., Morbyt U., Morris J., Moshreti A.,
RA Mount S.M., Moy M., Willshima N.V., Mobarry C., Morris J., Moshreti A.,
RA Mount S.M., Nelson K.A., Mykor K., Musskern D.R., F., Farleb J.M.,
Relson D.R., Nelson K.A., Warney R., Romery C., Shen H.,
RA Palnert K., Sannders R.D.C., Scheeler F., Shen H.,
Shee B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
RA Syleskas M., Tector C., Jurner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao D.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao D.A.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
Scheeder X.H., Zhong F.N., Zhong W., Zhon S., Zhu X., Zhun K.,
Shiener Z.B72185, Zaysen L.S.,
Scheeder C., Stather J.C.,
Scheeder C., Stather J.C.,
Scheeder X.H., Zhong W., Zhong X., Zhu S., Zhu X., Smith H.O.,
RM Chbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
Scheeder C., Stather J.C.,
Scheeder C., Stather J.C.,
Scheeder X.H., Zhong W., Zhong X., Zhu S., Zhu X., Smith H.O.,
Scheeder X.H., Zhong W., Rubin G.M., Venter J.C.,
Scheeder C., Stather J.C.,
Scheeder C., Stather J.C.,
Scheeder C., Stather J.C.,
Scheeder X.H., Zhong W., Shong W., Wenter J.C.,
Scheeder X.H., Zhong W., Shong W., Scheeder J.C.,
Scheeder X.H., Zhong W., Shong W., Shong W., Shith B.O.,
Scheeder X.H., Zhong W., Shong W., Shith B.O.,
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Scheeder C., Stather J.C.,
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100.0%; Pred. No. 45;
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EMBL: AJJ48288; CAB50F2.1; -1
Hypothetical protein; Complete proteome.
SEQUENCE: 108 AA; 12527 NW; 17027AAA8A659C1 CMC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA; 12104 MW; AE21FB9EF5/7163A CRC64;
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01-MAY-2000 (TrEMBLrel. 13. Last sequence update)
01.JUN-2000 (TrEMBLrel. 14. Last annotation update)
HYPOTHETICAL 12.5 KDA PROTEIN.
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SEQUENCE 107 AA; 12134 MW:
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.....COKTIOQLETVLCEPLQSYF 2144 05170 Scoring table: Sequence.

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562222 scqs, 172994929 residues Scarched:

9 Word size : 18464 Total number of hits satisfying chosen parameters:

Minimum DB seq length. 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

sp\_fung1:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organe!le:\* sp\_vertebrate:\*
sp\_unclassified:\* sp\_rvirus:\* sp\_bacteriap:\* SPTREMBL\_19:\* l: sp\_archea:\* 2: sp\_bacteria:\* sp\_plant:\*
sp\_rodent:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

#### SUMMARIES

| Desertption                   | Q96es5 homo sapien | U9y8c3 coprinus ci | Q9w467 drosophila | Oguxul pyrococcus  | garxay demococcus | O57720 pyrococcus | Q9yd74 aeropyrum p | Q9q144 macaca mula | Q9v2d5 pyrococcus | Q91f40 arabidopsis | Ogjmet listeria mo | Q975w6 sulfolobus | vý6kcz homo sapien | Q9d4p0 mus musculu | Q92c81 listeria in | Q9k6g3 bacillus ha |
|-------------------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| B 15                          | 4 Q96ES5           | 3 09¥8€3           | 5 09W467          | 17 09U <b>x</b> U1 | 16 Q9RXU9         | 17 057720         |                    |                    | 17 Q9V2D5         |                    |                    | 17 Q975W6         |                    | 11 Q9D4P0          | 16 092081          | 16 Q9K6G3          |
| å<br>Query<br>Match Length DB |                    |                    | ,                 | ,                  | •                 |                   |                    |                    |                   |                    |                    | 0.4 167           |                    |                    |                    | 0.4 188            |
| O<br>Score M                  | 127                | œ                  | 30                | æ                  | 30                | œ                 | œ                  | œ                  | 80                | 00                 | 80                 | œ                 | 8                  | æ                  | <b>3</b> 0         | <b>3</b> 0         |
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RESULT

| 09aby8 caulobacter<br>09kts7 vibrio chol<br>09lan6 eriphyas po<br>099jil calman eroc | 745752 raenorhabdi<br>Q99188 mus musculu<br>714912 homo sapien<br>raenaf rana luteny | rana<br>homo<br>homo | 30 C 31                 | 4846                                             | 699492 hindebacter<br>699492 hindebacter<br>09ptwl campylobact<br>09ptwl campylobacter<br>691422 liberibacter |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| 16 Q9AHY8<br>16 Q9KTS7<br>12 Q91GN6<br>7 Q9GJN1                                      | 5 045352<br>11 099188<br>4 014912<br>8 045055                                        |                      | 000                     | 16 091284<br>11 091w08<br>16 098bw1<br>16 092r33 | \c                                                                                                            | 2 09FAA0<br>2 09FAA0<br>2 09A014<br>16 007A40<br>16 098K07<br>2 059K11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 213<br>234<br>251<br>253                                                             | 256<br>276<br>288                                                                    | 300<br>307<br>339    | 343<br>4194<br>94       | 431<br>439<br>453<br>456                         | 469<br>470<br>481                                                                                             | 4 4 8 1 4 8 8 1 4 8 8 1 4 8 8 1 4 8 8 1 4 8 8 1 4 8 8 1 4 8 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 4 8 1 8 1 |
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| ထဆငာေသာ                                                                              | ac ao ao 10                                                                          | ထောင်လေ              | ထထထင                    | ထထထထ                                             | ασα ασο ο                                                                                                     | ထေသထထထထ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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## ALLIGNMENTS

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APPLICANT: Chen, Xianleng
APPLICANT: Chen, Xianleng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: FIRMITS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)A
GURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12910
LENGTH: 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: et al.
TITLE OF INVENTION: Plant Receptors and Ligands
FILE PREPERENTE: 1066P
CURRENT APPLICATION NUMBEP. HS/6n/382,898
CURRENT PILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 1344
SOFTWARE: FASISEO for Windows Version 4.0
SEQ ID NO 332
LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(624)
OTHER INFORMATION: unsure at all Xaa locations
             US-60-360-039-12910
; Sequence 12910, Application US/60360039
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 332, Application US/60382898
GENERAL INFORMATION:
APPLICANT: Hudson, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana
US-60-382-898-332
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Aspergillus nidulans
                                                                                                  APPLICANT: Cao, Yongwei
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US-60-382-898-332
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APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHORS THEREOF CAPA
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE PEPERENCE: 2759-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT PILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 9919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POSTUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
TITLE OF INVENTION: MODULATING VARIOUS PESSONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-03-24
NUMBER OF SEQ ID NOS: 33136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 8; DB 5; Length 603;
100.0%; Pred. No. 1.2c+02;
Lve. 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.1e+02;
Sive 0; Mismatches 0;
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0.4%; Score 8; DH 5; Ler
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 6;
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US-09-935-625-9919
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OTHER INFORMATION: Ceres Sec. ID no. 3086967
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tive 0; Mismatches
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; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Hest Local Similarity 180.v
-hea 8; Conservative
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Rest Local Similarity 100.0
Matches 8; Conservative
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                                         US-09-573-655B-1077
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                                                                                                                      THEO FINVENTION: NOTLER ACTO AND AMINO ACTO SEQUENCES RELATING TO BACTEROIDES FRA
THE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 1001-001
CORRENT APPLICATION NUMBER: 08,794,740,204R
CORRENT FILING DATE: 2000 04-04
NUMBER OF SEQ 10 NOS: 10444
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-0876P
CHIER REFERENCE: 2750-0876P
CHIER REFERENCE: 2750-0876P
CHIER APPLICATION UNMARK: US/09/573.6558
NUMBER FILING DATE: 20.00-05-18
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APPLICANT: chan, xiantenq
APPLICANT: dolan, Barry S.
APPLICANT: Hinkle, Gredory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: FXFRESSION OF MICPORIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 18-10/52052)A
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100.0%; Pred. No. 94;
1ve 0; Mismatches
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Fred. No.
                                                         ; Sequence 8954, Application US/09540209B; GENERAL INFORMATION:
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00.0%; Pre
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Best Local Similarity 100.0
East Local 8; Conservative
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Rest Local Similarity 00.0
Matches 8: Conservative
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US 09-540-2098-8954
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Sequence 1077, Applic
GENERAL INFORMATION:
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US 60 360 039 20635
                                  US-09-540 209B 8954
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LENGTH: 543
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LENGTH: 467
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US-10-105-299-4155
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US-09-688-017-299
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100 0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
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CURRENT FILING DATE. 2002.03-26
NUMBER OF SEQ ID NOS: 15197
PLICA Application removed - See File Wrapper or Palm ScriwARE. Patchtin Ver. 2 0
SEQ ID NO 4155
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CURRENT FILING DATE. 2002-04-05
NUMBER OF SEQ. ID NOS: 763
NUMBER OF SEQ. ID NOS: 763
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION: al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
              PRIOR APPLICATION NUMBER: US 60/196,267
PPING PILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/195,400
PRIOR PILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEC 10 NOWER: US 60/196,528
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEC 10 NOS: 383
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US-10-116-355-211
Sequence 211, Application US/10116355
GHNERAL INFORMATION:
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Best Loral Similarity 100.09
warrhes 8; Conservative
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Best Local Similarity 100 C
Matches 8, Conservative
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US-10-116-355-211
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LENGTH: 78
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TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
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0.4%; Score 8; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels
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DB 6; Length 179;
                                        0; Indels
0.4%; Score 8; DH 6;
100.0%; Pred. No. 38;
tive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 18999
                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 38-21(15:40) TO PUAL CURRENT APPLICATION NUMBER. US/10/155,881 CURRENT FILING DATE: 2002-05-22 NUMBER OF SEQ 1D NOS: 37595
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GENERAL INFORMATION.
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; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 8; Conservative
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OPGANISM: Glycine max
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US-10-155-881-32064
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Best Local Similarity
Matches 8; Conserv
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US-10-155-881-32064
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PRIOR APPLICATION NUMBER: US 60/176,195
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PPIOP APPLICATION NUMBER-
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US-09-688-017-299
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SOFTWARE, FAST
SEQ ID NO 276
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TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
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PRIOR FILLING DATE: 2000-04-11
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PRIOR PELLING DATE: 2000-05-12
PRIOR PELLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 09/570.118
PRIOR APPLICATION NUMBER: US 09/570.364
PRIOR APPLICATION NUMBER: US 09/588.017
PRIOR PELLING DATE: 2000-05-12
PRIOR FILLING DATE: 2000-05-13
PRIOR FILLING DATE: 2000-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : OTHER INFORMATION: TAX TP 43 PTV domain 1
US-09-710 059-276
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CURRENT FILING DATE: 2000-11-24
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162.493
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170-454
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PRIOR APPLITATION NUMBER: US 60/7162,498
PRIOR FILING DATE: 1999-10-29
PRIOR PILING IN NUMBER: US 60/770,453
PRIOR FILING DATE: 1999-12-13
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/156,528
PRIOR FILING DATE: 2000-04-11
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PRIOR APPLICATION NUMBER: US 60/160,860
                                                                                                                                                                                                               MMBER: US 50/182.295
2000-02-14
                                                                                                                                                                                                                                                                                       PRIOR FILLNG DATE: 2000-04 11
PRIOR APPLICATION NUMBER: US &0.7196 460
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PRIOR APPLICATION NUMBER: US 60/154/117
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PRIOR APPLICATION NUMBER: US 68/134,11#
                                                                                                                                  PRIOR FILLING DAFE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176.195
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US ADVIGA 267
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rabinowitz, Joshua D. APPLICANT: Schweizer, Johannes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    020054 - 00112208
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ORGANISM: Artilicial Sequence
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                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-03
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Best Local Similarity
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APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: 020054-0011100S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 8: 58 Scott 72; Best Local Similarity 100.0%; Pred. No. 16; Matches 8; Conservative 0: Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 09/570,118
PRIOR FILING DATE: 2000-05-12
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PRIOR FILING DATE: 2000-10-13
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PRIOR PILLING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR PILLING DATE: 1999-10-21
PRIOR PILLING DATE: 1999-10-21
PRIOR PILLING DATE: 1999-10-22
PRIOR PILLING DATE: 1999-10-25
PRIOR PILLING DATE: 1999-10-25
PRIOR PILLING DATE: 1999-10-25
PRIOR PILLING DATE: 1999-10-15
PRIOR PILLING DATE: 1999-12-13
PRIOR PILLING DATE: 2000-01-14
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THE REPERBECE: 020054-001110US
CURRENT APPLICATION NUMBER: US/09/688.017
CURRENT FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
                                                                                      PRIOR APPLICATION NUMBER. US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                                                                   FILLING DATE: 2000-04-11
APPLICATION NUMBER- 9S 69,196,128
FILING DATE: 2000-04-11
PRIOR FILLING DATE: 2000-01-14
FRICE APPLICATION NUMBER: US PO/182,296
PRIOR FILING DATE: 2000-02-14
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PRIOR FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 299, Application US/U9668017
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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GenCore version 4.5 copyright (c) 1993 - 2000 Compagen Ltd.
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UM protein - protein search, using sw model

July 2, 20e2, 15:35:17 ; Scarch time 43 Seconds Run on:

(without alignments) 5036.685 Million cell updates/sec

CONTIQUETVICEPLOSYF 2144 US-09-603-665-5 Perfect scure:

1 MTSLAQQLORLALPQSDASL 0[11]0 Scoring table: Sequence

Gapop 60 0 , Gapext 60.0

307805 seqs, 101015595 residues

Word size :

Searched:

10746 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New.\*

1. /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*

2. /cgn2\_e/prodata/1/paa/US06\_NEW\_COMB.pep:\*

3. /cgn2\_e/Fi-data/1/paa/US07\_NEW\_COMB.pep:\* /cgn2\_b/ptodata/1/paa/USGR\_NFW\_CMB.pep:\*/cgn2\_b/ptodata/1/paa/USG\_NFW\_CMB.pep:\*/cgn2\_b/ptodata/1/paa/USIO\_NFW\_COMB.pep:\*/cgn2\_b/ptodata/1/paa/USiO\_NFW\_COMB.pep:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

0; Gaps

Query Match 0.5%; Score 10; DB 6; Length 565: Best Local Similarity 100.0%; Pred. No. 1.3; Matches 13; Conservative 0, Mismatches 0; Indels

|               |       | œ              |                       |     |                                   |                   |
|---------------|-------|----------------|-----------------------|-----|-----------------------------------|-------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length | DB  | ID                                | Description       |
|               | 10    | 0.5            | 595                   | ۵   | US-10-141-675-2                   | Sequence 2, Appli |
| C             | 80    | 0.4            |                       | 2   | US-09-710-059-276                 | Sequence 276, App |
| 8             | 80    | 0.4            | 7.5                   | 5   | US-09-722-069-276                 |                   |
| 4             | 8     | 0.4            |                       | 2   | US-09-688-017-299                 | 299,              |
| ហ             | œ     | 0.4            | 44                    | ٥   | US-10-116-355 211                 | Sequence 211, App |
| 9             | œ     | 0.4            | 179                   | ÿ   | US-10-105-299-4155                | Sequence 4155, Ap |
| 7             | 80    | 0.4            | 205                   | 9   | US-10-155-881-32064               | Sequence 32064, A |
| 8             | æ     | 4.0            | 200                   | ٥   | US-1U-155-881-18999               | 18999,            |
| 6             | œ     | 4.0            | 467                   | Ľ:  | US-09-540-209H-8954               | Sequence 8954, Ap |
| 16            | Ġ     | 10.4           | 5.4.3                 | _   | 58 -60 360-039 20635              | 20635,            |
| 11            | 80    | 4.0            | 554                   | 5   | US-09-573 655B-1077               |                   |
| 15            | œ     | 0.4            | 603                   | Ľ   | US-06-632-652-6016                |                   |
| 13            | 80    | 0.4            | 909                   | ľ   | 8166-520-336-6080                 | Sequence 9918, Ap |
| 14            | 80    | 0.4            | 624                   | 7   | US-60-360-039-12910               | ò                 |
| Υ.            | œ     | 0 4            | 664                   | 7   | US-60-382-898-332                 | Sequence 332, App |
| 16            | - œ   | 4.0            | 418                   | 7   | HS-60-360-039-18355               | Sequence 18355, A |
| 17            | 00    | 0.4            | 1082                  | Ľ   | 118-09-935-625-25456              | Sequence 25456. A |
| 18            | 8     | 0.4            | 1192                  | ر ۲ | US-09 935-625-25455               | Sequence 25455, A |
| 19            | 80    | 0.4            | 1215                  | un: | US U9-935 625-25454               | -                 |
| 20            | 8     | 7.0            | 1357                  | u D | US 09-573 6558-2227               | Sequence 2227, Ap |
| [2            | 30    | ÷.             |                       | 7   | 4.5 - 6.0 - 36.0 - 0339 - 6.34 6. | Sequence 6346, Ap |
| 22            | 7     | 0.3            | 15                    |     | US-10-134-519 1                   | γpp               |
| 23            | 7     | 0.3            | 57                    |     | -155                              | 6943,             |
| 24            | 7     | 0.3            | 58                    | LΊ  |                                   |                   |
| 2.5           | 7     | 0.3            | 3                     | LT. | US:09:620 3938:2792               | 2792,             |
| 36            | 7     | 0.3            | 2 Û                   | L"  | 08 09 620 - 144B 3023             | Sequence 3023, Ap |

APPLICANT: Schauzer, Johannes
APPLICANT: Schauzer, Johannes
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
FILE PEPERNCE 020054 0011200S

Rabinowitz, Joshua D. Schweizer, Johannes Arbor Vita Corporation

APPLICANT.

Sequence 276, Application US/09710059 GENERAL INFORMATION: APPLICANT: Lu, Peter S.

RESULT 2 US 09-710-059-276

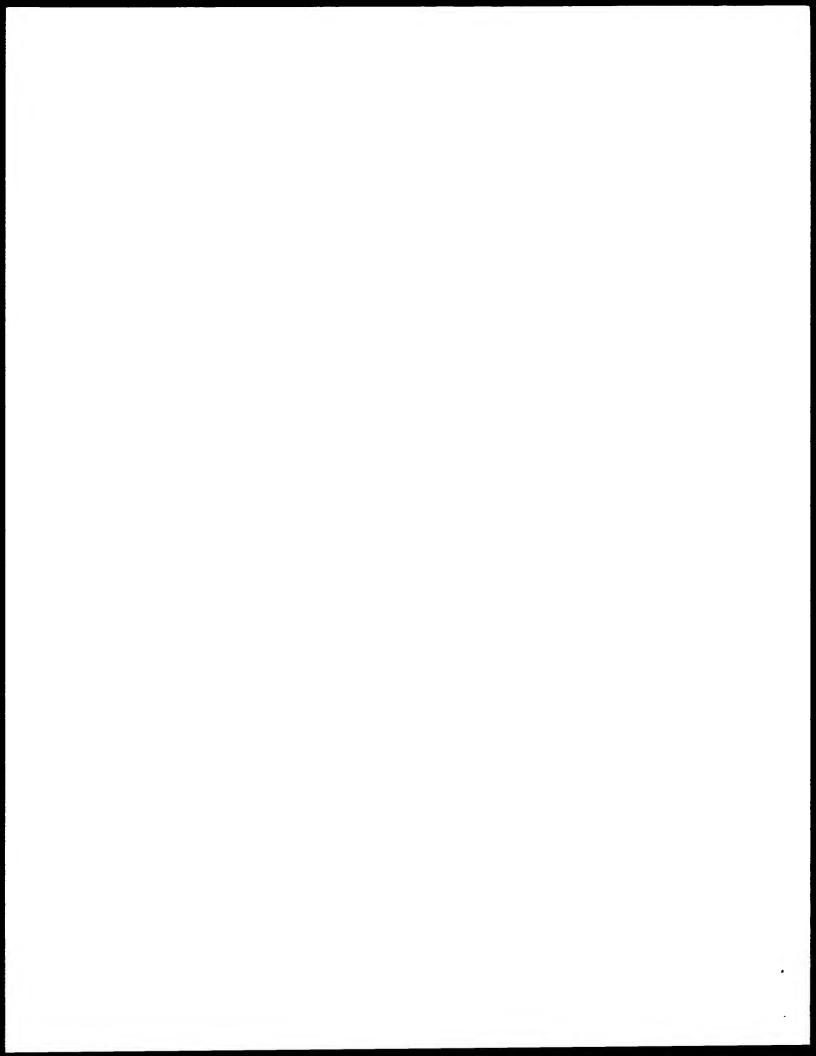
CURRENT APPLICATION NUMBER - US/09/710,059 CURRENT FILLING DATE: 2000-10-11

CURRENT FILING DATE:

PRIOR ADVILGATION NUMBER: US 60.134.111
PRIOR FILING DATE: 1999-05-14
PRIOR PLING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR PADLICATION NUMBER: US 60/134,117

PPIOR FILLING DATE: 1999-05-14

| 27 7 0.3 77 5 US-09-620-3938-3022 28 7 0.3 88 5 US-09-620-3938-3022 30 7 0.3 89 5 US-09-920-620-898-89 31 7 0.3 90 6 US-10-15-881-8021 32 7 0.3 90 6 US-10-13-881-8021 33 7 0.3 102 5 US-09-32-525-30858 34 7 0.3 102 5 US-09-620-3938-3021 35 7 0.3 102 5 US-09-620-3938-3021 36 7 0.3 104 6 US-10-106-698-4689 38 7 0.3 111 1 PCT-IL02-00174-31 37 7 0.3 112 6 US-10-106-688-4689 38 7 0.3 118 6 US-10-106-688-4689 38 7 0.3 118 6 US-10-106-688-4689 40 7 0.3 123 6 US-10-144-702-685 42 7 0.3 123 6 US-10-144-702-685 43 7 0.3 138 5 US-09-935-625-30857 44 7 0.3 138 5 US-09-935-625-30857 45 80 US-08-8 US-                                                                                                                                                                                                                                                                                                                                                                                     | Sequence<br>Sequence               | ტგგ9 — ჯ <del>ი</del> ლონობი 10859, გ<br>ტგნგ — ჯილონობი 10858, გ | Sequence        | Sequence       | i Sequence      |                | Sequence bool    | 31 Sequence 31, Appl | andantag        | Seduction                | Sequence         | 1011410000      | Sequence        | econences       | 0675 Sequence   | Sequence       |            | orter Family                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 0.3                                |                                                                   | n.0             | 0.3            | 0.3             | 0.3            | 0.3              | e. 0                 | 5.0             | ~. ~                     |                  |                 | . e.            | F.0             | 0.3             | 0.3            |            | US-10-141 675-2 Sequence 2. Applicat GENERAL INFORMATION: APPLICANT CURTIS, TITLE OF INVENTION FILE REFERENCE: MPI CURRENT FILING DATE: PROW FILING DATE: PROW FILING DATE: PROW FILING DATE: NUMBER OF SEQ ID NO SOFTWARE: FastSEQ F SEQ ID NO SOFTWARE: FastSEQ F SEQ ID NO TYPE: PRT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |



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RESULT 15
S44768
C2964.7 protein - Cacmorhabditis elegans
C;Species: Cacmorhabditis clegans
C;Species: Cacmorhabditis clegans
C;Date: 14-Sep-1994 #sequence_revision 12 May-1995 #text_change 23-Mar 2001
C;Accession: $44768
K;Wilson, R.
Submitted to the EMBL Data Library, September 1993
A;Description: Sequence of the C. elegans cosmid C2964.
A;Recference number: $44788
A;Accession: $44768
A;Accession: $44768
A;Status: preliminary
A;Molecule type: DNA
A;Residuaes: 1-250 <WILD-
A;Cross-references: EMH:.L23651; NID:g388575; PID:g388579
C;Genetics:
A;Introns: 49/2; 122/3; 165/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guery Match
Hest Local Similarity 100.0%; Prod. No. 29;
Matches 8, Conservative 0; Mismatches 0; Indels
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684 VEDLISVG 691
                         80 VEDLISVG 87
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                                          <u>q</u>
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Search completed: July 2, 2002, 15:37:28 Tob time: 236 sec

C; Genetics:

RESULT 11

Sdps

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R.Nolling, J.; Breton, G.; Omeicheuko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, K.; L.; Daly, M.J.; Bennett, G.N.; Kconin, E.V.; Smith, D.R.
J. Hacteriol. 183, 4823-4838, 2001
A.TILL: Conference and Companative Analysis of the Solvent Producing Harterium A.Feference number: A96909, MUH:21359325; PM(D:2) 469325
A.Aeression: B97109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Sequence and arrangement of genes encoding sigma factors in Clostridium acer
A; Peterene number: 140626: MIL): 95189110
A; Accession: 140627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AjGene: sigE
C;Superfamily: transcription in tiation factor sigma K; transcription initiation fact
C;Keywords. DNA binding: sigma factor, transcription initiation
F;60-235/Domain: transcription :nitiation factor sigma katE homology <KTE>
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A:Cross-references: GB:AE001437; PIDN:AAK79641.1; PID:q15024459; GSPDH:GNob148
A:Experimental source: Clostridium acetobutylicum A:CC824
                                                                                                                                                                                                                                                                                                                   probable transcription initiation factor sigma E - Clostridium arctobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 12 Aug 1996 #sequence_rrvision 12 Aug 1996 #text_shunge 15 oct-1999 C;Accession: 140627; S34309 EWHOLG, J.; Sass, C., Bennett, G.N. Gene 153, 89-92, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species, Ciustridium acetobutýlicum
C.Date. 14:Sep-2001 #sequence_revision 14:Sep 2001 #text_change 30:Sep-2001
C.Accession: B97109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross references: EMBL:U07420: NID:g705344; PIDN:AAC433U9.1; PID:g4659971 R.Sauct, U., Treuuet, A., Buchholz, M.; Duerre, P. submitted to the EMBL Data Library, June 1993.
A:Degcription: Sigma factor homologous genes in C. aretobutylicum.
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                                        Indels
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Rest Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches
      Pred. No. 28;
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Matches 8; Conservative 0; Mismatches
                                     Mismatches
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C
      100.0%;
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A.Recession: $14309
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 46-146, P',148-235
A.Cross-references: EMBL:223079
                                     Conservative
          Best Local Similarity
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A, Residues: 1-235 <RES>
                                                                                                  1038 AEQULEKI 1045
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                                     Matches
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A)Cross-reterences: GB:AE004166; GB:AE003852; NID-q9655259; PIDN-AAF93975.1; GSPDB:GN001
A:Experimental source: serogroup ol; strain N16961; blotype El Tor
                                                            A,kesidues: 1–188 / SIO.
A:Cross references: GR:APO01519; GR:BAOCOOCA; NID:q10175109; PIDN:BAB07485.1; GSPDB:GNOC
A:Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Elsen, J.; Heidelberg, J. H.; Jauly, M.C.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolod n. S.; Lim, Levis, M. White, D., Sallskard, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414; Z.D.; Zool n. Complete Genome Sequence of Caulobacter crescentus.
A.Felerence number: AR7249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charession, GB1276
RiHeidelberg, J.F.; Elsen, T.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.N.; Vamathevan, J.; Hass, S.; Oin, H.; Dragol, I.; Sellers,
L. R.R.; Mokalanos, J.J.; Varter, J.C.; Fraser, C.M.
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hypothetical protein VCO811 [imported] - Vibrio cholerae (strain N16961 serogroup Ol)
C.Species: Vibrio cholerae
C.Date: 18 Aug. 2000 #sequence_recision 20-Aug-2000 #fext_change 02 Feb-2001
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A:Acression: GB22756
A:Status: Preliminary
A:Status: Preliminary
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Cigenetics:
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C.Date: 20 Apr.2001 #sequence_revision 20.Apr.2001 #Lext_change 20 Apr.2001
C.Arcession: A87259
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hypothetical protein 050082 [limported] - Caulobacter crescentus
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C:Supertamily: Bacillus subtilis hypothetical protein ywld
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[00.0%; Pred, No. 23;
.ve 0: Mismatches
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Best Local Similarity (00....
Eng 8, Conservative
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A; Residues: 1-213 (Slo)
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196 1.I.SRDEVA 203
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A:Status: preliminary
A:Molecule type: DNA
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A:Gene: 000082

Ouery Match

Matches

RESULT 12

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R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Fsihl, Johnes, L.M.; Karst, U.
Sciantor 2: M.; Karst, U.
Sciantor 2: M.; Rarst, U.
Sciantor 2: M.; Rarst, U.; Simoes, N.; Ticrez, A.; Vacquez-Boland, J.A.; Voss, H.; Wehla A; J.; Litle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MITD-21537279; PMID:11679669
A; Status: proliminary
A; Sciants: proliminary
A; Sciants: proliminary
A; Sciants: Draw A; Substantial Sciants: Status: Status: Ciphl26
C; Genetics: A; Signal poptidase I sipS
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Macno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Fes. 28, 4317-4331, 2000
Nucleic Acids Fes. 28, 4317-4331, 2000
Ancleic Complete genome sequence of the alkaliphilic bacterium Haciilus halodurans a
A,Perience number: Aki650; MHID 20512582; FMIC:11058132
A,Accession: F84120
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Authors: Kreft, J.; Kuhn, M.; Terrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A.Reference number: AB1077; MIID-21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal peptidase I homolog Imo1271 [imported] – Listeria monocytogenes (strain EGD-e)
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C.Date: 27-Nov-2601 #sequence_revision 27-Nov 2001 #fext_change 14 hec.2601
C.Accession: AG1233
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C.Date: 01-Dec-2000 #sequence_revision 01-Por-2000 #text_change 15-Jun-2001
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illarity 100.0%; Pred. No. 22;
Conservative 0; Mismatches
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0; Mismatches
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Rest Loral Similarity 100.0%; Pred. No
Matches 8; Conservative 0; Mismat
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C.Superfamily: signal peptidase 1 sipS
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A:Residues: 1-180 <GLA>
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submitted to the Protein Sequence Database, August 2000
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A;Accession: H75201
A;Accession: H75201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1/146 «KAM»
A)Cross references: GB:AJZ48283; GB:ALÖ96835, NIL.95457433, FIDN:CAR49063.1, PID:e151499
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C;Date, 27 Nov-2001 #Sequence_L=vision 27-Nov 2001 #Text_-bhange 14-Der 2001
C;Accession: AE1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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C;Species: Arabidopsis thalland (Mouse car cress)
C;Dute: 18-And-2000 #sequence_revision 18-And 2000 #text_change 18-Aug 2000
C;Accession: T51520
                                                                                                                                                                                                                                                                                                              CiSpecies: Pyrococcus abyssi
Cibate: 20-Aug-1909 #sequence_revision 20 Aug 1999 #fext change ux-Sep.2000
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C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088
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A,Experimental source: cuitivar Columbia, BAC clone T20K14
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100 0%; Pred. No. 18;
ive 0; Mismatches
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100.0%; Pred. No 19;
Live 0; Mismatches
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R;anonymous, Genoscope
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A; Molecule type: DNA
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A;Note: T20K14_30
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granulocyte-macrophage colony-stimulating factor precursor [validated] - human N.Alternate names: colony-stimulating factor 2; GM-CSF C.Species: Homo sapiens (man) - C.Species: Homo sapiens (man) - C.Species: Homo sapiens (man) - C.Sate C.S
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R.Kaaslabaky, K., O'faira, P.J.: Berknot, K.; segal, G.M.; Hagen, F.S.: Adamson, J.W.
B.Kaaslabaky, K., O'faira, P.J.: Berknot, R.; segal, G.M.; Hagen, F.S.: Adamson, J.W.
Proc. Natl. Acad. Seri. U.S.A. 81, 3101-3105, 1986
A.Tille: Genomic cloning, characterization, and multilineare growth promoting activit
A.Reterence number: 159065, MUID:86205844
A.Accession: 159065
A.Status: translated from GA/EMHI./DDBJ
A.Molecule type: DNA
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Alfitle: Cloning, sequence, and expression of a human granulocyte,/macrophage colony s. A.Reterence number: A25169; MUID:85298329.
A.Reterence number: A25169; MUID:85298329.
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A:Residues: 1-144 <CAN>
A:Residues: 1-144 <CAN>
A:Cross-references: GBIN1/34; NID:q181149; PIDN:AAA52122.1; PID:q181150

K.icc, F., Yokota, T., Gtsuka, T., Gemmed J. i., iatson, N.; imb, J.; Aral, K.; Mennic Proc. Natl. Acad. Sci. U.S.A. 8; 4360-4364, 1985

A:Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating fact A:Relerence number: A01853; MUID:85242684

A:Relerence number: A01853
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F.Wong, G.C., Wifek, J.S.: Temple, P.A.; Wilkens, K.M.: Leary, A.C.: Luxenberg, D.P.:
A.; Clark, S.C.
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ACTA Hockim. Biophys. Sin, 25, 651-655, 1993.
ANTIELE. Amplification of human grandlocyte marrophage colony stimulating factor cluna.
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C.Reywords, cytokine, glycoprotein, growth factor, macrophage, monomer, T cell
E]1-17/Domain: signal sequence #status predicted <SIG>
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A)Cross-references- GR-MIG663, NID:q181145, FIDN:AAA52121.1, PID:q181146
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A;Introns: 53/3; 67/3; 109/3
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A;Accession: JC1090
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A;Residues: 1-144 <MIY>
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C:Datc: 20 Aug-1999 #sequenre_revision 20 Aug 1999 #fext_chunge 20 Jun-2000
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C:Date: 03 Dec:1999 #sequence_revision 03-Dec-1999 #text_change 31 Mar-2000
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    Score 8; DB 1;
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    c; Supertamily: cytidine deaminase
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                                                                                    Conservative
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                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Molecule type: DNA
A:Residues: 1 123 *KAW.
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DB 1; Length 144;

0.4%; Score 8; DB l 100.0%; Pred. No. 18;

Query Match Best Local Similarity

GenCore version 4.5 Copyright (c) 1993 - 2000 rompugen Ltd.

protein search, using sw model OM pretein July 2, 2002, 15 33 32 , Search time 40 91 Seconds Run on:

(without alignments) 5035 824 Million rell updates/ser

US-09-603-665-5 Perfect score:

COKTTODILETVIJEPLOSYF 2144 2144 1 MTSIAQQIQRLALPQSDASI..

01710 Scoring table: Sednence:

283138 sods, 46089334 residues Searched.

Gapop 60.0 , Gapext 60.0

Word size :

11028 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000030000

Post-processing: Listing first 45 summaries

PIR\_71.\* 1: pir1:\* pir3:\* pir4:\* pir2:\* Database ·

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|                  | Description           | hypothetical profe | hypothetical prote | probable cytidine | hypothetical prote |        | hypothetical prote | hypothetical prote |        | signal peptidase I | hypothetical prote |        |        | =      | DNA dependent PNA | Case4 7 protein | hypothoctical prote |        | conserved hypother | oxidoreductase Atu | C02D5.3 protein | hemocyanin - giant | phosphoglycerate k | probable vesicular | probable obemetaxi | probable terminal | 3-1Sopropylmalate | ryanide insensitiv | hypothetical prote | betal syntrophin - |
|------------------|-----------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------|-------------------|-----------------|---------------------|--------|--------------------|--------------------|-----------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|
| SUMMAPIES        | 110                   | 875029             | G71214             | 302325            | B75546             | FOHUGM | H75201             | T51520             | AE1596 | AG1233             | F84120             | AR7259 | CP2276 | 140627 | Fe4.7 11194       | 5447ER          | 1.0406              | D98344 | AC2938             | ACA221             | 344745          | A31137             | 868151             | 140014             | G83404             | A:10546           | A81270            | 147273             | 128687             | 159291             |
|                  | OB                    | 7                  |                    | ۲.                | 7                  | -      | C1                 | ୍ୟ                 | ~      | ್                  | C                  | C i    | Ci     | C.1    | ٠,                | ٠,              | e a                 | ٠.     | (4                 | C 1                | :4              | 7                  | C 1                | C1                 | CA                 | ~ )               |                   | •                  | C 4                | CA                 |
|                  | Query<br>Match Length | 108                | 123                | 123               | 123                | 144    | 146                | 159                | 180    | 180                | 188                | 213    | 5 ₹ 4  | 5 × C  | 45                | C v             | 1117                | 309    | 304                | 429                | 379             | 399                | 417                | 419                | 431                | 467               | 470               | 4 B B              | 다<br>(1            | 538                |
| a <del>k</del> o | Query<br>Match        | 4.0                | 4.0                | 0                 | 0.4                | 0.4    | 0.4                | <b>4</b> .0        | 0.4    | 0.4                | 4.0                | 0      | 0.4    | O<br>4 | 0                 | ت<br>4          | • <del>•</del>      | C      | 0.4                | 0                  | 0.4             | 0.4                | 0.4                | 0.4                | ∪<br>4             | 0.4               | O.4               | ∪ 4                | ٥.4                | 0.4                |
|                  | Score                 | - 30               | œ                  | æ                 | ဆ                  | 80     | 80                 | œ                  | œ      | æ                  | æ                  | œ      | Œ      | œ      | æ                 | 8               | œ                   | æ      | æ                  | æ                  | æ               | œ                  | 30                 | æ                  | α·                 | œ                 | 20                | α                  | α                  | ဆ                  |
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| probable impoprate | L-lactate permease | FFP14 23 protein - | probable protein k | hypothetical prote | hypothetical prote | endopeptidase Clp | hypothetical prote | cation-transportin | hypothetical prote | hypothetical prote | probable DNA polym | probable disease r | micropia polyprote | trichohyalin' she | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| 873383             | A70038             | G86449             | C84747             | T08932             | AC2023             | E35905            | T30023             | F86709             | T.73 540           | T35548             | T36761             | H84513             | \$02021            | A40691            | AD2443             |
| ~                  | ~                  | C)                 | 7                  | 7                  | C 1                | ,_                | C 4                | 7                  | ٠,                 | ~1                 | 7                  | <b>~1</b>          | C 1                | Ţ                 | 74                 |
| 541                | 563                | 60A                | 664                | RNA                | 819                | 862               | 875                | 918                | g ¥.<br>₹.         | 1171               | 1185               | 1215               | 1291               | 1549              | Tally<br>T         |
| _<br>•             | 0.4                | 0 4                | 0.4                | <b>₽</b>           | 0.4                | 0.4               | Ü                  | 0.4                | : 4                | 0.4                | 0.4                | 0.4                | 0.4                | 0.4               | 9.4                |
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| œ                  |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |                   |                    |

### ALIGNMENTS

RESULT

hypothetical protein PAB1179 - Pyrococcus abyssi (strain Orsay) C,Species. Pyrococcus abyssi C,Date. J0 Aug 1999 #Seguence\_revision 20.Aug 1999 #text\_change 20-Jun-2000

C. Accession: B75029
B. Annonymous, Genesation: B75029
B. Annonymous, Genesation: B75029
B. Annonymous, Genesation: B75029
B. Annonymous, Genesation: B75029
B. A. Reference number: A75001
B. A. Reference number: A75001
B. A. Recalled to the BML Day of General Sequence insights into archaeal chromosome s. A. Reference number: A75003
B. Status: preliminary
B. Molecule Uppe: DNA
B. Residues: 1 108 cKAW
B. Residues

A; Gene: PAB1179

C.Supertamily, Methanococcus januaschii conserved hypothetical protoic MIO223

Gaps ., O Length 108; u; Indels DH 2; э. 14; Query Match 0.4%; Score 8; DH 2 Best Local Similarity 100.0%; Pred. No. 14; Matches 6; Conservative 0; Mismatches

0

TESS KKKEGERE TAKE

62 KKKKGEEF 69 qq

RESULT

Apportectional protectin PH1983 - Pytococcus horikoshii CiSpecties: Pytococcus horikoshii CiSpecties: Pytococcus horikoshii CiPerci 10 Septembra Escapedae Fevision 10 Sept1999 #fext\_change 21 Jul 2000 CiSpecties 371214 Fixawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamameto, S.; Sept. Pytoniku, Y.; Fumanashi, T.; Tanaka, T.; Rudeh, Y.; Yamaraki, T.; Eushida, N.; Oqu Angler escapedae sequence and gene organization of the geneme of a hyper-thermophility A;Reference number: A71000, MD10-98344137

A.Arression: 071214 A.Status. preliminary: nucleic acid sequence not shown, translation not shown A.Molecule type: DNA

A)Residues: 1123 KKM>
A)Residues: 1123 KKM>
A)Cross-references. GB.A-000007, N.D.92230134; PIDN.BAA31110.1; PID.93258127
A)Experimental source: strain orga
A)Croce. this accession replaces an interim accession for a sequence replaced by GenBa C)Genetics:

A;Gene: PH1983

C.Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0223

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lo, Conservative
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                               ; ORGANISM: HUMAN
US-60-230-445-1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-60-230-445-1930
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                                                                                                                                                                                                            SEQ ID NO 1772
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                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                    Matches
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100.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 10; DR 26; Length 512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Indels
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TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0149 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. ...
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US-60-216-547-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/822,863 CURRENT FILING DATE: 2001-04-02 NUMBER OF EDID NOS: 4 SOFTWARE: FastEBO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/216,547
                                                Sanjanwala, Madhu Sudan
Baughn, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09822863
; GENERAL INFORMATION:
                                                                                                                                                      Hafalia, April
Tribouley, Catherine M.
Walia, Narinder K.
                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-07-07 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PERL Program
                                                                                                                     Patterson, Chandra
Gandhi, Ameena R.
                                    Greene, Barrie D.
                                                                                                                                                                                                     Au-Young, Janice
Walsh, Roddy
Ramkumar, Jaya
                                                                                                                                                                                                                                                                        Lu, Dyung Aina M.
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Matches 10; Conservative
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                                                                                     Yan, Monique G
   Harland, Lee
Burford, Nell
                                                                                                       Yang, Junming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORCANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                           Lu, Yan
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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPOPTER PPOTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER FRCTEIHS,
TITLE OF INVENTION: AND USES THEREOF
FILL REPRESENCE: CLOGO765
CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT PILLING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3051
SOUTHARDER OF SEQ ID NOS: 3051
SOUTHARDER PESESEQ IOF WINDOWS VEFSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NICLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND HSES THEREOF FILE REFERENCE: CLOODAS
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lbu.0%; Pred No 12;
tive 0; Mismatches 0; Indels
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100.0%; Fred. No. 12;
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Five 0, Mismutches
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CURRENT APPLICATION NUMBER: US/60/230,445
CURRENT FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1930, Application US/60230445
     US-60-230-445-1772; Sequence 1772, Application US/60230445; GENERAL, INFORMATION:
RESULT
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89 SVRRKALDLL 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2064. Apptheation US/EUG96409A
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
LITTE OF INVENTION: FOR DIAGNOSTICS AND PHERAPEUTICS
NECTFIC ACID MOLECTIES FUCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                     0.5%; Score 10; DB 26; Length 64;
100.0%; Pred, No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                   0: Indels
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                             CORRENT APPLICATION NUMBER: US/66/196,712 CURRENT FILING DATE: 2000 04-13 NUMBER OF SED ID NOS - 844. SOFTWAKE: FastSED for Windows Version 4.0 SED ID NO 4126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT APPLICATION NUMBER: US/60/096.409A CURRENT FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28206 SEQ ID NO 20694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/248 794
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock of al
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ORGANISM: Candida albicans
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US 09-248-796-20694
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Matches 10; Conservative
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TITLE OF INVENTION:
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US-60 096-409-20694
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LENGTH: 241
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TITLE OF INVENTION: Novel Nucleic Acids and
JITLE OF INVENTION: Polypertides
FILE REFERENCE: 807
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PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PILLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/56,875
PRIOR APPLICATION NUMBER: US 09/56,875
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/517,409
PRIOR PRIOR DATE: 2000-05-18
PRIOR PILLING DATE: 2000-05-18
PRIOR PILLING DATE: 2000-05-19
PRIOR PRILLING DATE: 2000-05-19
PRIOR PILLING DATE: 2000-06-19
PRIOR PILLING DATE: 2000-08-23
PRIOR PILLING DATE: 2000-08-23
PRIOR PILLING DATE: 2000-08-23
PRIOR PILLING DATE: 2000-08-31
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/66/322,511 CURRENT FILING DATE: 2001-09-13
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                              ; Sequence 640, Application US/60322511
; GENERAL INFORMATION:
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Thornton, Michael
Ding, Li
Yue, Henry
Tang, Y.Tom
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                                                                                                                        Yang, Yonghong
Wang, Zhiwei
Weng, Gezhi
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US-60-322-511-640
                                                                                          APPLICANT: Tang, Y. TOM
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US-60-322-511-640
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APPLICANT:
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us-09-603-665-5.olig6.rapm

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OTHER INFORMATION: Xaa equals any of the naturally occurring L'amino acids
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                                                                                                                                                                                                                                                                    44 KVVETLPHFISPYLEGILSQVIHLEKITSEMGSASQANIRLTSLKKTLATTLAPRVLLPA 103
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                                                                                                                                              Ouery Match 3.4%; Score 72; DB 21; Length 135; Best Local Similarity 100.0%; Pred. No. 1.1e-60; Matches 72; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER - US/09/757.028
CURRENT FILING DATE: 2001-01-09
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CURRENT APPLICATION NUMBER: US/09/757,028
CURRENT FILING DATE: 2001-01-09
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GENERAL INFORMATION:
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                                                               ORGANISM: Homo sapiens
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US-09-757-028-2541
                                                                                      US-09-757-028-2590
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LENGTH: 105
SEQ ID NO 2590
                      LENGIH: 135
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APPLICANT: BODAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPHER INFORMATION. Now equals any of the naturally occurring Leamino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; Pted, No. 4.88-42;
; Translobus 0; Indels
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Local Similarity 100.08; Pred. No. 4.86
nes 53; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/60/196,710
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7166
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PRIOR APPLICATION NUMBER: 60/179,065
                       PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
                                                            PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1640
LENGTH: 170
                                                                                                                                                                                               ORGANISM: Homo sapiens
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Best Local Similarity
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US-60-196-710-5862
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LOCATION: (166)
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FILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICHOAPPAY
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EST_HUMAN HIT: ALO40338.1, EVALUE 8.00e-37
SWISSPROT HIT: P42945, EVALUE 2.00e-03
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N: EXPRESED IN HERAL, SIGNAL - 1.4
N: EXPRESED IN HERAL, SIGNAL - 1.7
N: EXPRESED IN FETAL LIVER, SIGNAL - 1.8
N: EXPRESED IN HELIOO, SIGNAL - 1.8
N: EXPRESED IN HELIOO, SIGNAL - 1.8
N: EXPRESED IN HEALN, SIGNAL - 1.8
N: EXPRESED IN HEALN, SIGNAL - 1.3
N: EXPRESED IN HAMIN, SIGNAL - 1.3
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                                                                                                FILE OF INVENTED AND CORRECT SCOOTS AND COURTEN APPLICATION NUMBER: US/09/864,761
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PRIOR FILING DALE: 2001-01-30
PRIOR PELIANI DALE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PG1/ANGAGA
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PRIOR FILING DATE: 2001 01-90
PRIOR APPLICATION NUMBER: PUT/USEL/OBERGE
PRIOR FILING DATE: 2001-09-30
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER - IIS SUZISO 412
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR FILING DATE: 2001-01-29
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                         David K.
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                                                Then, Wensheng
Rank, David R.
Hanzel, David
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PRIOF APPLICATION NUMBER:
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PRIOR FILING DATE: 2001 0
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PRIOR APPLICATION NUMBER:
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3.6%: Score 77: DB 22: Length 77;
             100.0%; Pred. No. 8.9e-56;
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1350 SDSGDSTEVSKNVEETVVKLLSVFVDALPHVPEHRRIPTLVQLVDTLGAEKFLWILLILL 1419

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Best Local Similarity Matches 77, Causers

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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC AND PROMES USEFUL F
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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1 SDSGDSTEVSRNVERTVVKTTSVEVDALPHVPEHRRLPTLVQLVDTLGAERFTWITLILL 60
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N: EXPRESSED IN HELA, SIGNAL. - 1.8
N: EXPRESSED IN HELA, SIGNAL. - 1.4
N: EXPRESSED IN HELA, SIGNAL. - 1.4
N: EXPRESSED IN ADULT LIVER, SIGNAL. - 1.7
N: EXPRESSED IN FETAL LIVER, SIGNAL. - 1.8
N: EXPRESSED IN HALTOU, SIGNAL. - 1.8
N: EXPRESSED IN HALTOU, SIGNAL. - 1.3
N: EXPRESSED IN LUNG, SIGNAL. - 1.3
N: EXPRESSED IN LUNG, SIGNAL. - 1.7
N: EXPRESSED IN LUNG, SIGNAL. - 1.7
N: EXPRESSED IN LONG, SIGNAL. - 1.7
N: EXPRESSED IN LONG, SIGNAL. - 1.7
N: EXPRESSED IN BONE MARROW, SIGNAL. - 1.4
N: EXPRESSED IN BONE MARROW, SIGNAL. - 1.4
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CURRENT FILING DATE: 2000-09-27
FFILING DATE: 2000-09-27
FFILING TOTAL NUMBER: US E0/207,456
PRIOR FLING TO NOS. 21709
SOFTWARE: MOLECULAR Dynamics Sequence Listing Engine
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                                                                                                                                                                                                                                                 Sequence 19127, Application tS/60236359 GENERAL INFORMATION:
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; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-01-31
PELOE APPLICATION NUMBER: 60,180.628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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                                                         1420 FEQYVTKTVLAAAYGEK 14:6
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Rank, David R.
Hanzel, David K.
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LENGTH: 77
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; OHHER INFORMATION: Xad equals any of the naturally occurring L-amino acids
US-09-758-449-1058
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                                                                                                                                                        Sequence 2412, Application PC/TUS0118569
GENERAL INFORMATION:
APPLICART: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PALS FOT
CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT APPLICATION NUMBER: 60/259,467
PRIOR APPLICATION NUMBER: 60/259,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4560
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100.0%; Fred No. 2.4e-113;
ative 0, Mismatches 0;
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PHIOR APPLICATION NUMBER: 60/179,065
PHIOR PLING DATE: 2000-01-31
PHIOR PLING DATE: 2000-01-31
PHIOR PILING DATE: 2000-01-31
SOFTWARE: FILING DATE: 2000-03
SOFTWARE: PALENTING TO NOS: 1478
SOFTWARE: PALENTIN VET 2.0
SOFTWARE: PALENTIN VET 2.0
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1959 VKPEADIL 1966
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APPLICANT: Penn, Sharron G.
APPLICANT: Pank, David R
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HIMAN GENOME-DEPIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
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            3.7%; Score 79; DB 21; Length 164; 100 0%; Pred No. 2e-67; tive 0; Mismatches 0; Indels
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PRIOR FILING DATE: 21 SEPTEMBER 2000 (21.09.00)
PRIOR FILING DATE: 30 June 2000 (30.06.00)
WUMBER OF SEQ ID NOS: 38837
SOFTWARE: Molecular Dynamics Sequence Listing Engine
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tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APLLICATION NUMBER: US 60/207,456
PRIOR APLLICATION NUMBER: US 2000 (03.3.3.3.46
PRIOR APLLICATION NUMBER: US 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/234,687
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; Sequence 37036, Application US/09864761
; GENERAL INFORMATION:
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Query Match
Bost Local Similarity 100 0%
.....nos 79; Conservative
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Matches 77; Conservative
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                                                 90 AEVISTLEALAIPQLPSLMPSLITTMKNTSELVSSFVYIISALAALQKVVETLPHFISPY 149
                                                                                                                                                                                                                                     150 LEGILSOVIHIFKITSSMGSASGANIRLISLKKTLATTLAPRVLLPAIKKTYKQIEKNWK 209
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99.6%; Pred. No. 2.8e-133;
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APPLICANT: Baer, Richard
LIFLE OF UNVENTION: Compositions and Methods Comprising
LIFLE OF INVENTION: MARDI and other HRCAL Binding Proteins
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ER: TISD:499F2D
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STREET: P.O. Box 4433
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OPERATING SYSTEM: PC-DOS/MS DOS
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REGISTRATION NUMBER: P 41,07
REFERENCE CONTROL NUMBER: TLEED ON TREATMENT ON TREATMENT ON THE CONTROL NUMBER OF THE CONTROL OF THE CO
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512/474-7577
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CORRESPONDENCE ADDRESS:
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US-60-042-611-52
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08 60:042 611 52
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1839 NHMGPFMSILQEHIGXMKKEELISHQSQLIAFFLEALDFRAQHSENDLEEVGKTENTID 1898
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                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods Comprising TITLE OF INVENTION: HARD1 and Other BRCA1 Hinding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                       Sequence 52, Application US/60042985 GENFRAL INFORMATION:
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                                                                                                                                                                                                                                                                                                        APPLICANT: Bowcock, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                          1959 VKPFADTL 1966
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APPLICANT: DIMMANAC, RADOJE T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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PRIOR PILLING DATE: 2000 - 222
PRIOR PLILOR DATE: 2000 - 222
PRIOR PLILOR DATE: 2000 - 222
PRIOR PLILOR DATE: 2000 - 01-25
PRIOR PLILOR DATE: 2000 - 01-25
PRIOR PLILOR DATE: 2000 - 01-25
PRIOR PLILOR DATE: 2000 - 03
PRIOR PLILOR DATE: 2000 - 04-37
PRIOR PLILOR DATE: 2001 03-65
PRIOR PLILOR DATE: 2000 - 03
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CURRENT FILING DATE: 2002-03-12
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PRIOR FLING DATE: 2001-03-30
PRIOR PLING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: HS 09/752, 929
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR PLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/USO1/08656
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APPLICATION NUMBER: PCT/USO1/04927
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PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
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APPLICATION NUMBER: US 09/577,409
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PRIOR APPLICATION NUMBER: US 09/552,317
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                                                                                                                                                                                                  Application US/60339453
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SOFTWARE: pt_FL_genes Version 6.0
SEQ ID NO 167
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                                                                                                                                                                                                                                                                                         Wang, Zhiwei
Wang, Jian-Rui
Ghosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                             Boyle, Bryan J
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OPGANISM Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    Weng, Gezhi
                                                                                                                                                                                                        Sequence 167, Applic
GENERAL INFORMATION:
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1378 KIISVFVDALPHVPEHRRIDILVQLVDTIGAEKFIMIIJIILFEQYVTKTVIAAAYGEKD 1437
1258 CLENICYKLSFDGGKIPKDILDEEKFNVELIVQCIRLSEMPQTHHHALLLLGTVAGIFPD 1317
                                                                           1318 KVLHNIMSIFTFMGANVMRLDDTYSFQVINKTVKMVIPALIQSDSGDSIEVSRNVEEIVV 1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BARD1 and Other BRCA1 Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions and Methods Comprising
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                                                                                                                                                                                                                                 1438 ALLEADTEFWESVCCEFSVQHQIQSLMNILQYLLKLPEEKE 1478
                                                                                                                                                                                                                                                    593 ALLEADYEEPWESVCCEFSVOHOTOSLANTLOYLLKUPERKE 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.C, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 60/042,985
                                                                                                                                                                                                                                                                                                                                                                   Sequence 52. Application US/08936487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-41,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFERENCE/DOCKET NUMBER: IT:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bowcock, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHAPACTERISTICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: Concurre CLASSIFICATION 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-APR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SECUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas
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US-08-936-487-52
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1713 AEVTSTLEALAIPQLPSLMPSLLTTMKNTSELVSSEVYLLSALAALQKVVETLPHFISPY 1778

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Length 1149; Indels

10.3%, Score 221, 58.26, U. 100.0%; Pred. No. 3.9e-205; Live. 0; Mismatches 0;

10.38; Pre 100.0%; Pre

Matches 221; Conservative

Best Local Similarity

Query Match

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1108 EKTIKPFFAATSDEKVQQKILIRMLFDLLVNCKNSHCAQTVSSVFKGTSVNAEQVRIELEP 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1288 IVOCTRUSEMPOTHHHALLLLGTVAGTFTDKVLHNIMSTFTFMGANVMRLDDTYSFQVIN 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1202 IVQCTRUSEMPQTHHHALLILIGIVAGTEPDKVIJHNIMSTETEMGANVMRLDDTYSEQVIN 1261
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                                                                                                                                                                                                                                                          988 KKLKSHQKLSETLKNILSCVYSCPSYTAKDI MKVLQGVNGEMVLSQLI PMAEQLLEKIQK 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 PDKAKPLGTVQQKRRQKMQQKKSQDLESVQEVGSYWQPVTLILELLQHKKKLPSPQ1LV 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1082 POKAKPIGTVQUKRRQKMQQKKSQDLESVQEVGGSYWQRVTLILELLQHKKKLRSPQTLV 1141
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                                                                                                                                                                                         902 KKLKSHÇKIŞLLIKNILISCVI SÇESI TANDIMKVINĞVNĞEMVISQLILIMAFULLERIQK. 951
                    928 GUIVKHVERAATGTGAGSSVASTEYLLIDHLISKAHDITSDAAYVIQDATLEELIQKE 987
                                                                                    858 - SVIARTYGSSI, SNIVLINFTVRTVI QTQALTVGTAMESSQKT (ÇTRHQLASTSSIVVLSTILLINI) - 927
808 KODIWWNPEQLKFDSPNYLHTIALFEMMINAANHFPVLMKLFIKVHLEDVFQLFKFC 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1468 OYLLKI PEPKETTI PKAVSENKSESÖEBMIJOVENVELHI SKOLLHEKFLSVSPMSOLLISS
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FITLE OF INVENTION: Novel Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 358, Application US/60339453
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Zhiwei
Wang, Jian-Rui
Chosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weng, Gezhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Y. Tom
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61 SPEQFEAPLFSQLAKTLEPSVQTKAVNKQLDFNISLFLIHLSPYFLLKPAQKCLEWLIHR 120
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ilarity 190.9%; Pred. No. 4.1e 227;
Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: WS 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/649,167
PRIOR PLILING DATE: 2000-08-23
PRIOR PELLING DATE: 2000-08-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PILLING DATE: 2000-02-23
PRIOR PILLING DATE: 2000-02-23
PRIOR PILLING DATE: 2000-02-33
PRIOR PILLING DATE: 2000-02-33
PRIOR PILLING DATE: 2000-02-33
PRIOR PILLING DATE: 2001-02-25
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 812
CURRENT APPLICATION NUMBER: US/60/339,453
                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PELING DATE: 2000-02-03
PRIOR PELING PATE: 2000-04-27
PRIOR APPLICATION NUMBER: 94-27
PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PC,/USUI/UNRESP
PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                                                             PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
                                                                                                                                                                                                                                                                      PRIOR PILLIGATION NUMBER OS 09/491,404
PRIOR FILLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCITUSO1/02623
PRIOR FILLING DATE: 2001-01-25
                                                                                                        PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/552,317
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SOPTWARE: pt_FL_genes Version 6.0
                                                                                    2002-03-12
                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-25
                                                                                                                                       PRIOR FILING DATE: 2000-01-21
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                                                                               CURRENT FILLING DATE:
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1321 HAIMSIETEMGANVMRLDDTYSFQVINKTVKMVIPALIQSDSGDSIEVSPNVEETVVKII 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAVEDSVELVESLKKFIYALKAPKSFPKGPIWWNPEQLKENSPRYLHLLIGLFEMMLNGA 840
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                                            421 LNEQFLPLIRLLESKYPRTLDVVLEEHLKEIADLKKQELFHQFVSLSTSGGKYQFLADSD 480
                                                                                                      FETFKEHFSSEVTISNILNIFORAELSKNGEWYEVIKTAADILLIKEETI.SENDOLSNQVV 600
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LOCATION: (416)...(427) FIRE INFORMATION Caseins alpha/beta proteins domain identified by eMATRIX, OTHER INFORMATION: accession number BL00306R, p-value-7.300e-09, raw score of 8.2
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CHRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45591, Application PC/TUS0108631 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/649,167
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offHER INFORMATION: potential membrane-spanning segment, TopPred Program
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APPLICANT: Bouqueleret, Lydie
APPLICANT: Chumakov, Hya
APPLICANT: Chumakov, Hya
TILLE OF INVENTION: A NOVEL BAP28 GENE AND PROTEIN
FILE REFERENCE: GENSET.063PRF
CURRENT APPLICATION NUMBER: US/A0/2141 323
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NOMBER OF SEQ TO NOS: 5
SOFTWARE: Patent.pm
SEQ TO NO 4
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LOCATION: 1987..2007
OTHER INFORMATION: potential membrane spanning segment, TopPred Program
                                              membrane-spanning segment, lopPred Program
                                                                                                             LOCATION: 700.,720
CTHER INFORMATION: potential membrane-spanning segment, TopPred Program
                                                                                                                                                                                                      LOCATION: 8611.881
OTHER INFORMATION: Potential membrane-spanning segment, TopPret Proteam
                                                                                                                                                                                                                                                                                                                   OPHER INFORMATION: potentia membrane-spanning sequent, LopPred Program
                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 911..931 crime membrane-spanning segment, TopPred Program
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OTHER INFORMALION: DOTENTIAL membrane-spanning segment, Topbied Program
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OTHER INFORMATION: Potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: Polential membrane-spanning segment, TopPred Program
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US-60-141-323-3
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C.
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GIHER INFORMATION: potentia
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                                                 61 SFEQFEAPLF/SQLAKTLERSVQT/KAVNKQL/DENISLF/J.HILSPYFLLKPAQKCLEWL/HR 120
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APPLICANT: Barry, Caroline
APPLICANT: Bouquelerel, Lydie
APPLICANT: Choumakov, 11ya
FILLE REPERENCE: 67. US2. PRO
CURRENT APPLICATION NUMBEP 115,60/176,880
CURRENT FILLIS PATE: 2000-01-18
EARLIER APPLICATION NUMBEP 155,60/141,323
EARLIER APPLICATION NUMBEP 155
NUMBER OF SEQ ID NOS: 12
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100.0%; Pred. No 0
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OTHER INFORMATION:
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                                                301 LSCLIVILGEGKPESIGKKPFPHLCNVPDLITILHGISETYDVSPLLKYMLPHLVVSIIH 360
                                                                                               361 HVTGEETEGMDGQIYKRHLEAILTKISLKNNLDHLLASLLFEEYISYSSQEEMDSNKVSL 420
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: OTHER INFORMATION: Xaa-Gly or Glu
US 09:603-665-5
                      CHER INFORMATION: XBA-ASP OF ASD
                                        NAME/KEY: VARIANT LOCATION: 2017
LOCATION:
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61 SFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENISLFLIHLSPYFLLKPAQKGLEWLIHR 120 121 FHIHLYNQDSLIAGVLPYHETRIFVRVIQLLKINNSKHRWFWLLPVKQSGVPLAKGTLIT 180 241 KLFPYIQKGLKSSLPDYRAATYMIICQISVKVTMENTFVNSLASQIIKTLTKIPSLIKDG 300 360 420 480 099 780 721 THEPFAIRVESLLOKKIKKLESVITAVEIPSEWHIELMLDRGIPVELWAHYVEELNSTQR 780 781 VAVEDSVELVESLKKFIYALKAPKSFPKGDIWWNPEQLKEDSRDYLHLLIGLFEMMLNGA 840 781 VAVEDSVEDVESTRKETYALKAPKSFPKGDIWWNPEQLKEDSRDYLHLLIGLFEMMINGA 840 1 MTSLAGOLORLALPGSDASILISRDFVASILFDPKEAATIDRDTAFAIGCTGLEELLGIDP 60 1 MISLAUGLURLALPUSDASLLSRDEVASLLFDPKEAATIDRDTAFAIGCTGLEELLGIDP 121 FHIHLYNQDSLIACVLPYHETRIFVRVIQLLKINNSKHRWFWLLPVKQSGVPLAKGTLIT 181 HOYKDLÖFMDETCSLVIKSVKVFAEYRGSSAQLRVLLAEYASTIVSALVAAEDVSDNITA 181 HCYKDLAPMOFICSLVIKSVKVFARYPGSSAQLPVLLAFYASTIVSALVAAEDVSDNIIA LSCLIVILQRQKPESLGKKPFPHLCNVPDLITILHGISETYDVSPLLRYMLPHLVVSIIH 4.21 LINEOFLIPLIRLLESKYPRTLDVVLEEHLKETADLKKQELFHQFVSLSTSGGKYGFLADSD 541 FELFKEHESSEVLISNIUNLEQKAELSKNÖEMYEVUKTAADILIKEETLISENDOLSNQVV 541 FEIFKEHFSSEVTISNLLNLFORAELSKNGEWYEVLKIAADILIKEEILSENDOLSNOVV 601 VOLLPEVVINNODIESAEMKIAIYLSKSGIOSLHPLLRGWEEALENVIKSIKPGKLIGVA VOLLPEVVINNDDTESAEMKIATYLSKSGTCSLHPLLRGWEFALENVIKSTKPGKLIGVA 661 NORMIETLADNINGSPESSMLKMVERLISVGEFESENLKOKVTFHVILSVLVSGGSSLKE 721 THEPFATRVESTLÖKKTKKLESVITAVETPSEWHIELMLDRGTPVELWAHYVEELNSTQR DAVIIFRALMKLFIKVILEBVFQLFKFCSVLWTYGSSLSNPLNGSVKTVLQTQALYVGCAM DAVHFRVLMKLFIKVHLEDVFQLFKFFSVLWTYGSSLSNPLNCSVKTVLQTQALYVGCAM HVTGEETBOMDGOTYKRHLEATLIKISLANNLDHLLASLLEEYISYSSOEEMDSNKVSL 421 LNEOFLPLIRLLESKYPRILDVVLEEHLKEIADIKKQELFHQFVSLSISGGKYQFLADSD 481 TSLMLSLNHPLAPVRILAMNHLKKIMKTSKEGVDESFIKEAVLARLGDDNIDVVLSAISA ; 0 99.8%; Score 2140; DB 20; Length 2144; 100.0%; Pred. No. 0; Indels 0: 0; Mismatches Conservative Similarity Matches 2144; Query Match Best Local s 161 144 101 109 Š 2 Š ŝ ć 3 ;· 3 5 ŝ 5 â 3 ŝ Ś 2 Š â ŝ ŝ <u>^</u> 5 5 â ŝ = ŝ â ŝ

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4728-953 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   |                    |                |                |                  | 358 Sequence 358, App |                |                |
|-----------|-------------------------------|--------------------|----------------|----------------|------------------|-----------------------|----------------|----------------|
| SUMMARIES | ID                            | 20 US-09-603-665-5 | US-60 176 880- | US-60-141-323- | PCT-11501-08631- | US-60-339 453 358     | US-60-339 453- | US-08-936-487- |
|           | DB                            | 20                 | .⊒<br>-1       | 92             | _                | 36                    | 5              | 13             |
|           | %<br>Ouery<br>Match Length DB | 2144               | ₹]44           | 2144           | 1569             | 325                   | 1149           | 515            |
|           | %<br>Ouery<br>Match           | 9.66               | 8.66           | 82.3           | 42 4             | 11.3                  | 10.3           | 6.9            |
|           | Score                         | 2140               | 2140           | 1764           | 908              | 243                   | 221            | 147            |
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| φονιμων.Μων.ΟΙΟς ΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦΦ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | • • • • • • • • • • • • • • • • • • •                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 147<br>747<br>777<br>777<br>777<br>777<br>777<br>777<br>777<br>777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | σο σω σω σα                                                                                                                                                                                                                                                                                                                                                                                                          |
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### ALIGNMENTS

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AFFLICANT. Chumakov, IIya
AFFLICANT. Cohen Akenine, Annick
IITLE OF INVENTION: A NOVEL BAP28 GENE AND PROTEIN
FILE PEPERWICE. GENSET. 063AUS
CURRENT AFFLICATION NUMBER: US/U9/603,665
CURRENT FILING DATE: ZUUU-U0-23
CURRENT FILING DATE: ZUUU-U0-23
                                                                                                                                                                                                                                                         PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/176,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: 1694
OTHER INFORMATION: Xaa-Ser of Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION. 1854
OTHER INFORMATION. Xaa-Ala or Val
                  ; Sequence 5, Application US/09603665
; GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                    2000-01-18
                                                                                   Bougueleret, Lydie
                                                             APPLICANT: Barry, Caroline
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEG 1D NOS: 63
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
OPGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      PPIOP FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY, VARIANT
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2144
US-09-603-665-5
                                                                                   APPLICANT.
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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WPI: 2001-649462/74.

WAS MASS6647.

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XX

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensies, dene mapping, identification of mutations processing tresponsible for genetic disorders or other traits and to assess problematical to the processing tresponsible for genetic disorders or other traits and to assess processing to be a polypeptide (II) sequences. (I) is useful as hybridisation probes, or polypeptide (II) sequences. (I) is useful as hybridisation probes, or polypeptide (II) sequences. (I) is useful as hybridisation probes, or proposed to the sequence to the polymerase chain reaction (EVB) primers, olidomers, and for chromosome polymerase chain reaction (EVB) primers, olidomers, and for chromosome or for identifying expressed genes. (I) is useful in green therapy techniques of identifying expressed genes. (I) is useful in genes in the topyperpride in tissue, as molecular weight markers and as food supplement. (I.) and its binding partners are useful in receipting of a food supplement. (I.) and its binding partners are useful in receipting of a food supplement. (I.) and its binding partners are useful in receipting of disorders involving aberrant protein expression or biological activity. In produce and polymerical in the sequences have applied and polymerical in the printed diagnostics, lorensies, quee mapping, identification of mulations of and to produce other types of data and products dependent on DNA and diagnostics amino acid sequences of the invention. One of the printed of special call of the angle product acid sequences of the invention. In the printed of special or heart and to appear in the printed of special call of the p
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Ourry Match
Best Local Similarity 100.0%; Pred, No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

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OY 1655 KKKEGEEE 1662 [1111111 Db 29 KKKegeee 36 Search completed: July 2, 2002, 15:36:21 Job time: 484 sec 20

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Protain
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                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                        New isolated numbers acid detection reagent for detecting 1000 or more genes from Dresophila and for elumidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            cell-cell interactions in higher eukaryotes for the development of insecticides, therapeuties and pharmaceutical drugs. The invention discloses genomic iAN sequences (ABL)6176 AHL30511), expressed DNA sequences (ABL)6175 and the encoded proteins (ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of leader polypeptide of human GM-CSF used in mammalian coli expression system for secretion of a polypoptide analog of human granulocyte colony stimulating factor (hpC CSF)
                  Drosophila, developmental biology, eeli signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 22518, 21pp + Sequence Listing, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maematopoietic disorders; therapy; aplastic anaemla;
Drosophila melanogaster polypeptide SEQ ID NO 22518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone marrow transplant; burn wounds; leukaemia.
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100.0%; Pred. No. 66;
tive 0; Mismatches
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                                                                                                                 23-MAR-2801; 2801W0-4809231.
                                                                                                                                                11-jūi,-2000; 2000us-0614150.
                                                                                                                                     23-MAR-2000; 2000ms-191637P
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Matches 9; Conservative
                                                   Drosophila melanogaster
                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                             WPI; 2001-65686U/75.
                                                                                                                                                                                                                                                                                                                                                                                                                               2096 AA;
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                                                                        WO200171042-A2.
                              pharmaceutical
                                                                                                                                                                                                                                                              interactions
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                                                                                             27-SEP-2001.
                                                                                                                                                                                         Venter JC,
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The examples describe procedures for the designing of probes for hpG-CSF winh and genomic clones, both of which are claimed Specifically claimed are DNA sequences coding for (Ala 1)hpG-CSF; (Ser 36,42,64 and 74)hpG-CSF and the corresp. Met.1 cpds. The novelty is that hpG-CSF is the prod. of procaryotic or eucaryotic expression of an examples.
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                                                                                                                                                                                                                                                                                                                                                                                                           Poly,peptide with granulocyte colony stimulating factor activity obtd. by recombinant DNA procedures for treating hacmatopoletic
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100 0%; Pred No 7 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example, p52; 79pp; English.
                                                                                                                                                        85US-0768959.
85US-0768954.
                                                                                                                                     86US-0835548.
                                                                                       86WO-11001708.
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Bost Local Similarity 100 C
Matches 8; Conservative
                                                                                                                                                                                                                                 (KIRI-) KIRIN-AMGEN INC.
                                                                                                                                                                                                                                                    (KIRI ) KIRIN-AMGEN INC
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                                                                                                                                                                                                                                                                                                                                              WPI; 1987-064855/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
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                                                                                         22-AUG-1986;
                                                                                                                                     03-MAR-1986;
                                                                                                                                                                                   23-AUG-1985;
                                                                                                                                                                23-AUG-1985;
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W08701132-A.
                                         26-FEB-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
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09-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             see AATTHIS-AAIS7546). The present sequence is a peptide encoded by one such probe. The probes are useful tor producing a microarray for predicting, measuring and displaying apen expression in samples derived from human placenta. The probes are useful for antendal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention relates to single exon sucheic acid probes (SENP:
                                                                                                                        Peptide #3919 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1360 SDSGDSIEVSRNVEEIVVKIISVFVDALPHVPEHRRLPHLVQLVDTLGAEKFLWILLILL 1419
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                                                                                                                                            Probe; microarray; human; placenta, antenatal diagnosis;
genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 3(151; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                  Penn Si, Hanzel DK, Chen W. Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAMU5057 standard: Protein; 77 AA.
                                                                 AAM29882 standard; Protein; 77 AA
                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                40-JAN-2001; 2001WO-US00663.
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20000S-0234687.
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                                                                                                                                                                                                                                                                                                           2000GB-0024263.
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1420 FEQYVIKIVLAAAYGEK 1436
                                                                                                       (tirst entry)
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          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 AA;
                                                                                                                                                                                          WO200157272 A2.
                                                                                                                                                                                                                                                                             04-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                    04 FFR 2000;
                                                                                                                                                                                                                                                                                                  27 - SEP - 2000;
04 - OCT - 2000;
                                                                                                                                                                                                                                                            26 - MAY - 2000;
10 - JUN - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                   AAM29882;
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                                                         AAM29882
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The present invention relates to novel single exon nucleic acid probes (see AAIGOOD-AAIGOOT). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gence expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, monitoring and prognosing diseases of the human breast, particularly those diseases with polymenic actiology. The diseases include: breast cancer, disorders of development inflammatory diseases of the breast, librocystic changes, proliferative breast disease and non-carrinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WHEO at the whop.int/published_pet_sequences.
                                                                                   inflammatory disease, proliferative breast disease, non carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression
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                                                       Probe; human; breast disease; breast, cancer; development disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
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200008-0608409.
200008-0632366.
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                  W0200157270-A2.
                                                                                                                                              Homo sapiens.
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27-SEP-2000;
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1360 SDSGDSTEVSRNVEETVVKIISVEVDALPHVPEHRRIPHLYQLVOTLGAEKFLWILLILL 1419

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, lenkaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
discases such as Alzheimer's discase, multiple seletosis, sehizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                   1360 SDSGDSTEVSRNVEETVVKLISVEVDALPHVPEHRRLPILVQLVDTLGAEKFLMILLILL 1419
                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                             the present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone mairow expressed probe encoded profein SEQ ID NO: 29848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO: 29848; 658pp + Sequence Listing; English.
                                                                                                                                                                                           3.6%; Score 77; DB 22; Length 77;
L00.0%; Pred No. 9 7e-68;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing gene expression in human bone marrow
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100.0%; Pr-
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2000US-0207456.
2000US-0608408.
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2000US-0236359
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Matches 77; Conservative
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                                                                                                                       77 AA;
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27-SEP-2000;
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                                                                                                                       Sequence
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Gaps

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0; Indels

Pred. No. 9.7e-68,

Query Match 3.6%; Score 77; DB 22; Bost Local Similarity 100.0%; Fred. No. 9.7e-68, Matches 77; Conservative 0; Mismatches 0;

Length 77;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be used to produce a single exon microarray, which can be used for measuring button gene expression in a sample delived from human cervical cpithelial cells, ay measuring gene expression, the process are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Probe; human; microarray; gene expression; cervical epithelial cell;
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100.0%; Pred. No. 9.7e-68
:ive 0, Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                            AAM17368 standard, Protein, 77 AA
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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30-JUN 2000; 2000US-0608408.
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                                                1420 FEQYVTKTVLAAAYGEK 1436
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Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                       cervical cancer.
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                                                                                      measuring howen gene expression in a sumple derived iron homes feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying your expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exennected exid probe of the invention.
                                                                                                                                                                                                                                                                                                                           1350 SDSGDSTEVSENVELLVVKTISVEVDALPHVPEHRRIJPILVQLVDTIGAEKFTWILLILL 1419
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                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at 1tp.wipo.inf/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes for
Human genome derived Single exon nucleic acid probes useful for
analyzing gene expression in human fetal liver
                                                                         The invention relates to a single exon nucleis acid probe for
                                          Claim 27; SEQ 15 No 29019; 639pp · sequence listing: English
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                                                                                                                                                                                                                                                                  3.6%; Score 77; DB 22; Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypertension: cardiac arrhythmia;
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2000US-0236359.
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                                                                                                                                                                                                                                                                                             77: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular disease;
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30 - JUN - 2000;
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27-SEP 2000;
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measuring human gene expression in a sample derived from human heart (see MSALISS) ABALISOS. The present sequence is a protein encoded by one son probe. The probes may be used for predicting, medsuring and displaying gene expression in samples derived from the human heart via microariays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain rell samples, which may enable the diagnosis and improved treatment of nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluman brain expressed single exon probe encoded protein SEQ ID No: 29251.
                                                                   By measuring gene expression, the probes are useful for predicting, diagnosing, grading, stading, mobilecture, motivated and prounosing diseases of the human heart and vascular system etc. Cardiocaccular disease, hypertension, cardiac arrhythmias and congenital heart disease. Outc. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed at ftp.wipo.int/pub/published_pet_sequences.
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                                                                                                                                                                                                                                                                     100.0%; Pred. no.
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26-MAY 2000; 2000US 0207456.
30-JUN-2000; ZUDOUS-DADMAD8
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27-SEP-2000;
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seguence and an objeonationtide comprising a sequence complementary to a polynuclectide which comprises a 3° and sequence, where the objeonated objectide comprises a 1° and sequence, where the combination of the 5° end sequence is selected from those defined in the specification The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods AAMIG166 to AAMIB3C2 to AAMIB3C3 to AAMIBACA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2018 ALMMPLVDQLENKLGGEEKFQERVTKHLIPCIAQFSVAMADDSLWKPLNYQILLKTRDSS 2077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 almmplvdqlcnriggcckfqcrvtkhlipciaqfsvamaddslwkplnygillktrdss 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #3836 encoded by breast ceil single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                      5-98; Source 127; FR 22; benuffb 44-
160.08; Pred. No. 1.1e 116; 0, 164s18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%, Preus no.
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Matches 127, Conservative
                                                                                                                                                                                                                                                                                                                                          of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                           349 AA;
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-SEP-2000;
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21-SEP-2
27-SEP-2
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from human breast and Michaells, the method involves contacting the probes with a collection of detectably labelled nucleic acids derived from human breast, and then measuring the label bound to each probe of them increarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognessing the toxicity of chemical expression analysis is useful for deservable the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less hias than expressed sequence tag microarrays. The method is suitable for rapid production of lunctional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1360 SDSGDSJEVSRNVEETVVK11SVPVDALPHVPEHRRIPTLVQLVDTLGAEKFFIWITLLTL 1419
                                             The invention relates to a spatially-addressable set of single exonnucleic acid probes for measuring gene expression in a sample derived
                                                                                                                                                                                                                                                                                                                       Note, The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formal directly from WIPO at ftp wipo inf/pub/published_port_sequences.
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              Claim 27; SEQ ID NO 14153; 327pp / sequence listing, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 22; Length 77;
Pred. No. 9.7e-68;
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200008-0234687.
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Matches 77; Conserv
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\mathbf{x} \otimes \mathbf{x} \in \mathbb{C}
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1928 INFLERVVESOPEILEGFEFFIETVIGYISAVACSMEPNAFFITVEFWPALLSMAYDL 1587
                                   1468 OYLLKLPERKERTIPKAVSPNKSESQEEMLQVENVETHISKQLRHPKPLSVSPMSCLLSS 1527
                                                                                                                                                                                                                                                                                                                                                                 DNA sequence encoding BARDI, F123, RF2, RF14, RF31 or F1445 - Whas breast cancer antiqen, HRCAI, binding proteins are useful to identify patient having or at risk of developing cancer
                                                                                                                                                                                                      BAMP1: ring protein; BRGAl; breast cancer; risk; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 287-288; 348pp; English
                                                                                                                                            AAW54099 standard; Protein; 515 AA.
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940S-0(25296)
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The present invention describes primer sets for synthesistra $602 full-length CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the somehouse strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprising a sequence complementary to the complementary strand of a folynucleotide which comprises a 5'-end
                                                             1695 TAVKLIAPEPKEEKNVUGSALUUJAEVISTLEALAIPULPSLMESLLIIMPNISELVSSE 1754
                                                                                                                                                                                                                                                         1875 IDEPAQHSENDLEEVGKTENCTIDCLVAMVVKLSEVTEPPLEFKLEUWAKTEDAPKDRLL 1944
                                                                              Frimer sets for synthesizing polymorheotides, particularly the 5692 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abrormality of the proteins encoded by the
                                   Gabbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, primer, detection, diagnosis, antisense therapy; gene therapy.
                                                                                                                            1755 VYLLSALAALQKVVETLPHFISPYLEGILSQVIHLEKIISEMGSASQANIRLTSLKKTLA
                                                                                                                                                                                          1815 TO LAPROGUALATIKATYKOTPK VWKNHMGPPMSTLOPHTGXMKKEBLITSHQSGLITAFFLEA
                                                                                                                                                                                                                          186 ttlaprvllpaikktykgieknwknhmgpfmsilgenigamkkeeltshgsgltattlea
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 Longth 515;
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Score 171; DB 19;
Pred. No. 3.6e-160;
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                                Mismatches
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8.08;
99.68;
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11-JAN-2000; 2000UP-0118776.
02 MAY 2000; 2000UP-0184767.
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                                Matches 271, Cosservative
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Query Match
Hest Local Similarity
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1741 LTIMKNISELVSSEVYLLSALAALQKVVETLPHFISPYLEGILSQVIHLEKIISEMGSAS 1800
                                          1801 QANTRIJESLKKTLATTLAPRVILIPATKKTYKQIEKNWKNHMGPPMSILIQEHIGXMKKEEL 1860
                                                                                                                                      1861 TSHQSQLTAFFLEALDFRAQHSENDLEEVGKTENCIIDGLVAMVVKLSEVTFRPLFFKLF 1920
                                                                                                                                                      DWAKTEDAPKDRLLTFYNLADGIAEKLKGLFTLFAGHLVKPFALTLXQVNISKTDRAFFD 1980
                                                                                                                                                                                                                                                 1981 SENDPERCCLLLÖFTLINCLYKTFLEDTÖHFTSKERAXALMMPLVDOLENRLGGEEKFQER 2040
                                                                                                                                                                                                                                                                                                      2041 VTKHLIPCIAQESVAMADESLWKPLNYQILLKTRESSPKVPFAALITVLALAEKLKENYI 2100
lb8i igaenpdpivpvixtavkliaperkeeknvigsaliciaevustiealaipgipsimpsi 1740
                                                                                                                                                                                                                                                              diagnostics, forensics, gene mapping, identification of matations responsible for genetic disorders or other traits and to assess
                                                                                              Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                         2101 vlipesipflaelmedeceevehqcqkiqqletvlqeplqsyf 2144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #15223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAP-2606; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200008-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS79419.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCA) primers, oliqumers, and for chromosome and gene mapping, and in recombinant production of (II). The

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polymoreleatides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (i) is useful in gene therapy techniques to restain north arithity of (II) or no treal disease states involving (II). (II) is useful for generating antibodies against 1t, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (I) are useful for treating disoiders involving abenant protein expression or biological activity. The polypertide and polymorleades equences have applications in
                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations and trapnostics to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Absolutio-Abs30377 represent movel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              808 KGDTWWNPEQLKEDSRDYLHLLIGLFEMMINGADAVHFRVI,MKLFTKVHLEDVFQLFKFC 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928 GSPVKEVRRAA1QCLQALSGVASPPYL,ITDHL,ISKAEETTSDAAYVIQDLA'FLFEELQPE 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868 SVIMTYGSSLSNPINGSVKTVLGTGALYVGYMLSSGKTGYKHGLASISSPVVTSLLINL 927
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106.0%; Pred No. 0;
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Wed Jul

Cohen Akenine As Chumakov I. Bougueleret '., Barry C, 

WPI; 2001-367032/38

N PSDB; AAF83909, AAF83910.

for diagnosing prostato fumors, e g by hybridization or New BAP28 polynucirotides and polypeptides everexpressed in prestate polymerase chain reaction assays cancer cells

Claim 14; Page 297-304; 349pp; English.

The invention is directed to BAP2B polypeptides, JAP2B polynucleotide sequences and regulatory region located at the 3° and 5° ends of the BAP2B could recombine the BAP2B polynucleotides can be expressed by standard recombinant methodology BAP2B polynucleotides and polypeptides have been found to be over expressed in prostate tumour cells, therefore levels of BAP2B expression and/or activity may be assayed (or 3° by polymease chair reaction (PCR) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies specific for the BAP2B polypeptides are useful as diagnostic reagents. Bialbelic markers of the BAP2B apreams are useful and analysis. The present sequence represents a protein encoded by a lirst cDNA sequence of the BAP2B gene consisting of the exons 1 to 45.

2144 AA; Seduence

0; 241 KLEPYTÖKGLKSSLEDYRAATYMITCOTSVKYIMENTEVNSLASOTIKTLIKTPSLIKDG 300 301 LSCLIVLLQRQKPESLARKPFPHLCNVPDLITTLHGISETYDVSPLLRYMLPHLVVSIIH 360 541 FELFKEHFSSEVTISNILNEPOPAELSKNGEWYEVLKIAADILIKEETLSENDOLSNQVV 600 61 SPEGFEAPLESQUAKTLERSVOTKAVNKÖLDENTSLETLIHLSPYFILIKPAQKCLEWLIHR 120 61 steqteaplfsqlaktlersvqtkavnkqldenislflihlspyfllkpaqkclewlihr 120 121 FHIHLYNGDSLIACVLPYHETRIFVRVIQLLKINNSKHRWFWLLPVKQSGVPLAKGTLIT 180 181 HCYKDLGFMDFICSLVTKSVKVFAEYPGSSAQLRVLLAFYASTIVSALVAAEDVSDNIIA 240 361 HVTGEETEGMDGQIYKRHLEAILTKISLKNNLDHLLASLLFEEYISYSSQEEMDSNKVSL 420 421 LINEGELPLIRLLESKYPRTLDVVLEEHLKETADLKKQELFHQFVSLSTSGGKYQFTADSD 480 421 Ineqtiplirileskyprtidvvleehikeiadikkqelthqivsistsqqkyqtladsd 480 6.01 VOLEPEVVENNDIYLESAPMKTALYLSKSGTGSLHPILLRGWEFALENVEKSTKPGKLIGVA 660 1 MISTAQQIQRLALPQSDASLLSRDFVASLLFDPKEAATIDRDIAFAIGGTGLEELLGIDP 50 1 mtslaqqqqqrlalpqqqdasllsrdevasllfdpkeaatidrdtafaigctgleellgidp 60 491 TSEMESENHPEAPPRILAMNHEKKIMKTSKEGVDESFIKEAVLAREGDDNIDVVESAISA 0 Score 2140: DB 22; Length 2144; Pred. No. 0; Indels 0; 0; Mismatches 130.0%; 99.88; Matches 2144; Conservative Hest Local Similarity Query Match g <u>a</u> 5 9 ò g ŝ <del>2</del> ŝ 6 5. n C 5 ò a 0.7 5

FGAENDOPFVPVLXTAVKLJAFERKEEKNVLGSALJCJAEVTSTLEALATPOLFSLMPSL, 1740 HNIMSTETEMGANVMRLDDTYSFQVINKTVKMV1PAL.1QSDSGDSTEVSRNVEETVVK11 1380 SLDIFIKAVRITKELYAGMPTIQITALEKITKPFFAATSDEKVOOKLI.RMLFDLLVNCKN 1140 1081 sldifikavhttkelyagmptigitalekitkpffaaisdekvqqkllrml1dllvnckn 1140 1141 SHCAQTVSSVEKGISVNAPQVETFILPPPIKAKPIGTVQQKPPQRKMQQKKSQIN PSVQEVG 1200 1201 GSYWQRVTLILELIAGHKKKIRSPQILVPTLFNLLSEALEPLPQEQGGNMEYTKQLILSCLL 1260 NICQKI,SPDGGKIPKD11,DEEKFNVELIVQCIRI,SRMPQTHHHAIJ,LI,GTVAGIFPDKV1, 1320 1441 BADTEFWESVCCEFSVQHQ1QSLMN11,0YLJ,KLPEEKEET1PKAVSFNKSESQHEML,0VF 1500 1501 NVETHTSKQLRHFKFLSVSFMSQLLSSNNFLKKVVESGGPELLKGLEERLLETVLGY1SA 1560 DELINIKELÖÖNI SWKKTI VTRFILKEVPDILLA I VORKKKEGEEFØATING TALYTIKLICKN | 1680 1021 VLQGVNGEMVLSQLLPMAEQLLEKIQKEPTAVLKDEAMVLHLTLGKYNEFSVSLLNEDPK 1080 hnimsiftfmganvmrlddtysfqvinktvkmvipaliqsdsgdsiovsrnvooivvkii 1280 961 SKARETTSDAAYVIQDLATLFEELQREKKIJKSHQKIJSETLKNIJJSCVYSCPSYTAKDIJMK 1020 901 LSSQKTQCKHQLASISSEVVISLLINLÖSEVKEVKKAAIQCLQALSGVASFEYLJIDHIJ 960 661 NQKMIELLADNINLGDPSSMLKMVEDLISVGEEESFNLKQKVTFHVILSVLVSCCSSLKE 720 DAVHFRVLMKLFIKVHLEDVFÇLFKFCSVLWTYGSSLSNPLNCSVKTVLQTQALYVGCAM 900 THEPPATRVESLLOKKTRKLESVITAVETPSEWHITE, MEDROTPVET, WAHYVETLINGTOR 780 VAVEDSVFLVFSLKKF1YALKAPKSFPKGD1WWNPEQ1.KFDSRDY1.HT.L.IGL.FEMML.NGA 840 nvethtskglrhfkflsvsfmsgllssnnflkkvvesggpeilkgleerlletvlgyisa 1561 VAQSMEPNADKLTVKFWRALLSKAYDLLDKVNALLPTETFIPVIRGLVGNPLPSVRRKAL SVFVDALPHVPEHRRLPILVQIVDTLGAEKFLWILLILLFEQYVTKTVLAAAYGEKDAIL 1081 1261 1261 1321 1381 1381 1621 1621 721 721 81 781 901 1681 1321 1501 qq qq q q qq q ò δŏ ò g qq 5 οy q òγ Op ò οy qq δλ ò ò ò ò 9 ö ò 3 ŝ نے 3 οy 9 5

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GenCore version 4.5
Copyright (c) 1993 - 2000 - Compugen Ltd
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OM protein - protein search, using sw model

July 2, 2802, 15:29:57; Scarch time 52.51 Seconds (without all-unments) 4535.178 Million cell updates/sec Kun on:

US-09-603-665-5 Perfect score:

COKTLOQUETVIGEPLOSYE 2144

2144 1 MTSLADOLOPLALÞOSDASL OFIGO Scoring table: Sequence.

747574 seqs, 111073796 residues Searched:

Gapop 60.0 , Gapext 60.0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

/SIDS1/qcqdata/hold-qeneseq/qeneseqp-emb1/AA1989.DAT:\* /SIDSI/geddata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*/SIDSI/geddata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*/SIDSI/geddata/hold-geneseq/geneseqp-embl/AA1992.DAT:\* /SIDsTygradata/nold-geneseqg-geneseqg-embi/AA1995 (AF)\*
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/SIDSI/gcgdata/hold-genescq/genescap.embl/AA15000.DAT:\* /SIDSI/degdata/hold-geneseq/geneseqf\_embl/AA1994\_DAT:\* /SIDSI/qeqdata/hold\_geneseq/geneseqp-embl/AA1994\_DAT:\* /SIDSI/qcqdatta/hold-qeneseq/qeneseqF-embl/AA1982.DAT:\*/SIDSI/qcqdatta/hold-qeneseqp-embl/AA1982.DAT:\*/SIDSI/qcqdata/hold-qeneseqp-embl/AA1984 DAT:\*/SIDSI/qcqdata/hold-qeneseqy/qeneseqp-embl/AA1984 DAT:\*/SIDSI/qcqdata/hold-geneseqy/qeneseqp-embl/AA1984 DAT:\* /S11817/gradata/hold-geneses/genesesp-embl/AA1986.nat:\*/S1081/gcgdata/hold-geneses/genesesp-embl/AA1987.nat:\*/S1081/gcgdata/hold-geneses/genesesp-embl/AA1988.DAT:\* /8158/7g-gdata/bold-g-in-seq/-joincseqp-enc)/AAT980.0AT+ /81081/qegdata/bold-geneseq/-joincseqp-enci/AAT9AT-A A\_Geneseq\_032802:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/qcqdata/hold-qeneseq/qeneseqp-embl/AA2001

Human protein sequi Peptide #3836 enco Peptide #3890 enco Protein #337 enco Human brain express Human bone marrow Peptide #3802 enco Peptide #3919 enco Novel human diagno Homo sapiens BAP28 Protein encoded by Description SUMMARIES AAH92729 ABB31185 ABB36384 AAM57146 AAM69542 AARREDDG AAM17368 AAW54099 ABB21738 AAM29882 <u>-</u> Sucry Congth DB 力をち 8 66 Score 2140 90¢ Result

| Peptide #3739 enco | Drosophila melanog | Sequence of leader | Novel human diagno | PDZ encoded domain | Human tax interact | Human tax interact | Human parereatic c | Human digestive sy | Drosophila melanog | Putative P. abyssi | Human granulocyte | CM-CSF (N- and O-1 | Colony stimulating | Human granulocyte | Sequence of a huma | Sequence of a huma | Granulocyte macrop | Sequence of human | Sequence of human | Metapyrocatechase | GM-CSF encoded by | GM-CSF (N-linked s | CM-CSF (one N-link | Human GM-CSF. Hom | Muman granulocyte | Amino acid sequenc | Human granulecyte- | Amino acid sequenc | Human GM CSF. Hom | Himan protein sequ | Haman scoreted pro | Human secreted pro | Human ARE-like pro |
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| AAM05057           | ABB65242           | AAP70733           | ABG02460           | AAB55838           | AAB57629           | AAH58039           | ABB10562           | AAM92098           | ABB65755           | AAB96435           | AAP94855          | AAW0 1933          | AAPFOF45           | AAP60418          | AAP70656           | AAP70657           | AAP80527           | AAP81886          | AAP81885          | AAR04098          | AAR71118          | AAW03932           | AAW0 3/9/34        | AAR92800          | AAWSON 31         | AAB18633           | AAR23002           | AAB84602           | AAB50871          | AAR97:80           | AAR6.4.1.38        | AAB64492           | AABBEBBB           |
| C                  | Ci                 | ·x                 | CI<br>CI           | 22                 | C4                 | 22                 | 디디                 | CI<br>CI           | C1                 | C1                 | 10                | 17                 | 7                  | 7                 | 80                 | œ                  | σ                  | 5                 | σ                 | 11                | 16                | 17                 | 17                 | 17                | 10                | 21                 | ៊                  | 다                  | C1                | a                  | C+                 | CI<br>CI           | 55                 |
| 77                 | 2096               | 1)7                | 68                 | 7.8                | 78                 | 78                 | 93                 | 93                 | 107                | ŢÓB                | 142               | 142                | 144                | 144               | 144                | 144                | 144                | 144               | 144               | 144               | 144               | 144                | 144                | 144               | 144               | 144                | 144                | 144                | 144               | 174                | 179                | 179                | 179                |
| 3.6                | 0.4                | =                  | 0.4                | 4.0                | 0.4                | 0.4                | C.4                | <b>₹</b> .0        | 4.0                | <b>→</b>           | 0.4               | 0.4                | <b>+</b>           | 0.4               | 0.4                | 0.4                | 4.0                | 0.4               | 0.4               | 7.0               | 0.4               | 4.0                | 4.0                | 0.4               | <b>ਦ</b><br>C     | 0.4                | C                  | 0.4                | 0.4               | ₽<br>()            | <del>.</del>       | 0.4                | <b>₽</b>           |
| 77                 | 6                  | x                  | œ                  | œ                  | ထ                  | æ                  | ဃ                  | œ                  | ಹ                  | α                  | œ                 | <b>c</b> c         | α                  | œ                 | æ                  | æ                  | æ                  | 8                 | æ                 | œ                 | œ                 | œ                  | 8                  | 80                | α                 | œ                  | α                  | 8                  | 80                | æ                  | œ                  | æ                  | œ                  |
| 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 6.                 | 07                 | 21                 | C.                 | 2.3               | 77                 | 25                 | 26                | 27                 | 28                 | 29                 | 30                | 3.1               | 32                | 33                | 34                 | 35                 | 36                | 3.7               | 38                 | 30                 | 40                 | 41                | 17 17              | 43                 | 44                 | 4.5                |

## ALIGNMENIS

HAF28, prostate, tumour; cancer; diagnostic; genetic analysis Protein encoded by MAP28 constraing of exons 1 to 45. AAB85029 standard, Frotein; 2144 AA Location/Qualifiers /label- Ser or Asn /label- Asp or Asn /label+ Gly or Glu /label- Ala or Val us-Aud-2001 (first entry) Mise-difference 1694 Misc-difference 1854 Misc-difference 1967 Misc-difference Homo sapiens. AARRS029; AAB85029 RESULT 

MOSDER OBERS-NO 04-JAN-2001

23-JUN 2000; 2000WO-1B01183.

25-JUN-1999; 99US-0141323. 18-JAN-2000; 2000US-0176880.

(GEST ) CHNSET

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10 HLVKPFA 16

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RESULT 15
US-10-041-018-109
Sequence 309, Application US/10041018
Sequence 309, Application US/10041018
GENERAL INFORMATION: Diterbride to the Applicant Hart, Elizabeth A.
APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Diterpres-Producing Unicellular Organism
FILE PRESENCE: PO2080USJ/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT APPLICATION NUMBER: US 60/259880
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: Patentin version 3.1
SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: PATENTIAL TO SECONDATE OF THE SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: PATENTIAL TO SECONDATE OF THE SEQ ID NO 309
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SOFTWARE: PATENTIAL TO SECONDATE OF THE SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: PATENTIAL TO SECONDATE OF THE SEQ ID NO 309
INMURER OF SEQ ID NOS 413
SOFTWARE: PATENTIAL TO SECONDATE OF THE SEQ ID NO 309
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Search completed,  $\mathrm{Jul}_T(2)$  2002, 16-16-47 Job time: 824 sec

DB 6; Length 1945;

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3.5%; Score 7; DB 6; Ler
100.3%; Pred. No. 1.4e·02;
tive 0, Mismatches 0,
                                                                                             : OKGANISM: Saccharomyces cerevisiae US-10-041-018-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
  SOFTWARE: Patentin version 3.1
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NUMBER OF SEQ ID NOS: 413
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cs 7: Conserv
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US-10-041-018-264
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LENGTH: 1045
                                             LENGTH: 1045
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                         SEQ ID NO 199
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Best Local S
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APPLICANT: Hinkle, Greqory J.
APPLICANT: Hinkle, Greqory J.
APPLICANT: Slater, Steven C.
LITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF THILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 18-10(52052)
                                                                                   APPLICANT: Goldman, BAITY S.
APPLICANT: Hinkle, Greqory J.
APPLICANT: Hinkle, Greven C.
TITLE OF INVENTION: EXPRESSION OF MICHGIAL PROTEINS IN PLANTS FOR PRODUCTION OF THIS OF INVENTION: DIANIS WITH IMPROVED PROPERTIES.
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PRICK APPLICATION NUMBER: US-502-80
PRICK FILING DATE: 2002-01-07
PRICK FILING DATE: 2001-(1-05)
NUMBER OF SEQ ID NOS: 41*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.5%; Score 7; DB 7; Length 852; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                      LITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 48 10 ($2.62.)A CURRENT APPLICATION NUMBER: US/A0/2460,034 CURRENT FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47.874
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CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9821
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; Sequence 9821, Application US/K0360039
Sequence 8006, Application US/60360039
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Rhodobacter sphaeroides
US-60 360-039 8006
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Matches 7; Conservative
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APPLICANF: Chen, Xianfeng
APPLICANF: Goldman, Barry
                                             APPLICANI: Cao, Yongwei
APPLICANI: Chen, Xianfeng
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                    GENERAL INFORMATION:
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US 10-041-018-199
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LENGTH: 852
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                                                                                    APPLICANT: Hart, Elizabeth A.
TITLE OF INVENTION: Disterpere-Producing Unicellular Organism
FILE REFERENCE: 522863171025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-C1-07
PRIOR APPLICATION NUMBER: US 60/259880
PRIOR APPLICATION NUMBER: US 60/259880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 264, Application US/10041018
GENERAL INFORMATION:
APPLICANT: Matsuda, Scalichi F.T.
APPLICANT: Matsuda, Scalichi F.T.
TITLE OF INVENTION. Diterperer-Producing Unicellular Granism FILE PEPERENT - PO2080031/10(25547)
GURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILE OF INVENTION TOWER: US/00/041,018
PRIOR PULICALION NUMBER: US/00/059880
PRIOR FILING DATE: 2001-01-05
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Best Lodal Similarity 106.0%: Fred. No. 1.4c.62;
Matches 7; Conservative 0; Mismatches 0;
; Sequence 218, Application US/10041018; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OKGANISM: Saccharomyces cerevisiae US-10-041-018-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPGANISM: Saccharomyces cerevisiae US-10-041-018-264
                                                           APPLICANT: Matsuda, Seiichi P.T.
APPLICANT: Hart, Elizabeth A.
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APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
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                                  Conservative
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; OKCAN!SM: Oryra sativa
US-10-155-881-27684
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Query Match
Best Local Similarity
Matches 7; Conserva
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; GENERAL INFORMATION:
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                                                                       175 LAEKLIKE 181
                                                                                                              272 LAEKLKE 278
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US-10-155-881-27684
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LENGTH: 409
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LENGTH: 415
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APPLICANT: GOLDMAN, MATTY S.
APPLICANT: States, Gregory J.
APPLICANT: States, Steven C.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: CS/60/360,039
CURRENT FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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GTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-137-337-685
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                                                                                                  3.5%; Score 7; DB 5; Length 367; 100.0%; Pred. No. 55; atlive 0; Mismatches 0; Indels
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100.0%; Pred. No. 59;
Eive 0; Mismatches
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CURRENT PUBLICATION NUMBER: US/758,447
PRIOR APPLICATION NUMBER: 06/1758,447
PRIOR PILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
STRING SEQ ID NOS: 812
SOFTWARE: PALENTIN VORE: 2000-03-04
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
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US-60-360-039-17151
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                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-8
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Best Local Similarity
7; Conserve
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Matches 7; Conserv
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                                                                                                                  Query Match
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APPLICANT: HIARLE, Gregory J.
APPLICANT: State's Gregory J.
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFRENCE: 38-10(5.205.2)
CURRENT APPLICATION UNBER: US/60/360,039
CURRENT FILING DATE. 2002 02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LULfiyya, Linda L.
APPLICANT: LULfiyya, Linda L.
APPLICANT: MICHAINCH, James
TILLE OF INVENTION: UCCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TILLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REPRENCE: 38-21(15300) J
CURRENT PPLICATION NUMBER US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 3/595
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3.5%; Score 7; DB 7; Length 393;
100 0%; Pred. No. 59;
Live 0; Mismatches 0; Indels
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100 0%; Pred. Nc. 62;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                              , Sequence 27684, Application US/10155881; GENERAL INFORMATION:
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US-60-360-039-8006
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262 VIALAEK 268
                                                                                                                                     US - 10 - 106 - 698 - 4568
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                                                                                                                              Ouery March 8.5%: Score 7: DH 7: Length 317; Rest Loral Similarity 100.0%; Fred. No. 46; Marches 7: Conservative 0: Mismatches 0; Indels
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0, 54;
                                                                                                                                                                                                     0; Indels
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Bost Local Similarity 100.0%; Pred. No. 54;
Matches 7: Conservation 0; Mismatches
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TITLE OF INVENTION: SECRETORY MOLECULES
FILE REFERENCE: PT 1232 PCT
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GENERAL INFORMATION:
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PERALIA, Careyna H.
DEGANISM: Caemorhabditis elegans
US 60 350 039-6822
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JoNES, Anissa L.
IRAN, Alamna-Phung H.
DAHL, Christopher R.
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DAM, Tam C.
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CHINN, Joyce
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FLORES, Vincent
MARWAHA, Rakesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Le, Audrey
LAN, Ruth Y.
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175 LAEKLKE 181

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sequence 4558, Application 05/10106698
GENERAL INFORMATION
APPLICATE WHEN ELSE
TITLE OF INVENTION. Colon and Colon Gamer Associated Polynucleutides and Polypopt
FILE REPREMENCE: PA00591
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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CURRENT APPLICATION NUMBER: 15/09/991,150
CURRENT FILING DATE: 2001-11-15
Prior Application removed see File Wrapper of Faim
NUMBER OF SEQ ID NOS: 532
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Rest Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches
                                                                                                                                     CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/25524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PLILING DATE: 1999-11-03
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s GENERAL INFORMATION:
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Garrey,Austin I.
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Fong, Sherman
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                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                              : ORGANISM: Homo sapiens
US:10-106-698-4568
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Copyright (c) 1993 - 2090 - Compugun A.td.
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protein search, using sw model OM protein

July 2, 2002, 16.16.40 , Search time 59.99 Seconds Run or.

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Minimum DB seq length: 0 Maximum DB seq length: 20ununubum

Post-processing: Listing first 45 summaries

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/cgnz\_b/ptodata/l/paa/USUB\_NEW\_COMB.pcp.\*
/cgnz\_b/ptodata/l/paa/USIO\_NEW\_COMB.pcp.\*
/cqnz\_6/ptodata/l/paa/USIO\_NEW\_COMB.pcp.\* /eqn2\_6/ptodata/1/paa/PCT\_NEW\_COMB\_pep:\*/cgn2\_6/ptodata/1/paa/USO5\_NEW\_COMB.pep:\*/cgn2\_6/ptodata/1/paa/HSO7\_NEW\_COMR\_pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

|        |       | o <del>s</del> o |          |     |                      |                   |
|--------|-------|------------------|----------|-----|----------------------|-------------------|
| Result | ,     | Query            | Query    | a.  | -                    |                   |
| 0      | 31000 | Match            | na faran |     |                      | Descripcion       |
| 7      | 7     | 3.5              | 307      | 7   | US-60-360-039-21343  | Sequence 21343, A |
| C1     | r-    | ш<br>М           | 317      | ۲   | US-60-360-036-0877   | Sequence 6822, Ap |
| *1     | 7     | 3.5              | 352      | _   | P/T-IIS02-09921-696  | Sequence 696, App |
| 4      | 7     | 3.5              | 353      | 9   | US-10-106-598-4558   | Sequence 4568, Ap |
| 5      | 7     | 3.5              | 367      | S   | US-09-991-150-8      | Sequence 8, Appli |
| 9      | 7     | 3.5              | 392      | G   | US 10 137 337 685    |                   |
| 7      | 7     | 3.5              | 343      | 7   | 118-60-360-039-17151 | 1715              |
| œ      | 7     | 3.5              | 409      | 9   | US-10-155-881-27684  |                   |
| 6      | 7     | 3.               | 415      | ^   | 115-60-460-004-2667  | Sequence 2667, Ap |
| 10     | 7     | 3.5              | 852      | 7   | 11S-60-440-038-8006  | Seguence Book, Ap |
| 11     | 7     | 3.5              | # f. B   | 7   | 1786 650 035-03-86   | Sequence 9821, Ap |
| 12     | 7     | 3,5              | 1045     | (ۍ  | US-10-041-018-199    | 199,              |
| 13     | 7     | 3.5              | 1045     | 9   | US-10-041-018-218    | 218,              |
| 14     | 7     | 3.5              | 1045     | ŗ   | US-10-041-018-264    | Sequence 264, App |
| 15     | 7     | 3.5              | 1045     | 9   | US-10-041-018-309    | Sequence 309, App |
| 16     | 7     | κ.               | 1045     | æ   | US-10-041-018-336    | 336,              |
| 1.7    | 7     | 3.5              | 1045     | 7   | US-60-360-039-1836   | 1836,             |
| 18     | 1     | ي.<br>ئ.         |          |     | US-56-360-039-22781  | _                 |
| 19     | 7     | ي<br>ا           | 1572     | اکا | 48-64-645-625-1959   | Sequence lasa, Ap |
| 50     | ~     | J. F.            | 1572     |     | US-09-935-625-18337  | ~                 |
|        | ۲.    | tr<br>or         | 1612     |     | 775 60 460 044 1628  |                   |
| Ci     | 7     | ς:<br>Γ:         | 1762     | u": | US-09-935 645 1958   | Seguence 1958, Ap |
| 53     | 7     |                  | 1762     | Ç   | US-09-935-625-18336  | Sequence 18335, A |
| č      | ۲-    | 3.5              | 1830     | u:  | US-09-935 625 1957   | Sequence 1957, Ap |
| 25     | 7     |                  | 1830     | 5   | -625-                |                   |
|        | 7     | ~                | 2368     | Ľ,  | TIS-00-035-625-1963  | Sequence 1963, Ap |

| 1 Sequence | Sequence 1962, Ap  | · ·                 | ,                  | 9 Sequence 18339, A | 3,                 | Sequence 240, App  | Sequence 244, App  | Sequence 240, App | Sequence 244, App | Sequence 240,      | Sequence 244, App  | Sequence 240, App  | Soquence 244, App | Sequence 240, App | Sequence 244, App | Sequence 67, Appl | Sequence 58, Appl | Sequence 67, Appl |
|------------|--------------------|---------------------|--------------------|---------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 1          | T961 ST9 J86 60 SD | 11S-19-935-625 1834 | US-09-935-625-1961 | US-09-935-625-18339 | ES-10-105-299-4193 | 115-09-453-834-240 | 115-09-453-834 244 | US-09-453-841-240 | US-09-453-841-244 | US-10-099-574A-240 | HS-10-099-574A-244 | TIS-10-147-849-240 | US-10-147-849-244 | US-10-147-993-240 | US 10 147 993 244 | POT-0801-42202-67 | US-09-736-968A-58 | 115-04-687-837-67 |
| 2368 5     | 2647 5             | 26.47 5             | 2704 5             | 2704 5              | 16 6               | 18 5               | ur.<br>ŒF1         | 18 5              | 18                | IB O               | 18 6               | 1я б               | 18 €              | 18 6              | 18 6              | 6.0               | <u>60</u>         | 60 5              |
| 3.5        | ع.<br>ت.           | ۳.                  | 3.5                | 3.5                 | 3.0                | 0                  | C                  | 3.0               | 3. £              | 3.0                | ()<br>~            | ∪<br>*             | C                 | 3.0               | 3.0               | ÷                 | 3.0               | C .x              |
| 7          | 7                  | 7                   | 7                  | 7                   | v.                 | ¥                  | Æ                  | ٥                 | د                 | Q                  | ų.                 | v                  | œ                 | 9                 | Q                 | £                 | 9                 | ¥                 |
| 27         | 803                | 62                  | 3.0                | 31                  | 32                 | 33                 | 77.                | 35                | 36                | 3.7                | œ.                 | 96                 | 4 0               | 4.1               | 42                | 4 4               | 44                | 4 ጉ               |

# ALIGNMENTS

```
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S
APPLICANT: Goldman, Barry S
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C
TITLE OF INVENTION: LEMESSION OF MICHORIAL PROFITINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: LAMESSION OF MICHORIAL PROFITIES
FILE PEPPENCE: 38-10($2052)A
FILE PEPPENCE: 38-10($2052)A
FILE PEPPENCE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                  Sequence 21343, Application US/60360039; GENERAL INFORMATION.
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Archaeoglobus fulgidus US-60-36C-039-21343
                         US-60-360-039-21343
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ 1D NO 21343
LENGTH: 307
RESULT
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### .: Gaps 0 Length 307; 0; Indels DB 7; 3.5%; Score 7; DB 7; 100.0%; Pred. No. 47; ive 0; Mismatches Oucry Match Best Local Similarity 100.v

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinlib, Grogory J.
APPLICANT: Hinlib, Grogory J.
APPLICANT: Slater, Steven C.
Hille OF HINLIB. EXTRESSION OF MICHOHIA: PROPERTIES
HILLE OF INVENITON. PLANTS WITH IMPROVED PROPERTIES
FILLE EBEREMINE: 38 10 (5.462.)A
CUPERNIT APPLICATION NUMBER: 18,567,460,039
CUPERNI FILLING LAHE: 2662.02
NUMBER OF SEQ ID NOS: 47374
LENGTH: 317
                                                                                                                                                                                                                                                                                 CONTROL OF SECTION OF SECTION OF STREETS OF SECTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Xianfenq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
                                                                                                                                                US 50 (50 039-6822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT .
RESULT
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LOCATION: (43) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                APPLICANT: BOSEN CE al.
FILE PEPERENCE. PMOJA
CURRENT APPLICATION NUCLEIC ACIDS, Proteins, and Antibodics
FILE PEPERENCE. PMOJA
CURRENT APPLICATION NUMBER: US/09/758,451
CURRENT FILING DATE: 2001-01-11
PRIOR PPLING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/780,628
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
SEQ ID NOS: 316
SEQ ID NO 374
US-09-758-451-174; Sequence 174, Application US/09758451; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMAT
US-09-758-451-174
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Caps
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Query Match 3.5%; Score 7: DB 21; Length 48: Hest Local Similarity 100.0%; Pred. No. 87; Matches 7; Conservative 0; Mismatches 0; Indels
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74 LLLQFIL 80 22 LLLQFIL 28 qq

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Sequence 4290, Application US/U9521976
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENERT 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ 10 NOS: 19335
SOFTWARE: PATENT.PM
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-621-976-4290
RESULT 15
US-09-621-976-4290
                                                                                                                                                                                                                                                                                                         SEQ ID NO 4290
LENGTH: 61
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..
                                                         0; Gaps
Query Match 3.5%, Score 7; DB 20; Length 61; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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180 KENYIVI, 186 30 KENYIVL 36 δŏ

Search completed. July 2, 2002, 16:14:39 Job time: 696 sec

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US-08-417-872A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN
OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
IS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                          OTHER INFORMATION: MAE TO ACOUS 229.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN HRAIN, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN INFO. SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5%; Score 7; DB 22; Length 36; 100.0%; Pred, No. 66; ative 0; Mismatches 0; Indels
                                                                                                     SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID No 44493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07 APE 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds
1155 Avenue of the Americas
PRIOR APPLICATION NUMBER: 35 09/608.40H WENTOR FILLING DATE: 2000-06-30
PRIOR PLIANG TOTAL 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774.203
PRIOR FILLING DAIE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERALING SYSTEM: PC-00S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-417-872A-32
: Sequence 42, Application US/08417872A
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISIRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9040
THEREAR: 212-869-9741/8864
TRIEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANI: SPAKKS, ANDREW H
APPLICANI: HOFFMAN, NOAH
APPLICANI: KAY, BRIAN K.
IITLE OF INVENTION: POLYPEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMALTON FOR SEQ TO NOT 32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMALION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Cucry Match
Hest Local Similarity 100.0
' w 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                    NUMBER OF SEC 1D Nos: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOPOLNGY: Linear MOLECULE TYPE: profein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pengle &
                                                                                                                                                                  TYPE: PRI
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 GGEEKFQ 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET
                                                                                                                                              LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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FOWLKES, Dena M. McCONNELL, Stephen J. McCONNELL, Stephen J. McCONNELL, Stephen J. TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL. DEMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                edeb (0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 41;
                                                  u; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
    Tength 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERAIING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
Ouery Match 3.5%; Score 7; DH 8; Best Local Similarity 100.0%; Pred. No. 75; Matches 7; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSME: Pennic & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oucry Match
Hest Local Similarity 100.0%; Prod. No. 75;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1101-174 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-879-957-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (222) 863-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: .Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                   Sequence 79, Application US/U9879957 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lestie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew H. HOFFMAN, Noah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 41 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                 KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                         66 ENDPEKC 72
                                                                                                                                    29 ENDPEKC 35
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US-09-879-957-79
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APPLICANT:
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                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hamada, Tohru
TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS
TITLE OF INVENTION: 0SING GYRASE GENE AS AN INDICATOR
FILE REFERENCE: 12817-004001
CURRENT APPLICATION INTHREE: US/09/823,829
CURRENT FILING DATE: 2001-03-30
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                                                                                                                                DB 22, Length 220;
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                                                                                                                                                                           0; Indels
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207.456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 03 AUGUST 2000 (03 08 00) PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                  4.0%, Score 8, DB 2;
106.0%; Pred. No. 32;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 24 May 2000 (24 05 00)
PRIOR APPLICATION NUMBER: US 09,7632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 34446, Application PC/TUS0100663; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/208, 588
PRIOR PILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: JP 97/343316
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Molecular Dynamics, Inc.
                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09823829 GENFPAL INFORMATION:
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                                                         ORGANISM: Chitinophaga pinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn version 2.0
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Rank, David R.
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Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamamoto, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                      Shoko
                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 8; Conservative
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Kasai, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura,
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                 LENGTH: 220
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                                      TYPE: PRT
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SEQ 1D NO 6
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APPLICANT: Chen, Worsheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS HY MICROARRAY
FILE REFERENCE: Acomica.A. 1
CURRENT APPLICATION NUMBER: 18/09/864.761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Prod No 66;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MAP TO ACROS229.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL + 0.96
                                                                                                                                                                                                                                          SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 34446
                                                                                      PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR PELING NUMBER: US 09/608,408
PRIOR PILING DATE: 30 June 2000 (30.05.00)
NUMBER OF SEQ ID NOS: 38837
PRIOR FILLING DATE: 03 October 2000 (03.10.00) PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR FILLING DATE: 27 September 2000 (27.09.00)
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PRIOR APPLICATION NUMBER: PET/ISOL/000669
PRIOR APPLICATION NUMBER: PET/ISOL/00669
PRIOR APPLICATION NUMBER: PET/USOL/00665
PRIOR FILLING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PET/USOL/00668
PRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING TATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
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Hanzel, David K.
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Best Local Similarity 1900.
Note 7; Conservative
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Query Match
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OTHER INFORMATION: potential membrane-spanning segment, TopFred Program
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11file of invention: A Novel, BAP28 GENE AND PROTEIN
                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCL/USDL/08631
PRIOR FILING DATE: 2010-03-30
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US-09/770,160
PRIOR PILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
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CURPENT FILINS DATE: 1949-06-25
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                         PRIOR FILLING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: PCT/US01/04941
PRIOR FILLING DATE: 2001-03-05
                                                                    PRIOR APPLICATION NUMBER: PCI/USGI/04627
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                              PRIOR AFPLICATION NUMBER: US 04/540_217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/649,167
PRIOR FILLING DATE: 2008-02-28
PRIOR APPLICATION NUMBER: US 09/577,409
                                                                                                                                           PRIOR FILING DATE: 2006-03-07
PRIOR APPLICATION NUMBER: US 09/574,454
                                                                                                                       PRIOR APPLICATION NUMBER: US 197519,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/60141323
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NoS: 412
SUFTWARE: PL-EL-GENES VERSION 6.0
SEQ ID NO 167
                                                PRIOR FILING DAJE: 200(-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barry, Caroline
APPLICANI: Bougueleret, Lydie
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APPLICANT: Nakamura, Shoko
APPLICANT: Suzuki, Makoto
APPLICANT: Suzuki, Makoto
APPLICANT: Hamoda Tohru
TITLE OF INVENTION: MEHOD FOR IDENTIFICATION AND DETECTION OF MICHO-MGANISMS USIN
TITLE OF INVENTION: GENE AS AN INDICATOR
                                                                                    LOCATION: 861..881
OTHER INFORMATION: potential membrane-spanning segment. Toppred Program
                                                                                                                                                                                                                                                                                                                LOCATION: 911..931
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
                                                                                                                                                                                           ECYATION: 884..904
OTHER INFORMATION: potential membrane-spanning segment, TopFred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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J. OTHER INFORMATION: potential leucine zipper pattern, BLA Program
US-60-141-323-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.8%; Score 100; DB 26; Longth 2144; 100.0%; Pred. No. 1.7e-93;
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CORRENT APPLICATION NUMBER: US/09/823,823
CURRENT FILING DATE: 2001-0,-30
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PRIOR FILING DATE: 1997-12-12
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COUNTRY:
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                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods Comptising
TITLE OF INVENTION: BARD1 and Other BRCA1 Binding Proteins
NUMBER OF SEGUENCES: 115
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  REFERENCE/JOCKET NUMBER: UTSD:499PZ2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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                                                                                                                                                                                                                                                                                                   Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                     Sequence 52, Application 08/60042611
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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NAME: Hibler, David W.
REGISTRATION NUMBER: P-41
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CORRESPONDENCE ADDRESS:
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102 ALMMPLVDQLENRLGGEEKFQFRVTKHLIPCIAQFSVAMADDSLWKPLNYQILLKTRDSS 161
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                                                                                               PatentIn Release #1.0, Version #1.30
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000 12-22
PRIOR FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PRILING DATE: 2000-01-25
PRIOR PRILING DATE: 2000-01-25
PRIOR PRILING DATE: 2010-01-25
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TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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                                                                                                                        CHPPENT APPLICATION DATA: APPLICATION NUMBER: US/60/042,985
                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                            NAME: Hibler, David W. REGISTRATION NUMBER: P-41,071
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                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 515 amino acids
TYPE: amino acid
STRANDEDNESS:
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APPLICANT: Wang, Jian-Rui
APPLICANT: Ghosh, Malabika
APPLICANT: Weng, Gezhi
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Best Local Similarity 100.0
Matches 100; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-60-042-985-52
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                                                                                                                                                Longth 2144,
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                                                                                                                        99.0%; Seore 199; DB 20; 3x
100.0%; Pred No. 6.2e-196;
Hismatches 0;
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APPLICANT: Harry, Caroline
APPLICANT: Boughoferer, Liydie
APPLICANT: Chounakov, Liydie
TITLE OF INVENTION: A NeVEL BAP28 GENE AND PROTEIN,
FILE PERFERENTE: 67 1922-ER
CURRENT APPLICATION NUMBER: US/PU/176,880
CURRENT FILING DATE: 2060-01-18
EARLIEF APPLICATION NUMBER: US 60/141,323
EARLIEF FILING INTE: 1999-06-25
NUMBER OF SEQ ID NOS: 12
OTHER INFORMATION: Xaa-Asp of Ash NAME/KEY: VARIANT
                                                             2. OTHER INFORMATION: Xaa-Gly or Glu
US-09-603-665-5
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; Sequence 4, Application US/60176880
; GENERAL INFORMATION:
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60 176-880-4
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Hest Local Similarity
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                                                                         61 AFFDSENDPERCCLLLQFILINCLYRIFLFDTQHFISKERAXALMMPLVDQLENRLGGEER 120
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                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION. Compositions and Methods Comprising
TITLE OF INVENTION: BARDI and Other BRCAL Binding Proteins
NUMBER OF SEQUENCES: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION WINER: US/08/936,487
F11.1NG DATE: Concurrent.y Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/042,985
FILING DATE: 04-APR-1997
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                              2: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER - HS 60/9425,296
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,611
FILLING DATE: 03-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hibler, David W. REGISTRATION NUMBER: P-1,071
REFERENCE/DOCKET NUMBER: UTSD:499
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                RESULT 3
US-08-936-487-52
US-08-936-487
; SEQUENCE 11 SOURCH STORM STORM STORM
; GENERAL INFORMATION:
; APPLICANT: BOWCOCK, Anne M.
; APPLICANT: Haer, Richard
; APPLICANT: Haer, Richard
                                                                                                                                                                            2097 ENYIVLLPESIPFLABLMEDE 2117
                                                                                                                                                       181 ENYIVILPESTPFLAELMEDE 201
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amino acid
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Best Local Similarity 100.0
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPITTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING DATE. Concurr
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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US-08-936-487-52
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Length 2144,

Query Match 99.0%; Sorre 199, DR 2f, L Hest Local Similarity 100.0%; Pred. No. 6.2e-196, Matches 201; Conservative 0, Mismatches 0,

Query Match Hest Local Similarity

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Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

1619 2. 2002. 10 14 37 ; Seared time 50° 3 Seconds Run con

(without alignments) 140.012 Million cell updates/ser

115-08-603-665-5\_copy\_1917\_2117

1 PKLEDWAKTEDAPKORIJIE......NYIVIJESTPETABLMEDE 201 Perfect score: Sequence.

Gapop 60 0 , παραχε 60 0 05170 Scoring table:

3502263 segs. 351980561 residues Searched.

Word size .

1334 Total number of hits satisfying chosen parameters:

Maximum DR seg length: 200000000 Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

Databaso

/cgn2\_6/ptiodata/2/paa/HSOR1\_COMB\_pop.\*
//gn2\_6/ptiodata/2/paa/HSOR2\_COMH.pep.\*
//gn2\_6/ptiodata/2/paa/JSOR4\_COMR.pep.\*
/cgn2\_6/ptiodata/2/paa/JSOR4\_COMR.pep.\*
/cqn2\_6/ptiodata/2/paa/HSOR5\_COMB.pep.\*
/cqn2\_6/ptiodata/2/paa/HSOR5\_COMB.pep.\*
/cqn2\_6/ptiodata/2/paa/HSOR5\_COMB.pep.\* /cqu2\_6/prodata/2/paa/ms091\_coMB\_pep+\*/cqu2\_6/prodata/2/paa/ms092\_coMB\_pep+\*/cqn2\_6/prodata/2/paa/ms093\_coMB\_pep+\* /cgn2\_6/ptodata/2/paa/USO88\_COMB.pep:\* /cgn2\_6/ptodata/2/paa/USO89\_COMB.pep:\* /cgn2\_6/ptodata/2/paa/USO90\_COMB\_pop:\* Pyprodnia/2/paa/USHI4\_COMB\_pcp: \* 6/ptodnia/2/paa/US935\_COMB\_pcp: \* 6/ptodnia/2/paa/US69\_COMB\_pcp: \* 6/ptodnia/2/paa/US697\_COMB\_pcp: \* /cqn2\_6/ptodata/2/paa/US098\_COMB.pep.\* COMB. prop. 1 /rgi:2\_f/pt.odata/2/paa/USf01\_COMH\_prp.+ /cgis2\_6/ptodata/2/paa/US60\_COMB.pcp.+ /cgn2\_6/ptodata/2/pas/PCTUS\_CGMH prp \* ///gitz\_6/Et odat +/2/Eas/it306\_5@NE\_prip.\* /cgn2\_6/pt odat a/2/pas/it307\_c/MB\_pep.\* /cgn2\_6/pt odat a/2/pas/it3080\_c/oMB\_pep.\* MB /cgn2\_6/ptodata/2/paa/US097\_COMB. /cgn2\_6/ptoduta/2/pau/US106\_ .6./p1:::data/2/pu4/IIS099\_ Pending\_Patents\_AA\_Main:\* /cdn2\_ /udu:5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Description                      | Sequence 5, Appli | Scauence 4, Appli | Sognono 52, Appl | Sequence 52, Appl | Sequence 52, Appl | Sequence 167, App | Sequence 3, Appli |
|----------------------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|
| ID                               | 11S 09 603 665 5  | US+60+176 880 4   | US-08-946-487-52 | US-Eu-042-611-62  | TS-F0-042-98E E2  | US-60-339 453 167 | US 60-141-323-3   |
| 1 8                              | 20                | ŭ<br>G            | Ť                | 90                | ч<br>С•           | 26                | 9                 |
| %<br>Query<br>Match Length DB ID | 2144              | 2144              | 515              | 515               | 515               | 1149              | 2144              |
| %<br>Query<br>Match I            | 0 66              | 0 66              | 4 G X            | 49.8              | 4<br>9            | 49.8              | 49.8              |
| Score                            | 149               | 199               | 100              | 100               | 100               | 100               | 100               |
| Result.                          | 1                 | C1                |                  | 4                 | 2                 | 9                 | 7                 |

NAME/KEY. VARIANT

# ALIGNMENTS

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TITLE OF INVENTION: A NOVEL BAF28 GENE AND PROTEIN FILE FEFFHENCE GENSET.063AUS
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PRIOR APPLICATION NUMBER: US 60/176,880
PRIOR FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LCCATION. 1854
OTHER INFORMATION: Xaa-Ala or Val
                                                                                               Sequence 5, Application US/09503665
GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION, 1694
OTHER INFORMATION: Xaa=Ser or Asn
                                                                                                                                                                                                                                                                                                                                APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APFLICANT: Cohen Akenine, Annick
                                                                                                                                                                                                                                                           Barry, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
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TS-09-603-665-5
                                                                                                                                                                                                                                                  APPLICANT.
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 Length, 254,
3.5%, Score 7, DB 22, Longth 254
100.0%; Pred. No. 1.4e+02;
Live 0, Mishatches 0, Indels
                               7; Conservative
                 Best Local Similarity
 Ouery Match
                                Matches
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ABG01568 standard; Protein; 289 AA. ABG01568 ID ABG0 XX

# AHC01568;

(first entry) 13-FEB-2002

Novel human diagnostic protein #1559.

Human, chromosome mapping, gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic, genetic disorder.

WO200175067-A2.

11-0CT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000HS-0540217

23-AUG-2000; 2000US-0649167

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

N-PSDB; AAS65755.

WPI; 2001-639362/73

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, lorensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 20; SEQ ID No 31927; 103pp; English.

The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, Oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal artirity of (11) or of the respectivity of (11) or o quantitating a polypopide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging oil sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, foreusics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGNONIN-ABGNONIN represent novel human Note: The sequence data for this patient did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire,wipo.int/pub/published\_prt\_sequences. 

289 AA; Sequence

O. Gaps 3.5%; Score 7; DB 22; Length 289; 100 D%; Pred No 1 Kr(02; glabut 10 O; Mismatchos 100 08; Rest Loral Similarity 100 C Matches 7, Comservative 4 LLSALAA 10 Query Match

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73 11salaa 79

Search completed: July 2, 2002, 16.06.03 Job time: 180 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 5' end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in qune therapy. The primers are useful for synthesising pelynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in gene therapy. The primers are useful for synthosising polynucleotides, particularly full length CDNAs. The primers are also useful for the detection and/or disanosis of the abnormality of the proteins encoded by the full length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAHSULE for AAHSULE AAAHSULE AAHSULE AAAHSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: primer: detection; diagnosis: antisense therapy; gene therapy.
                                                                                                                              Caps
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Wakamatsu A. Nagai K. Otsuki F.
                                                                                                                              indels
100.0%; Prod. No. 1.20-02:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human profein sequence SEQ ID No-17369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95232 standard: Protein: 245 AA.
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27-AG5-1999; 99JP 0-00253.
11 JAN-2000; 2000JP 0118775.
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2000 tp - 0,41899.
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                                                                                                                        Conservative
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                                                         Best Local Similarity
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09 JUN - 2000;
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                                                                                                                  Matches
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AAB95242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for homologous nucleic acies which are required for cell proliferation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall D, Trawick JD, Carr GJ;
                                        Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a Wide variety of orjanisms. The present sequence represents an essential prekaryotic cellilar proliferation protein. Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotics, comprise sequences of antiscuse nucleic acids
   Length, 245;
                                    0; Indels
                                                                                                                                                                                                                                                                                               Helicobacter pylori cellular proliferation protein #181.
                                                                                                                                                                                                                                                                                                                               Antisense, prokaryotic cellular proliteration protein;
3.5%; Score 7; PB 22; 34
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                    antibiotic; antibacterial; drug design.
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                                                                                                                                                                                          AAU35868 standard; Protein; 254 AA.
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2000US - 253625P.
2000US - 257931P.
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                                    7; Conservative
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                    Best Local Similarity
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                                                                     129 SENDLEE 135
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                                                                                         W0200170955-A2.
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and contg. restriction enzyme sites. The gene is carried on the cloning vector pERISH7-alpha, in which the rcsB related gene is rcsB alpha which contains 7 substituted bases and the ampicillin resistance gene from pUCl8 (AATACT is substit. for tch Scal recognition site AGPACT). Using this new cloning vector the specific selection medium or chromogen for lac 2 is not required.
                                            The sequence is that of an resB related gene prod, having the same amino acid Sequence as the resB gene prod. (the cps regulatory gene)
                       Disclosure, Page 8, 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-040507/05
chromogen for lac 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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                                                                                                                                                                                                                                                                                 119 alaalqk 125
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                                                                                                                                                                                                                                                                                             contq. restriction enzyme sites. The gene is carried on the cloning vector pERISHS-alpha, in which the rosB related gene is rosB-alpha which contains 7 substituted bases and the ampicillin resistance gene from pUGHS. Using this new cloning vector the specific selection medium or chromogen for law 2 is not required.
                                                                                                                                                                                                                                                                                   amino acid sequence as the rcsB gene (the cps regulatory gene) and contq. restriction enzyme sites. The gene is carried on the
                                                                                                                                                                                                                                                                       The sequence is that of an resB related gene prod. having the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene cloning vector for easy selection—comprises regulatory qene with coding aminoacid sequence, and contg. numerous restriction enzyme sites, avoiding specific selection medium or
                                                                                                                                                                                 Gene cloning Vector for easy selection—comprises regulatory gene with coding aminoacid sequence, and contg. numerous restriction enzyme sites, avoiding specific selection medium or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ops regulatory gene; restriction enzyme site; lac Z; chromogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%, Score 7, DB 14, Length 216,
100 0%; Pred No 1 2±+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ResB related gene prod. from pERISH7-alpha.
                                                                                                                                                                                                                                                Disclosure; Page 7; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR36606 standard; Protein; 216 AA.
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                                                                       91JP-0254341.
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Best Local Similarity 100
Each Local 7; Conservative
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                                                                                                                        (NIGE-) NIPPON GENE KK.
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                                                                                                                                                                                                                          chromogen for lac Z
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  Escherichia coli.
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                        JP05091885-A.
                                                                         06-SEP-1991;
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                                                16-APR-1993.
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The sequence is produced by the rcsB gene region, the regulatory gene of E. coli capsular polysaccharde synthetic gene. The gene may be inserted in a wester and foreign DNA inserted at the rcsB gene locus. The ilyated vector (e.g. pERISHI) may be used to transform E. coli HBIOI cells, with only recombinant cells being cultured. The gene provides a method for selection of recombinant clones, without the need for replica or colour media.
                                                                          0; Gaps
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   Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli; capsular polysaccharide, synthetic gene: pERISH1;
                                                                          0; Indels
3 5%; Score 7; DB 14; Le
100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
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Length 216;

3.5%; Score 7; DB 14;

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27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein is used in a vaccine for protecting poultry against coccidiosis, i.e. intection by E. tenella, E. acervulina and E. maxima.
The dosage is 5.50 microg/kg, pref. 25 microg/kg, followed by booster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                          Gaps
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the Eimeria surface actigen.
A recombinant vector or virus conta, the DNA sequence encoding this
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C
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100.0%; Pred. No. 1.1e+02;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Eimeria merozolte surface antigen (24kD), DNA encoding it recombinant virus, useful in the produ. of vaccine against coeridiosis in poultry
                        Length 195;
                                       0; Indels
                       Score 7; DH 22; Lie
Pred. No. 1.1e:02;
                  4,5%; Sct.
100.0%; Pred. No. ...
                                                                                                                                                                     Eimeria merozoite surtace antigen precursor
                                                                                                                                                                                      Merespite: antiqens vicesmes cocondissis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Fig 1(a b): 40pp; English
                                                                                                                                                                                                                       Location/Qualificts
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                                                                                                                                                                                                                                                         /label- mat_peptide
                                                                                                                   AAR14165 standard; Protein; 200 AA.
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7: Conservative
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56 11Salaa 52
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1900 or more genes from brosphila. The invention is useful in developmental biology and in clucidating cell signalling and cell-cell interactions in higher cukaryotes for the development of insecticidas, therapeutics and pharmaceutical fungs. The invention discloses genomic DNA sequences (ABLL6176-ABL90511), expressed DNA sequences (ABL018176-ABL90511), expressed DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes from Drosophila and for elucidating \operatorname{cell} signalling and \operatorname{cell-cell} interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 33815; Zlpp + Sequence Listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%: Score 7; DB 22; tength 200;
100.0%, Fred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Drosophila melanogaster potypeptide SEG ID NO 33816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resh related gene prod. from pERISH6-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD, Myers EW;
ABB69008 standard; Protein: 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR36605 standard; Protein: 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-0S09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-29000; 200908-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1993 (Lirst entry)
                                                                                                                                            26-MAR-2002 (First entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WP1; 2001 656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL13111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 1.1.SA1.AA 10
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                                                                                                                                                                                                                                                                                                                          pharmaceutical.
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                                          polynucleutides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or no treat disease states involving
                                                                                                (II) Is useful for generaling artibodies against it, detecting or quantitating a polypertide in tissue, as molecular weight markers and us a food supplement. (I) and its binding partners are useful in medical imaging of sites expressing (I). (I) and (II) are useful in the dispeptide and polymented profession or binding a site and polymented are useful to treating disorders involving aberrant profession expression or binding artiful dispeptide and polymented tide sequences have applications in diagnostics, forension, gene inapping identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is concerned with the isolation of NIM1 homologues
                                                                                                                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from Willow at ftp.Wipo.int/pub/published_pet_sequences.
polymerase shala reaction (PCB) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and their coding sequences from Arabidopsis thaliana, Brassica mapus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Systemic acquired resistance, SAR, signal transduction cascade;
disease resistance, tobacce, remain, surflewer, sugarbact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel plant genes for enhancing systemic acquired resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and broad spectrum disease resistance in plants, are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 3.5%; Score 7; DH 2
Best Local Similarity 100 0%; Prod No. 57;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. vulgaris NIM1 homologue SEQ ID NO: 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologues of Arabidopsis NIM1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB27313 standard; Protein; 165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 111; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2000, 2000WG-EP01978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2000-594322/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA97216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TTLAPRV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ttlaprv 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200053762-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmeron JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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annuls and Solanum tuberosum, NIMT is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The protein and gene can be used to produce transgenic plants resistant to
                                                                    diseases caused by viruses, such as tobacco of cucumber accale virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phythophthora parasitica and Peromospota tabacilia, bacteria such as Pseudomontas syringae and ptabaci, insects, including aphids and lepidophera and memalodes such as Meleidogyne incognita. In particular they can be used against disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ARLIBITA-ARLIBIT), expressed DNA sequences (ARLIBITS) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila, developmental biology, cell signalling; insecticide;
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O
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                                                                                                                                                                                                                                                                                      Length 165;
                                                                                                                                                                                                                                                                                                                           0; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 17076.
                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                       0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                    3.5%; Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB63428 standard; Protein; 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                                    100.08;
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11-mu.-zono; zonous-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
                                                                                                                                                                                        organisms of maize.
                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                             165 AA;
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                                                                                                                                                                                                                                                                                                                                                             174 DAPKDRL 180
                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical
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                                                                                                                                                                                                                               Sednence
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                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                       Matches
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Ouery Match 3.5%; Score 7: DH 11; Length 98;
Hest Local Similarity 100.0%; Pred. No. 22;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps
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b 74 MVVKLSE 80

Search completed: July 2, 2002, 16:18:31 Job time: 864 sec

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STRAIN-569B,
                                                                                                                                                                                                                Gupta R.S.;
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031026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; CFB group; Flavoharteria; Flavohacteriaceae; Flavobacterium.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gupta R.S., Mukhiar T., Singh B.;
Ewolutionary relationships among photosynthetic prokaryotes
"Ewolutionary relationships among photosynthetic prokaryotes
Chlorobium repidum and Proteobacteria). implications regarding the
origin of photosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Protein phylogenies and signature sequences: A reappraisal of evolutionary relationships among archaebacteria, eubacteria, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                          4.0%; Score 8; DB 5; Length 895; 100.0%; Pred. No. 13; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 56,
                                                                                   Submitted (AUG-2001) to the EMBL/GenBank/DDHJ databases.
EMBL; U55857; AAA98035.2; -.
EMBL; U70855; AAB09160.2; -.
                                                                                                                                                 895 AA, 103130 MW, ESAFD/041F235037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AA; 6451 MW; 8623CEF781D184E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol. Mol. Biol. Rev. 62.1435-1491(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5%, Score 7, 1.
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol Mirrobiol 6.0-0(1999).
EMBL, ARISO451, AAD33469.1, AAD3469.1,
Interpre; IPRO02318; FRNN-synt_2c.
Pfam; PF01411; ERNN-synt_2c:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALANYL-TRNA SYNTHETASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDI, INE-99058143; PubMed=9841678,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flavobacterium ferrugineum.
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Best Local Similarity 100.0
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aminoacyl-tRNA synthetase.
                                                                                                                                                                                                                                     Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                 Waterston R.;
"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                           STRAIN-BRISTOL N2;
  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           696 ENDLEEVG 703
                                                                                                                                                                                                                                                                                                       17 ENDLERVG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 NINLERVG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_FaxID=249;
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01-JUN-2001
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NON_TER
SEQUENCE
                                                                                                                                                     SEQUENCE
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Bacteriā; CFB group; Flavobacteria, Flavobacteriaceae; Flavobacterium.
NCBI_TaxID=991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gupta R.S., Mukhtar T., Singh B.; "Evolutionary relationships among photosynthetic proxaryotes "Evolutionary relationships among photosynthetic proxaryotes (Heliobacterium chlorum, Chloroflexus amranticus, Cyanobacteria, Chlorobium tepidum and Proteobacteria): implications regarding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                   "Protein phylogenies and signature sequences: A reappraisal of
vortationary relationships among archaebacteria, eubacteria, and
eukaryotes,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 7; DB 2; Length 57; 100 0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kacwrakon P., Manning P.A.;
Submitted (SKP-1997) to the EMBL/GenBank/DDBJ databdses
FMRL; AF025662; AAB81983.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 98 AA; 11215 MW; 615AC1889B6D4FB4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ALANYL-TRNA SYNTHETASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                       eukaryotes.";
Microbiol Mol Riol Rev 62:1435-1491(1998).
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InterFor, IPP*07218; IPRA-3ynt_2c.
Pfam; PF01411; IRNA-8ynt_2c; 1.
Aminoacyl-tRNA synthetase.
                                                                                                                                                                                                           STRAIN-ATCC29551;
MEDLINE~99058143; PubMed=9841678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         origin of photosynthesis.";
Mol Microbiol 0:0-0(1999).
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                                                                             Cytophaga aquatilis.
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Best Local Similarity
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20 EKLKGLF 26
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A Galibert F. Finan T.P., Long S.R., Fuehler A., Abola P., Ampe F.,
A Galibert F. Finan T.P., Long S.R., Fuehler A., Abola P., Ampe F.,
A Barloy-Hubber E., Barrelt M.J., Becker A., Cadicu E., Capela D., Chain P.,
A Cowic A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
A Cowic A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
A Gloux S. Coatio T. Ceffegu A., Goldsog N., Souryal M.,
A Hernandez Lucas I., Hong A., Hulzar L., Hyman R.W., Jones T., Rahn D.,
A Rahn M.L., Kalman S., Reating D.H., Riss E., Komp C., Lelaure V.,
A Masyy D., Falm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
A Masyy D., Balm C., Weiding D.H., Wonder K., Yeh K.-C., Batut J.,
A vorboelret F.L., Weidner S., Wells D.H., Wond K., Yeh K.-C., Batut J.,
The composite decome of the lequme symbiont Sinothizobium meliloti.,
Seigence 29:4668-672(201).
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                                      "The cloaks genes from Dseudomonas acraqinosa code for a novel eyanide-
insensitive rerminal oxidase related to the eytochrome bd quinol
oxidases.";
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Barteria: Profedhacferia: alpha subdivision; Rhizobiaceae qroup;
Rhizobiaceae. Sinorhizobium.
NCBL_TaxID-382;
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Best Local Similarity 100.0%; Pred. No. 7 R.
Marches R. Conservative 0. Mismatches 0. Indels
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01-DEC 2001 (TrEMBLrel. 19, Last sequence update)
01-DEC 2001 (TrEMHLrel. 19, Last annotation update)
PUTATIVE QUINGL OXIDASE SUBUNII LIRANSMEMHRANE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 AA; 94235 MW; 30A3421H6H767553 CRC64,
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    Cummingham L., Pitt M., Williams H.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR002585; Bac.Ubq_Cox.
Plam: PE01654; Bac_Ubq_Cox; I.
Complete proteome.
                                                                                                                                                            Mol. Microbiol. 24:579-591(1997).
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Gaps.
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Rhabditidae, Peloderinae, Caenorhabditis.
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investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenHank/DDBJ databases.
EMBL: ACOUSTOS; AALOUB65.1: -.
HYDOTHELICAL PROLET PROLET BEGUEGE CEG64;
SEQUENCE 725 AA, 82788 MM; 18DC466B4C9D0A35 CEG64;
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"The sequence of C. elegans cosmid K08D10.";
Submitted (APR-1996) to the EMBL/Genbank/DOBJ databases.
                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01 DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                  725 AA
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                                                                                                                                                                                                                        HYPOTHETICAL 82.8 KDA PROTHIN.
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01-OCT-2001 (TEMBLEEL 18.
01-OCT-2001 (TEMBLEEL 18.
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                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 ENDLEEVG 530
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                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            021325; 094264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
                                                                                      095XA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K08D10.
                                                           095XA4
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RESULT 10
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                                    095XA4
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0; Gaps

Indels

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Matches

115 SENDPEKC 122

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-!- CATALYTIC ACTIVITY: ATP-DEPENDENT HREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
EMBL. AB032582; BAB13320.1; -- HSSP; P06982; LAJ6.
InterPro; IPR001241; DNA_LOPOISOII.
InterPro; IPR003594; HATP-ase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Phylogenetic analysis and taxonomic study of marine Cytophaga like bacteria, Proposal of Hacrentibaculum gen. nov. with Hacrentibaculum maritimum comb. nov. and Hacrentibaculum novolyticus comb. nov., and two new species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ò
                     -1- SIMILARITY- RELONGS TO THE TYPE II TOPOISOMERASE FAMILY EMBL; AH032581; HAB13319.1; -.
HSSP; P06982; TAJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 481;
5. 7.7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AA; 53735 MW; LE4FD8E3F4EEBA30 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TERMELLE). 16, Created)
01-MAR-2001 (TERMELLE). 16, Last sequence update)
01-DEC-2001 (TERMELLE). 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, CFB group, Flexibacter group, Flexibacter.
NCBL_Tax1D-1004;
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Live 0, Mismatches
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SMART; SM00433; TOP2c; 1.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 8;
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                                                                                                                                                                                                                                                                                               PRINTS: PRO0418; TP12FAMILY.
Probom: PROF0615; DMZ.toprisolI; 1
SMART: SMO0433; TOP2c: 1
PROSITE; PS00177; TOP0ISOMERASE_II: 1
                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Isomerase; Topoisomerase.
                                                                                                             Interpro; PR001241; FNA_topolsoll.
Interpro; IPR003594; HATPase_c.
Interpro; IPR002936; Toprim.
Pfam: PP00204; PNA_topolsoll: 1.
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Pfam; PF02518; HATPase_c, 1.
Pfam; PF01751; Toprim: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA GYRASE B SUBUNIT (FRAGMENT)
                                                                                                                                                                                                                                    Pfam; PF02518; HATPase_c; 1.
Pfam; PF01751; Toprim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00418; TPI2FAMILY.
OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki M., Yamaguchi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
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Best Local Similarity
Matches 8, Conservat
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QGFAW9
ID QGFA
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Length 481;

DB 2;

Query Match 4.0%, Score 8; I Best Local Similarity 100.0%; Pred No

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-i - CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOLBLE-STRANDED DNA
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                                                                                                                                                                                                                                                                                                                                                                             STRAIN-DSM 2588;
Suruki M. Takadera T., Harayama S., Vamamoto S.;
Takadera T. Cytophaga-like bacteria: Phylogenetic analysis
"Diversity of marine Cytophaga-like bacteria: Phylogenetic analysis
using gyrB sequences and their carotenoids profiles.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
EMBL: ABO48186; BAR43153 1; -
HSSP; P06982; laJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 8; DB 2; Length 481; 100 0%; Pred No. 7.7;
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                                                                                                                                                                                                                                                                                    Bacteria; CFB group; Flexibacter group: Chitinophaga.
NCBI_TaxID=79329;
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01-3TL-1997 (TrEMBLrel. 04, Last sequence update)
01 DEC 2001 (TEMBLREL. 19, Last amodation update)
                                                                                                                                                              01-TIN-2001 (TrEMBLrel. 17, Created)
01-TUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                          PRT; 481 AA.
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PROSITE; PS00177; T0P01SOMBRASE_11; 1.
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STRAIN-ATCC 15642 / PAO1;
MEDLINE-97323403; PubMed-9179851;
                                                                                                                                                                                                                              DNA GYPASE B SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00204, DNA_topoisoll, 1. Pfam; PF02518; HATPase_c; 1. Pfam; PF01751; Toprim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;PR002936, Toprim.
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Matches 8, Conservative
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                                                                                                                          PRELIMINARY;
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116 SENDPEKC 323
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NON_TER
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                                                                                                                                                09AQL.4;
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                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saps
                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria: Proteobacteria: alpha subdivision: Phizobiaceae group:
Phyllobacteriaceae: Mesorhizobium.
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Rhodobacter sphaeroides (Rhodopsendomonas sphaeroides).
Hacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.0%: Score 9; DB 16; Length 453; 100.0%: Pred. No. 7.3; 0; Indels of Indels
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Ptam: PF01654: Bac_Ubq_cox: 1.
SEQUENCE 465 AA; 51345 MW: 5C9F8091E567C910 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 AA; 49427 MW; ID2439E6E34BFA0F CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLINIV-1998 (IFEMBLIC), 08, Credicd)
01 NOV-1998 (TEEMBLIC), 08, Last sequence update)
01 DEC 2001 (TEEMBLIC), 19, Last annotation update)
01 off-2001 (TrEMBLrel. 18, Last, sequence update)
01 off-2001 (TrEMBLrel. 18, Last, annotation update)
001Not. OXIDASE SUBBILL 1.
MERA'24.
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EMBL: AF084032: AAC34673.1; ..
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MEDITINE-20519422; PubMed-11064196;
                                                                                                                                                                                                                    MEDIJINE-21082930; PubMed-11214958;
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; 198002585; Bac_Ubq_Gox.
Plam; PF01654: Bac_Ubq_Cox: ].
Complete profeceme.
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Host Local Similarity 100.0
Matches 8; Conservative
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"Phylogenetic analysis and taxonomic study of marine Cytophaga like bacteria. Proposal of Haerentibaculum gen. nov. with Haerentibaculum maritimum comb. nov. and Haerentibaculum ovolyticus comb. nov., and two new species.";

submitted (SEP-1999) to the EMBL/Genfank/PirRJ databases.
                                                                                                                                                                                                                                                                                              Submitted (SEP-1999) to the EMHL/GenBank/DDHJ databases.
-!- CATALYTIC ACTIVITY: AIP-DEPENDENT BREAKADE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                   STRAIN-IFO 16041;
Sucaki M., Yamaguchi K.;
Phyliogenetic analysis and taxonomic study of marine Cytophaga like bacteria. Proposal of Haerentibaculum qen. nov. with Haerentibaculum marttimum comb. nov. and Haerentibaculum evolyticus cumb. nov., and two new species.";
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01-MAR-2001 (TrEMBLrel. 16, fast sequence update)
01-MAR-2001 (TrEMBLrel. 19, last sequence update)
01-MC-2001 (TrEMBLrel. 19, last annotation update)
DNA GYRASE B SUHUNIT (FRAGMENT)
                                         01 MAR-2001 (TILMBLIE). 16, Created)
1-MAR-2001 (TIRMBLE). 16, Last sequence update)
01-DEC-2001 (TIEMBLE). 19, Last annotation update)
DNA GYRASE B SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; CFB group; Flexibacter group; Flexibacter
                                                                                                                                        group: Flexibacter group: Flexibacter
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                481 AA
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ATP-binding; Isomerase; Topoisomerase.
               PRT;
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PRINTS: PR00418; TP12FAMILY.
Probom; PD000616; DNA_topoisoII; 1.
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InterPro; IPR001241; DNA_topoisoll.
InterPro; IPR003594; HAIPase_c.
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Flam; PF00204; DNA_topoisoII; 1.
Plam; PF02518; HATPase_c; 1.
                PRET.IMINARY;
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Suzuki M., Yamaquchi K.;
                                                                                                                         Flexibacter japonensis.
Bacteria, CFB group: Fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00433; TOP2c;
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                                                                                                                                                       NCBI_TaxID-104662;
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GenCore version 4.5 Copyright, (c) 1993 - 2000 rompugen Ltd.
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OM protein - protein search, using sw model

July 2, 2002, 16:18-30 , Search time 96:19 Seconds (without alignments) 361 493 Million cell updates/sec

US-09-603-665-5_COPY_1867_2067 Title: Perfect score:

201 1 LTAFFLEALDFRAGHSENDI.

CIAQESVAMADDSLWKPLNY 201 Sequence:

OLIGO Gapop 60 0 , Gapext 60 0 Scoring table:

562222 segs, 372994929 residues Scarched:

Word size :

1169 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Listing lirst 45 summaries

SPTREMBL_19:* 1: Sp_archea:* Database :

sp_archea:*
sp_bacteria:*
sp_fung::*
sp_huma::*
sp_huma::*
sp_numa::*
sp_mamma::*
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Pred. No. is the number of results predicted by chance to .ave a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution sp_rvirus:* sp_bac_eriap:* sp_archeap:*

sp_unclassiticd:*

sp_virus:* sp_vercebrate:*

sp_rodent:* sp_plant::*

# SUMMARIES

Description	Ogées5 momosanten	098dw. rhizobium 1		09fax2 : lexibacter		Ogtaw9 Paribacter		007440 cseudomonas	092s67 -bizobium m	095xa4 caenorhabdi	021325 caenorhabdi	09x617 flevobacter	_		O9cte2 mus musculu	096215 sulfolobus
<u> </u>	Q96ES5	.6 Q98DW1	68080	Q9FAX2	OGFFAXO	O9FAW9	O9AQL4	6 007440	6 092567	095XA4	021325	. Q9 <b>X</b> 617	. 09 <b>x</b> 618	031026	1 Q9CTE2	7 096215
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PRT; 453 AA.

098DW1 PRELIMINARY; PRT; 098DW1; 01-OCT 2001 (TrEMBLical, 18, Greated)

RESULT 2 098DW1 ID 09 AC 09 ET 01

0994t0 homo sapien 090wt1 brachydanio 09a213 caulobacter 02603 helicobacter 02603 helicobacter 098hm1 rhizobium 1 09n045 macaca fasc 09au6 canlobacter 02108 caenorhabdi 097513 sultolobus 097513 columba livolobacter 097580 sus serota 095134 homo sapien 097644 bacillus ha 090vyp7 homo sapien 099vyp7 homo sapien 099vyp1 homo sapien 099vyp1 lactolococus 090vyp1 lactolococus 075226 homo sapien 029vyp1 lactolococus 075226 homo sapien 029vyp1 lactolococus	PRELIMINARY; PRT; 349 AA.  CC-2001 (TEMBLEE]. 19, Created) CC-2001 (TEMBLEE]. 19, Last sequence update) SC-2001 (TEMBLEE]. 19, Last sequence update) SC-2001 (TEMBLEE]. 19, Last sequence update) SAR TO HYDOMERICAL PROPERT FLJ10359. SAPTIENS (Human).  SAPTIENS (Human).  TAXID=9606; TAXID=9606
4 Q9Y4T0 13 Q90WT1 16 U2A213 16 U2A213 16 U2A213 16 Q9EM91 16 Q9AAU6 6 Q9AAU6 7 Q9XEB9 17 Q9XEB9 13 Q9Y137 2 007839 13 Q9Y137 2 007839 14 U2A518 6 Q975B9 4 Q9Y721 16 U2A518 16 U2A518 17 U2A518 18 U2A518 19 U2A518 19 U2A618 2 Q4R722 5 Q9EM6E4 2 Q9R721 10 U2M6E4 10 U2M6E4 2 Q9R721 2 Q4R722 5 Q9EM5 5 Q9EM5 5 Q9EM5 10 U2A665 11 U2A68 11 U2A68 11 U2A68 11 U2A68 12 U2A68 13 U2A68 14 U2A68 15 U2A68 16 U2A68 17 U2A68 18 U2A68 18 U2A68 18 U2A68 19 U2A68 19 U2A68 19 U2A68 19 U2A68 10 U	T. 1  5 GOBESS  9 PRELIMINARY; PRT; 349 AA.  90568S5  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 03 SEQUENCE FROM N.A.  11 SEQUENCE FROM N.A.  11 SEQUENCE 349 AA; 39921 MW; 3A359597E7079EB CRC64; 03 Match 04 Collega; AAH1983.1; 04 DAS SEQUENCE 349 AA; 39921 MW; 3A359597E7079EB CRC64; 03 Match 04 One of the Collega
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US-10-041-018-264
Sequence 264, Application US/10041018
Sequence 264, Application US/10041018
GENERAL INFORMATION:
APPLICANT: Matsuda, Selichi P.T.
APPLICANT: Matsuda, Selichi P.T.
TITLE OF INVENTION: Diterpene-Producing Unicellular Organism FILE REFERENCE: P02080USI/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
PRIOR FILING DATE: 2002-01-07
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SEGFTWARE: Patentin version 3.1
SEOFTWARE: Patentin version 3.1
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Indels
0, Mismatches
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7; Conservative
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FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/50/350.039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9821
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                                                                                                                                                                                                 APPLICANT: Chen, Xiantena
APPLICANT: Chen, Xiantena
APPLICANT: Gladau, Barry S.
APPLICANT: Gladau, Barry S.
APPLICANT: Gladau, Barry S.
APPLICANT: Black, Steven C.
APPLICANT: Black, Steven C.
TILLE APPLICANT: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38 10(52052)A
FILE REFERENCE: 38 10(52052)A
CORRENT FILING DATE: 2002-02-21
NUMHER OF SEQ ID N'S: 47374
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Greening J.
APPLICANT: Hinkle, Greening J.
APPLICANT: State Street Street J.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE; 38 10/52052)A.
FILE REFERENCE;
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APPLICANT: Chen, Xiantenq
APPLICANT: Chen, Xiantenq
APPLICANT: Goldman, Barry S.
APPLICANT: Brown Content of the Capture of the Capt
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; Sequence 9#21, Application US/60360039
; GENERAL INFORMATION:
                                                                             : Sequence 2667, Application US/Konthonst
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Book, Application 08,40340439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILLING DATE: 2002-02-21
NUMBER OF SEC ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Synechocystis sp. 
US 60 460 049-2667
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APPLICANT: Chen, Xianteng
                                                                                                                                                              APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 FLAELME 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 VI.ALAEK 145
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                                          US 60 360 039-2667
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LENGTH: 415
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RESULT 10
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APPLICANT: Hart, Elizabeth A.
APPLICANT: Hart, Elizabeth A.
FITLE OF UNENTION: Diterpone-Producing Unicellular Organism FILE REFERENCE: P02080051/1002547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT PELING DATE: 2002-0;.07
PRIOR FILING DATE: 2002-0:09
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Diterpene-Producing Unicellular Organism FILE REFERENCE: P0208051/10025547
CURRENT APPLICATION NUMBER: US/10/041,018
CURRENT FILING DATE: 2002-01-07
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                                                                                                                                     Ouery Match 3.6%; Score 7; DB 7; Length 894; Post Local Similarity 100 00; Pred. No. 1.26+02; Matches 7; Conservative 6; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e+62;
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Best Local Similarity 100.0%; Pred. No. 1.4
Matches 7; Conservative 0; Mismatches
; TYPE: PRT
; ORGANISM: Desultitobacterium hafniense
US-60-360-039-9821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/259880
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyres cerevisiae
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SOFTWARE: Patentin version 3.1
FAVOR: 1 FAVOR: 1
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SOFIWARE: Patentin version 3 1
SEQ ID NO 199
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Gaps

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3 6%; Score 7: DB 6: Length 392;
100.0%; Pred. No. 58;
Live 0: Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 47374
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Guery Match
Best Local Similarity 100.0
Matches 7; Conservative
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                                                              7; Conservative
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US-10-155-881-27684
                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei APPLICANT: Chen, Xianf
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                                           Best Local Similarity
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                                                                                                142 LAEKLKE 148
                                                                                                                                  111 LAEKLKE 117
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LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secreted and Transmembrane Folypeptides and Nacleic FITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 7; DB 5; Length 367;
100.0%; Pred. No. 54;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fosen et al. IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUPRENT FILING DATE: 2001-11-16
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 532
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CURRENT APPLICATION NUMBER: US/10/137,337
CUPPENT FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER - HS/09/991,150
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PRIOR PLICATION NUMBER: 09,758,447
PRIOR FILING DATE: 2001-01-11
PRIOR PLICATION NUMBER: 60,179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER: 05-52
SOFTWARE: PALENTIN VET: 2.0
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; GENERAL INFOPMATION
                                                                                                                                                                                            Grimaldi,J.Christopher
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                       Timothy A.
                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Stewart, Timothy A
                                                                                    Ferrara, Napoleone
                                                                                                                                           Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                   Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerber, Hanspeter
                                                                                                                                                                                                           Gurney, Austin L.
                                                                                                                                                                           Godowski, Paul J.
                                                                                                                                                                                                                                  Kljavin, Ivar J.
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                                   Botstein, David
                                                                                                                                                          Goddard, Audrey
                                                                                                                                                                                                                                                   Napier, Mary A.
Ashkenazi, Avi i
               Baker, Kevin P
                                                    Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                        Tumas, Daniel
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                                                                                                       Fong, Sherman
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                                                                   Eaton, Dan L.
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                                                                                                                                                                                                                                                                      Pan, James
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APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
APPLICANT: Hinke, Gregory J.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURPENT APPLICATION NIMBER: 18/60/3460.039
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100.0%; Pred. No.
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; Sequence 17151, Application US/60360039; GENERAL INFORMATION:
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3 (RCANISM: Carporhabditis elegans IIS-56: 460-039-6822

APPLICANI:

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FEATURE

LENGTH

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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 7; DB 1; Tength 454;
100.0%; Pred. No. 53;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 7; DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS905PCT CURRENT APPLICATION NUMBER: ECT/US02/09785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PA005P1
CURRENI APPLICATION NUMBER: US/10/105,698
                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-03-27
PRICK APPLICATION NUMBER: PC1/US00/26524
PRICK FILING DATE: 2000-09-28
PRICK APPLICATION NUMBER: US 60/157,137
PRICK APPLICATION NUMBER: US 60/163,280
PRICK APPLICATION NUMBER: US 60/163,280
PRICK FILING DATE: 1999-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Sequence 698, Application PC/IUS0209785; GENERAL INFORMATION:
                                                          ; Sequence 4568, Application US/10106698; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09991150
; GENERAL INFORMATION:
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Hest Local Similarity Tous
7, Conservative
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Matches 7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 VLALAEK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 TVLGEP1, 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 VLALAEK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 TVLGEPL 191
RESULT 4
US-10-106-698-4568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH.
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PRIOR APPLICATION UNMRER: 60/280, 667; 60/280, 668; 60/291, 280; 60/291, 849; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879; 60/291, 879;
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: OTHER INFORMATION: Incyte ID NO: LG:238456.10.ort3:2001MAR30
PCT-0502 09921 694
                               Length 317;
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                                                                                             0: indels
                        Query Match
Best Local Similarity 100.0%; Fred. No. 48;
Matches 7; Conservative 0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        Appligation PC/TUS0209921
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PERALIA, Carayna H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRAN, Alanna-Phung B.
DAHL, Christopher R.
GIETZEN. Darryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INCYTE GENOMINS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGUYEN, Duy Viet An
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LEWIS, Samantha A.
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AMSHEY, Stefan R.
DAUGHEKIY, Sean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAFFO, Abel
Jennes, Antissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URASHKA, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHINN, JOYCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jimmy Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAM, Lam C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEEFELD,
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                       139 VLALAER 145
                                                                                                                                                                                                                      234 VIALAEK 248
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OM protein - protein search, using sw model

Tuly 2, 2002, Inclh:47; Search time 54,44 Seconds

(without alignments) 328.355 Million cell updates/sec

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307805 seqs, 101015595 residues Searched:

Total number of hits satisfying chosen parameters:

Word size:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post processing: Listing first 45 summaries

Pending_Patents_AA_New:* 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB_pep.* 3: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB_pep.*

/cgn2_6/ptcddata/1/pda/USO7_NEW_COMB.pcp.* /cgn2_6/ptcddata/1/pda/USOB_NEW_COMB_pcp.*

/cgn2_6/ptodata/1/paa/usn9_unm_inomH_pep:*//cgn2_6/ptodata/1/paa/usn0_new_comB.pep.*//cgn2_6/ptodata/1/paa/US60_NEW_ioMH_pep.*

Pred. No. is the number of resuits predicted by chance to have a Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

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Result No.	Score	Ouery Match	Ouery Match Length	DB	£	Description
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7	7	3.6	307	^	US-60-360-039-21343	Sequence 21343, A
e.	7	W F	317	ŗ.	HS-60-360-039-6832	Sequence 6822, Ap
æ	7	3.6	352	-	PCT-HS02-04421-646	, 969
*	7	3.6	353	9	US-10-106-698-4568	
S	7	3.6	354	_	PCT-US02-09785 698	
9	7	3.6	367	r.	US-09-991-150-8	Seduence 8, Appli
7	7	3.6	392	9	US-10-137-337-685	
œ	7	3.6	393	7	US-60-360-039-17151	Sequence 17151, A
6	7	3.6	4 0 d	ď	TIS-10-155-881-27684	
10	7	3.6	415	7	US-60-460-039-2667	Sequence 2007, Ap
11	7	3.6	852	~	98-680-680-68066	8006
12	7	3.6	894	7	US 60 360 039 9821	9821,
13	7	3 6	1045	£	US-10-041-018-144	199' /
14	7	3.6	1045	c	US-10-041-018-218	Sequence 218, App
15	7	S)	1:145	c	115-10-041-018-264	Sequence 264, App
16	7	3.6	_	9	US-10-041-018-309	Sequence 309, App
17	7	3.6	1045	ع	115-10-041-018-336	136,
18	7	3 6	1045	7	US-60-360-039-1836	1836,
19	7	3 6	128 ←	~.	118-50-460-460-75781	
∪~7	7	3 6	1572	ک	115-09-445-625-1454	Sequence 1454, Ap
	7	3 6	1572	ď	118-00-038-628-18337	Sequence 18337, A
34	۲.	3.6	1752	dC	9541-579-586-60-56	Sequence 1958, Ap
53	7	3 6	1762	ď	US 09 935 625-18336	Segmence 18336, A
£.0	7	3.6	1830	٩'n	US US 335 615 1957	Sequence 1957, Ap
ยา (4	7	3.6	1830	un.	US 09 935-625-18335	
93	7	3.6	2368	ري	US-09-935-625-1963	Sequence 1963, Ap

7	3.6	2368	٦)	US-09-935-625-18341	Sednence	Sequence 18341, A	
	÷,	2547	اکا	US-09-935-625-1962	Sequence	1962, Ap	
	3.6	2547	ď)	US 09 935 625-18340	Sequence		
	3 6	2704	ľ	US-09-935-625 1961	Sequence	1961, Ap	
	3.6	2704	2	US-09-935-625 18339	Sequence		
	3.1	16	٧	US-10-105-299-4193	Sequence	4193, Ap	
	3.1	18	Ľ;	US-09-453-834-240	Sequence		
	-	ž	u ⁻	11S 09 454-834-244	Sequence	244	
	~	18	ď	118-09-453-841-240	Sequionee		
	3.1	20	'n	US-U9 453 841 244	Sequence	244,	
	3.1		٥	US-10-099-574A-240	Sequence	240,	
	. F.	18	Œ	HS-10-099-574A-244	eouelibes:	244,	
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	Ţ <b>,</b>	X.	·c	US-10-147-849-244	Sequention		
_	3.1	18	9	US-10-147-993-240	Sequence	240,	
_	3.1	18	9	US-10-147-993-244	Sequence	244,	
	- .*	5.4	-	M' 1 - USU 1 - 122112-67	Sednence	67, 4	
	3.1	09	5	US-09-736-968A-58	Sednence	58, Appl	
	3 1	9	r.	19-1831-60-Sn	Sequence	67, Appl	

# ALIGNMENTS

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APELICANT: STATE, STATE, STORY OF MICRORIAL PROTEINS IN PLANTS POR PRODUCTION OF TITLE OF INVENTION. EXPRESSION OF MICRORIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE PEPEPENGE. 94 -10 ($5052) A
FILE PEPEPENGE. 94 -10 ($5052) A
FURRENT APPLICATION NUMBER: 18/A0/4A0,034
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ 10 NOS: 47374
LENGTH-307
                         ; Sequence 21343, Application US/60360039; GENERAL INFORMATION: APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPGANISM: Archaeoglobus tulgidus
                                                                                                      Chen, Xianfeng
Goldman, Barry S.
Hinkle, Gregory J.
US-60-360-039-21343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-60-360-039-21343
                                                                                                      APPLICANT:
APPLICANT:
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or free cì Length 307; O, Indels DB 7; Ouery Match 3.6%; Score 7; DB 7; Best Local Similarity 100.0%; Pred. No. 46; Maiches 7; Conservative 0, Mismaiches

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Sequence 5822, Aprileation US/60360039 GENERAL INFORMATION: APPLICANT: Pao, Yongwei US-50-350-039-6822 PESIILT

THIRE OF INVENTION: EXPESSION OF MICROHIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE PEPPENTE: (4-10(\$-52)A
CURRENT APPLICATION NUMBER: 18/60/360,039
CURRENT PILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 317 APPLICANT: Chen, Xianfenq APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.

LENGTH, 31 TYPE: PRT

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                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                       uvery Match
Host Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodics FILE REFERENCE: PMO18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JODERT, S. T. TITLE GONERT OF INTITUTE REFERENCE: GONERT ON: HAND TOWN HAND OF INTITUTE REFERENCE: GENSET 0.54PR2 GONERT APPLICATION NUMBER: US/09/621,976 CURRENT FILLING DATE: 2000-07-21 SOFTWARE: PELCEL.PM NUMBER: PELCEL.PM SSO, ID NO. 4290 LENGTH: 61
                                                             TOPOLGGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-879-957-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/758,451 CURRENT FILING DATE: 2001-01-11 PRIOR APPLICATION NUMBER: 0.0/179,065 PRIOR FILING DATE: 2000-01-31 PRIOR FILING DATE: 2000-07-31 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 174, Application US/09758451; GENERAL INFORMATION:
                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                       LENGTH: 41 amino acids
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 316
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 LLLQFIL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 LLLQFIL 28
                                                                                                                                                                                                                                                                                                   33 ENDPEKC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-621-976-4290
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-758-451-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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Ouery Match 3.6%; Score 7; DB 20; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 147 KENVIVL 153
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Db 30 KENVIVL 36
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Search completed, July 2, 2002, 16:14:40 Job time: 697 sec

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APPLICANT: HOFFMAN, MOAH
APPLICANT: KAY, BRIAN K.
TITLE OF INVENTION: FOLYPEPTIDES HAVING A FUNCTIONAL DOMAIN
TITLE OF INVENTION: F INTEREST AND METHODS OF IDENTIFYING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO ACD05229.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 0 96
OTHER INFORMATION: EXPRESSED IN FEAL LIVER, SIGNAL - 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 0.86
US-09-864 761-44493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7: DB 22; Length 36;
Pred. No. 84;
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SOFTWARE: Annomax Sequence Lusting Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U; Mismatches
                                                                                                         PRIOR ATLLING DATE: 2011-01 30
PRIOR ATLLING DATE: 2011-01 30
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR PELLING DATE: 2001-01 30
PRIOR PELLING DATE: 2001-01 40
PRIOR PELLING DATE: 2001-01 40
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR APPLICATION NUMBER: PTI/USOL/0066/2
PRIOR APPLICATION NUMBER: PTI/USOL/006/2
PRIOR APPLICATION NUMBER: US 60/234,687
                                 PRIOR FILLING DALE: 2001-01-30
PRIOR APPLICATION NUMBER: PCL/3601/000664
PATE TO THE PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PT-EVE/MS-FVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application #S/084[7872A GENERAL INFORMATION:
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Hest Local Similarity (00.00
7; Conservative
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         PRIOR APPLICATION NUMBER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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New York
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                                                                                          PRIOR FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 46
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KAY, Brian K.
FOWLES, Data M.
MCCONNELL, Stephen J.
HITLE OF INVENTION: PO_YPEPTINES HAVING A FUNCTIONAL.
DGMAIN OF INTERES! AND METHODS OF IDENTIFYING AND
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100.0%; Pred. No. 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%; pred. No. 94;
Matches 7, Conservative 0; Mismatches
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FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1101-174 TELECOMMUNICATION INFOFMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/879,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
APPLIANCE DATE: 05.08,417,872A FILING DATE: 07-APR-1995 CLASIFICATION: 536 ATTORNEY/AGENT INPRMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELETAX. (212) 862-8864/9741
TELEX: 66141 PENNIE
THIEX: 66141 PENNIE
                                                                                                      REGISTRATION NUMBER: 18,872
PPEPPINCPZINGKET NUMBEP: 1191-193
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 79, Application US/09879957
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  TELEPAX: 212-790-9056
TELEPAX: 212-869-9741/E864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOFFMAN, Noah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                           LENGIH: 41 amino acids
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                          linear
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US-08-417-872A-32
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                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: 1
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PCT-US01-00663-34446
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                                                                                      APPLICANT:
                                                                                                           APPLICANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                              TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING OF TITLE OF INVENTION: GENE AS AN INDICATOR FILLE PERFERENCE: 12847-004-011.

CUPRENT APPLICATION NUMBER: US/09/823,823
CUBRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUZUKI, MAKOLO
APPLICANT: KASAL, HIFOAKI
APPLICANT: Hamada, Tobru
TITLE OF TWENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS
TITLE OF INVENTION: USING GYRASE GENE AS AN INDICATOR
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100.0%; Pred. No. 40;
Live 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22, Longth 220
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4.1%, Score 8, DB-25
Hest Loral Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismalches
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CURRENT APPLICATION NUMBER: US/09/823.829

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 09/208, b88

PRIOR APPLICATION NUMBER: US 09/343316

PRIOR APPLICATION NUMBER: UP 97/343316

PRIOR FILING DATE: 1998-12-10

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 82

SOFTWARE: PALENTIN VERSION 2.0
                                                                                                                                                                                                                                                                                                                   DRIOR APPLICATION NUMBER: US 09/208, 688
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 97/343316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genence 6, Application US/09823829
GENERAL INFORMATION:
                                                 Sequence 6, Application US/09823823
GENERAL INFORMATION:
APPLICANT: Yamamoto, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Chitinophaga pinensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin version 2.0
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamamoto, Satoshi
APPLICANT: Nakamura, Shoko
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                                                                                                                                        Nakamura, Shoko
Suzuki, Makoto
Hamoda, Tohru
                                                                                                                       Kasai, Hiroaki
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              RESULT
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RESULT 10

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TITLE OF INVENTION: HOMAN GENOME DIRIVED SINCIE EXON NUCLETÇ ACTO DECRES USPETIL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                        APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILLE REFERENCE: PB 0004 WO 7
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 0.96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234.687
PPIOR FILIN: DATE: 21 September 2000 (21 09 00)
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                  CHERENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 64 PERFUATY 2000 (04 02 00)
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 26 MAY 2000 (26.05 00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 03 AUGUST, 2000 (03.08.00)
PRIOR PHLING INTERES: US 02/283.6
PRIOR FILING INTERES: US 02/283.6
PRIOR PHLING INTERES: US 02/280.1000 (03.10.00)
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PRIOR PLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-18
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NUMBER OF SEQ ID NOS: 38837
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER · PCT/HSO1/00663
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PPIOP APPLICATION NUMBER: US 60/207,456
Sequence 34446, Application PC/TUS0100563
GENERAL INFORMATION:
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                                                      APPLICANT: Molecular Dynamics, Inc.
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                                                                                                  Penn, Sharron G.
Rank, David R.
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LENGTH: 36
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SOFTWARE: Patent.pm

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PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR PILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: POT/US01/03800
PRIOR APPLICATION NUMBER: POT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILLING DATE: 2000 013 07 PRIOR APPLICATION NUMBER: US 09/574.454 PRIOR PILLING DATE: 2000-05-19 PRIOR APPLICATION NUMBER: PCT/US01/04941 PRIOR FILLING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 04/540.217
PRIOR FILINI DATE: 2000 033-31
PRIOR FILINI DATE: 2000 038-34
PRIOR FILINI DATE: 2000 08-24
PRIOR FILINI DATE: 2000 08-24
PRIOR FILINI DATE: 2001 03-40
PRIOR FILINI DATE: 2001 03-40
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2001-02-26
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PRIOR FILING DATE: 2001-01-25
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PRIOR FILING DATE: 2001-04-18
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PRIOR FILLING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/577,409
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PRIOR FILING DAIE: 2000 03 07
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PRIOR FILING DATE: 2001 01-26
                           PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000 01-25
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SEQ 1D NO 167
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PRIOR FILLING DATE: 2000 12-22
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PRIOR AFFLIGATION PRIOR FILING DATE:
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# 5.1%: Store 127: DB 25: Length 1149:
100.0%: Pred. No. 4.5e-119:
tive 0; Mismatches 0; Indels 0; Gaps
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Ouery Match
Best Local Similarity 100.0
Matches 127: Conservative
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LOCATION: 91..111 Optential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Proutom
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Proq.am
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OTHER INFORMATION: potentia membrane spanning segment, TopPred Program
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OTHER INFORMATION, potential membrane-spanning sequent, TopPred Program
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OTHER INFORMATION: potential membrane spanning segment, TopPred Program
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OTHER INFORMATION: potential leucine zipper pattern, BLA Program
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Matches 127; Conservative 0; Mismatches
                                               ORGANISM: homo sapiens
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LENGTH: 2144
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                             NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                            COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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Matches 127; Conserv
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CLASSIFICATION:
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                                                                                                                 Texas
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                              449 PKVRFAALITVLALAEKEKENYIVLLPESIPFLAELMEDECEEVEHOOOKTIQULETVLG 508
   129 PKVRFAALLTVLALAEKLKENYIVLLPESIPFLAELMEDECERVEHQCQKTIQQLETVLG 188
                  65.1%; Score 127; DB 26; Length 515; 100.0%, Fred. No. 2.2e:119;
                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods Comprising
TITLE OF INVENTION: BARD1 and Other BRCA1 Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible oppEATING SYSTEM: PC-ONS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                       B: Arnold, White & Durkee
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/60/042,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/60042985 GENERAL INFOPMATION:
                                                                                                                                                                                ; Sequence 52, Application US/60042611
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hibler, David W. REGISTPATION NUMBER: P-41,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ 1D NO: 52: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bowcock, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                 APPLICANT: BOWCOCK, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 amino acids
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Best Local Similarity
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                                                                                                     509 EPLOSYF 515
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69 ALMMPLVDQLENRLAGEEKFQERVTKHILIFCIAQFSVAMADDSLWKFLNYQILLKTRESS 128
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Compositions and Methods Comprising
BARDI and Other BRCAL Binding Proteins
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 115/60/042,985
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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PRIOR APPLICATION NUMBER: PCT/US00/35017
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
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                                                                                            ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy ...
AMEDIUM TYPE: HAM PC COMPATIBLE
OC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
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512/474-7577
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APPLICANT: Wang, Jian-Rui
APPLICANT: Chosh, Malabika
APPLICANT: Weng, Gezhi
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2070 LLKTRDSSPKVRFAALITVLALAEKLKENYXVELFESIPFLAELMEDEVEEVEHGOGKTT 2129
1950 I.FTI.PAGHI.VKPPADTI.XOVNISKTDEAFFDSENDPFKCCI.J.QFTI.NCf.PKTFI.FDT QH 2669
                                       61 FISKERAXALMMPLVUQLENPLGGEEKFQFPVTKHLIPCIAQFSVAMADDSIWKPLNYQI 120
                                                                                                                  121 LLKTRDSSPKVRFAALLTVLALAEKLKENYTVLLPESTPFLAFIJMEDECEFVEHOCOKTT 180
                                                            2010 FISKERAXALAMPLVFQLENPLGGEEKFQEPVIKHUIPHHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                    2130 QQLETVLCEPLQSYF 2144
                                                                                                                                                                                               181 QULEIVLGEPLÜSYF 195
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                       Sength 2144;
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                                                                                                                                   93.0%; Score 193; DR 20;
130.0%; Pred. No. 1e-185;
Vienalistes 0;
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APPLICANT: Bouqueleret, Lydie
APPLICANT: Choumakov, Hya
TITLE OF INVENTION: A NOVEL HAP28 GENE AND PROTEIN
FILE REFERENCE: 67.US2.PRO
                                                                                                                                                                      ilarity 100.0%; Pred. No. leri
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER - US/60/176 RRO CURRENT FILING DATE: 2000-01-18 EAKLIER APPLICATION NUMBER: US/60/141,323
                                                        LOCATION: 2017 OTHER INFORMATION: Xaa-Gly \odot \mathcal{E} Gla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/60176880 GENERAL INFORMATION:
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                OTHER INFORMATION: Xad-Asp or Asn
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NUMBER OF SEC ID NOS: 12
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Matches 195; Conserva
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Best Local Similarity
Matches 195; Conserva
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                                       NAME/KEY:
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DOCAPION:
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                                                                                    Compositions and Methods Comprising BAFD1 and Other BECA1 Binding Proteins
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FILING DATE: 20-SEP-199£
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                        Arnold, White & Durkee
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Sequence 52, Application US/08936487 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
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INFORMATION FOR SEQ ID NO: 52:
                                        APPLICANT: Bowcock, Anne P. APPLICANT: Baer, Richard
TITLE OF INVENTION: Composit
(TILE OF INVENTION: BAFDI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILLING DATE: 04-APR-1997
ATTOPNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hibler, David W. REGISTRATION NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                CURPENT APPLICATION DATA:
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2000 Compagen Ltd.
GenCore version 4 5
Copyright (c) 1993 2000 Comp
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OM protein - protein search, using sw model

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US-09-603-665-5 COPY_1950 2144

POKTIQOLEIVDSEPUQSYP 195 195 1 LETLEAGHLVKPEADTLXQV Perfect score: Sequence.

OLIGO Capop 60 0 , Gapext 60 0 Scoring table:

3502263 seqs, 351980561 residues

Searched:

Word size :

Total number of hits satisfying chosen parameters:

2299

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Pending_Patents AA_Main:*	1: /cgn2_6/p!.odu!a/2/paa/Fr7118_chMB_p	2: /cqs2_6/ptodata/2/paa/0806_COMB_pP	3: /cgn2_6/ptodata/2/paa/US07_COMB.pe	
apase :				

/cgit__6/ttodatd/2/puu/USOBO_COMB.pcp.*
/cgnz_6/ptodatd/2/pau/USOBO_COMB.pcp.*
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//cgnz_6/ptodatd/2/pau/USOB_COMB.pcp.*

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/cgn2_6/ptodata/2/paa/US099_COMB.pcp.* /cgn2_6/ptodata/2/paa/US10_COMB.pep.* /cgn2_6/ptodata/2/paa/US10_COMB.pep.* /cgn2_6/ptodata/2/paa/US60_COMB.pep.* /cgn2_6/prodata/2/paa/US097_COMB.pcp. /cqn2_6/prodata/2/paa/US098_COMB_pcp.

/cgn2 6/ptodata/2/paa/US096_COMB.pep:

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Sequence 5, Appli	Sequence 4, Appli	Sequence 52, Appl	Sequence 52, Appl	Sequence 52, App)	Sequence 167, App	Sequence 3, Appli
		<u>a.</u>	US-09-603-665-5	US-60-176 880-4	US-08-936-487-52	US-60-042-611-52	US 60-042-985 52	US-60 339-453-167	US 60 141-323-3
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		Match Length DB ID	2144	1144	7.7.	7,17	n ; n	1149	2144
*	Query	Match	0.66	0.65	65.1	65.7	65.1	65.1	65.1
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Sequence 6, Appli Sequence 6, Appli	3444	444	Sequence 32, Appl	5 .	7 -	i č	Sequence 7436. Ap	. C1	33.	1	38	30438	61			670	083		7397	114	23	128	549	Sequence 145, App	612	612	104	109	Sequence 2146, Ap	57,	13298,	Sequence 65493, A	83089,	Sequence 70342, A	Sequence 1282, Ap
8 678 60 SI	PCT-US01-00663	US-09-864-761-4449	US-08-417-87	/ 56 - 6 / X - 50 - 50 - 50 - 50 - 50 - 50 - 50 -	せいきょうのく こからしのご	118-60-147-499	US-60-196-718	US-60-196-718	US-60-162 247	US-60-169-840	US-09-751-181-	PC-II-11S01-C	US-09-864	08-60-236	US-09-107	US-09-107	US-60-170	2-60-SN	PCT-US01-C	DS-60-170	11S-08-849	US-08-625	666 BO SO	US-60-181	US-09-897	US-60-215	US-09-732	US-60-169	US-60-140	US-09-339	US-03-675	-03-108-421-6	US-09-708-427-8308	US-09-708-427-7034	ŭs 60-142 896 1
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AFFLICANT. Chumakov, Ilya
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AFFLICANT. Cohen Akenine, Annick
ITHE OF TWENTIEN. A NEVEL BAL28 GENE AND PROFEIN
FILL REFERENCE: GENSELLUG3AUS
                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER TISSUS/NO.3,665
CURPENT FILING DATE: 2000-06-23
PELOR APPLICATION NUMBER INS AD/141,323
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US OU/176,880 PRIOR FILING DAFF: 2000-01-18 NUMBER OF SEQ ID NOS: 63 SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION, 1854
OTHER INFORMATION: Xaa-Ala or Val
NAME/KEY: VARIANT
                                             , Sequence 5, Application US/U9603665 : GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION, Xaa=Ser or Asn
NAME/KEY: VARIANT
                                                                                             APPLICANT: Barry, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2144
                         US-09-603-665-5
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SEQ ID NO 5
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RESULT
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RA Nordone F., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,
RA Sasabi H. Sale R., Schemebech C., Seya T., Shibata Y., Storch K.-F.,
RA Sasabi H. Sale R., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RA Hayashizaki Y.,
RI "Functional annotation of a full length mouse cDNA collection.";
RI "Emerican annotation of a full length mouse cDNA collection.";
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139 VLALAEK 145 +111111 151 VLALAEK 157

Query Match

Matches

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070473

RESULT 12

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Indels

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Rawai U. Shinagawa A. Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Kiyoshwa H., Gordo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kidota K., Maisuda H., Ashburner M., Balalov S., Casavant T., Picischmann W., Gasterland T., Gissi C., King H., Kochiwa H., Fucischmann W., Staubi F., Sazuki R., Tomita M., Wagner I., Washio T., Sakai K., Tomita M., Wagner I., Washio T., Sakai K., Tomita M., Wagner I., Washio T., Sakai K., Tomita M., Baldarelli R., Barsh G., Blake J., Bolielli D., Rojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fujita M., Gariboldi M., Gyens E., Marchionni L., Mashima J., Mazzarelli J., Mombacrts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           klee S.k., Nassif X., Kusecek B., Merker P., Beretti J.i., Achtman M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molocular and biological analysis of orght genetic islands that distinguish nelsseria meningitidis from the closely related pathogen neisseria genorthoseae":
Infect Immun 68:2082-2045(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria; beta subdivision, Neisseriaceae, Neisseria.
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.6%; Score 7; DB 2; Length 238; Rest Local Similarity 100.0%; Pred. No. 70; Matches 7; Conservative 9; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24830 MW; 52428P97A9A844H7 MPM64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61-JUN-2001 (TrEMBLIEL. 17, Created)
01-JUN-2001 (TrEMBLIEL. 17, Last sequence update)
01-DEC-2001 (TrEMBLIEL. 19, Last annotation update)
2610-213/RPIK PROTEIN (FRAGMENT).
AKPIAL OF 2610201A1RPIK.
                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                  01-oct-2000 (tremmirel, 15, Created)
01-oct-2000 (tremmirel, 15, Last sequence update)
01-mAr-2001 (tremmirel, 16, Last annotation update)
HYPCTHELICAL 24.8 KDA PROTEIN
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O
                                                                                                                                                                                                                                                                         238 AA.
0; Mismatches
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MEDLINE-21085660, PybMod-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2018/481; PubMed-10722605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
7; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 DSSPKVR 17
                                                         51 YKIFLFD 57
                                                                                               41 YKIFLFD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tinsley C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-72491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                            Q9JPE8;
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      Matches
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Thesis (2001), bepartment of Institute of Roology, Academia Sinica,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebralish) (Zebra danio).
Enkaryousi Metacau, Chordala, Cianiata, Vertebrata, Buteleostomi;
Actinopteryyii, Neopteryyii, Teleostei, Euteleostei; Östariophysi;
Cyprinformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota; Metazoa; Chordata; Craniáta; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Kodentia; Sciurognathi; Muridae; Cricetinae;
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      DB 11; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 228;
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01-DEC-2001 (TERMBLIEL, 19, Last annotation update)
CRYSTALLIN RI PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                     01-AGG-1998 (TERMELLE), 07, Created)
01-AGG-1998 (IMBELE), 07, Last sequence update)
01-DEC-2001 (IMBELE), 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
      3.6%; Score 7; DB 11
100.0%; Pred. No. 63;
.tive 0; Mismatches
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Pfam. PF00248: aldo ket.red: 1.
PRINTS: PROUGOS, ALDKETRUTASE.
PROSITE: PS00798: ALDOKETO_REDUCTASE_1: 1.
PROSITE: PS00062: ALDOKETO_REDUCTASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus (Chinese hamster).
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01-DEC-2001 (TREMBLREL. 19, LAST SCHU
01-DEC-2001 (TREMBLREL. 19, LAST ANDO
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EMBL; AJ317957; CAC84899.1; -.
SEGUENCE 232 AA, 26781 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALDEHYDE REDUCTASE (FRAGMENT).
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nes 7; Conservative
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Best Local Similarity
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                                            Hest Local Similarity
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                                                                                                                               139 VLALAEK 145
                                                                                                                                                                         123 VI.AI.AEK 129
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Query Match

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SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Bosidae;
eurosids II; Brassicales: Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville B.,
De Clerck R., De Keyser A., Neyt F., Rouze P., Van Den Daele H.,
Villaroci K., Gielen J., Van Montagu M., Bancrott I., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryola, Mehazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria: Primates, Catarthini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   ..
SEQUENCE FROM N.A.
MEDLINE: 89123097; PubMed-2644218;
Jacobson M.R., Brigle K.E., Bennett L.T., Setterquist R.A.,
Jacobson M.S., Cash W.L., Bryton J., Newton W.E., Dean D.R.;
"Physical and genetic map of the major nif gene cluster from
Acolobarter vinetandil.";
J. Barteriol. 171-1027(1989).
EMRL: M20588: AAA4421.1;
SEQUENCE 72 AA; 8004 MW; HCHCA20883035894 CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 7; DB 10; Length 165; 100.0%; Pred. No. 50; tive 0, Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0, Indels
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                       Length 72;
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Submitted (MAR-2000) to the EMBL/Genhank/DDRT databases
EMBL AL[62351; CARB2561.1; -...
Hyporbeticed profesin.
SEQUENCE 165 AA: 15002 MW: 2140B7CBAA98BA2B CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rudd S., Lemeke K., Mayer K.F.X.;
Submiffed (MAR-2000) to the EMBLAN-MARK/UDBEL databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01 OCT 2000 (TERMLER), 15, Created)
01 OCT 2000 (TERMLER), 15, Last sequence update)
01-OCT 2000 (TERMLER), 15, Last annotation update)
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01-NAY 2000 (TEMBLECL. 13, Last sequence update)
01-DEC-2001 (TEMBLECL. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                       DB 2;
. 23;
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                                                                                                                                                                                                                                                                                                                                                                                               0: Mismatches
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                                                                                                                                                                                                                                                                                                                                    1.5%; Score 7; I
00.0%; Pred, No.
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120115_180.
                                                                                                                                                                                                                                                                                                                                                                190.0%;
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Best Local Similarity 100....
7: Conservative
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Hest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 ALAEKLK 24
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CSLZVS
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REFAINCESTBL/63; TISSUB-EMBRYO;

KA RAWAI J. Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rarawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H. A., Ashburor M., Rasukawa I., Saito K.,

Radota K., Matsuda H. A., Shehoror M., Rasukawa I., Saito K.,

Radota K., Matsuda H. A., Shehoror M., Rasukawa I., Saito K.,

Radota K., Matsuda H. A., Shehoror M., Rasukawa I.,

Radota K., Matsuda H. A., Shehoror M., Gissi C., King B., Kochiwa H.,

Radota K., Okido T., Puruno M., Gissi C., Ring B., Kochiwa H.,

Rasuka K., Okido T., Puruno M., Aono H., Badarelli R., Barsh G.,

Rasakai K., Okido T., Puruno M., Anna H., Hadarelli R., Barsh G.,

Rasonstein M.J., Bult C., Tletcher C., Fujia M., Garibolai M.,

Romstein M.J., Bult C., Tletcher C., Fujia M., Garibolai M.,

Rasaki H., Sato K., Schochach C., Sakamoto N.,

Rasaki H., Sato K., Schochach C., Sakamoto N.,

Sasaki H., Zoyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I.,

Wangking R., Wang K.H., Weitz C., Whittaker C., Wilming I.,

Wangking R., Newyolisa P., Hasequwa Y., Rawaji H., Kehisuki S.,

Wangking R., Wang K.H., Weitz C., Whittaker C., Wilming I.,

Wangking R., Weitz C., Wanga I., Shibata S.,

Wangan R., Weitz C., Wanga I., R., Wanga I., Shibata S.,

Wangan R., Weitz C., Wanga I., R., Shibata S.,

Wangan R., Weitz C., Wanga I., R., Weitz R., Wanga I., Shibata S.,

Wangan R., Weitz C., Wanga I., R., Weitz R., Wanga I., Shibata S.,

Wangan R., Weitz C., Wanga I., R., Weitz R., Wan
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                              Ducsterhooff A., Lauber J., Mewes H.W., Gassenhinber J., Wiemann S. Submitted (AUG-1999) to the EMBL/GenHank/DDHJ databases.
E-HL. SIMILARITY: CONIAINS 2 WD REPEATS (TRP-ASP DOMAINS).
E-HL. ALILO160; CABS3665..;
InterPro: IPP601680; WD40
Plam; PF00400; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Melazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional annotation of a full-length mouse cDNA collection.":
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100.(%; Pred. No. 61;
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InterPro; IPR001395; Aldo_ket_red.
InterPro; IPR001395; Aldo_ket_red.
Ptam; PP00248; aldo_ket_red; I.
PRINTS: PP000069; AldowerP01ASE.
PROSITE: PS00062; AldowerP01ASE.
SEQUENCE: 214 AA; 24419 PW; 62A4H9AC136CEBES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 205 AA: 22537 MW; 972HTFF960460BT0 CRC64;
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Last annotation update)
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Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      SMART; SM00320; WD40; 2.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE: PS50082; WD_REPEATS_2; 1.
PROSITE; PS50244; WD_REPEATS_RESION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Repeat; WD repeat
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EMBL, AK011221; HAH27477.1; -.
HSSP; P14550; ZALR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel, 17, (TrEMBLrel, 19,
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IISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
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Gaps

4.1%, Score 8, DB 2; Length 481; 100.0%, Pred. No. 12; Live 0; Mismatches 0; Indels

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Best Local Similarity 100.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "phylogenetic analysis and taxonomic study of marine Cytophaga like barieria Proposal of Haerentibaculum qen. nov. with Haerentibaculum maritimum comb nov. and Haerentibaculum ovolyticus comb. nov., and
               two new species.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
maritimum comb, nov, and Haerentibaculum ovolyticus comb, nov., and
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-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
EMBL, AB022582; BAB13320.1; -.
HSSP: P06982; IAJ6.
InterPro; PR001241; DNA_topoiso11.
InterPro; PR001241; DNA_topoiso11.
                                                                                                                                            -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
EMBL; AB032581; BAB13319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.1%; Score 8; DB 2, Length 481;
100.0%; Pred. No. 12;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 4A; 53517 MW; 1F3AB57936BC10F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA; 53735 MW; 1E4FD8E3F4EEBA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hacteria; CFB group; Flexibacter group, Flexibacter.
NCBL_TaxID-1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (FTEMBLICE). 16, Created)
1-MAR-2001 (TEMBLICE). 16, Last sequence update)
01-DEC-2001 (TEMBLICE). 19, Last annotation update)
DNA GYRASE B SUBUNIT (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Isomerase: Topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00177; TOPOLSOMERASE_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding, Isometase, Topoisometase.
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Probom; PD000616; DNA_topoisoll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                              pfam; PF02518; HATPasc_c; 1.
Pfam; PF0751; Toprim; 1.
PRINTS; PH60418; TPT2FAMILY.
Probom; PD000616; DNA_topoisoII: 1.
                                                                                                                                                                                                                  HSSP; P06982; 1AJ6.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interPro; IPR002936; Toprim.
Piam; PF00204, DNA_LopoisoII; 1.
Piam; PF02518; HATDASe_c; 1.
Piam; PF01751; Toprim: 1.
                                                                                                                                                                                                                                                                                                     InterPro; IPR002936; Toprim.
Pfam; PF00204; DNA_topoisoll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki M., Yamaguchi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00433; TOP2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SMOO433; TOP20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hest Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flexibacter sancti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-1FO 15057:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two new species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 SENDPEKC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
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SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                              InterPro;
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Suzuki M., Takadera T., Harayama S., Yamamoto S.; "Diversity of marine Cytophaga-like bacteria: Phylogenetic analysis using gyrB sequences and their carotenoids profiles."; Submitted (AUG-2000) to the EMBL/CenHank/Dubu databases.
-!- CATALYTIC ACTITYTY: ATP-DEPENDENT HREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY. EMBL; AB048186; BAB33153.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 8, DB 2; Length 481;
100.0%; Pred. No. 12;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AA, 53681 MW, E8452H58879927F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; CFB group; Flexibacter group; Chitinophaga.
NCBI_TaxID-79329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrembLrel, 01, Last sequence update)
01-NOV-1998 (TremBLrel, 08, Last annotation update)
                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation opdate)
NNA GYRASE B SUBUNIT (FRAGMENT).
                                                                                                                                                  481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00177; TOPOISOMERASE_II: 1.
ATP-binding: Isomerase. Topoisomerase.
NON_TER
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                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P06982; 1AJ6.
Interpro; IPR001241; DNA_topoisoll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000616; DNA_topoisoll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; TPR002936; foprim.—
Ptam; PF00204; DNA_LopoisoII; 1.
Ptam; PF02518; HATPase_c; 1.
Ptam; PF01751; Toprim; 1.
PRINTS; PR00418; TP12FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Conservative
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                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00433; TOP2c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                         Chitinophaga pinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3est Local Similarity
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316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 SENDPEKC 39
316 SENDPEKC 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-DSM 2588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEÇUENCE
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                                                                                                                                                        09A01.4
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09A01.4
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"Ploning Sequence and genomic structure of MHC class II antigens from the Speciacled cannon. Calman crocodilus.";
Submitted (MAR 2000) to the EMHL/Genhank/DDHJ databases.
                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus halodutans and genomic sequence comparison with Facillus subtilis"; Nucleic Acids Res. 28:4317-4331(2000).
EMBL: ANODISI9; BABO7485.1: -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       STRAIN-C-125 / JCM 9153, MEDLINE-20512582; FubNed 11058132. Machine-20512582; FubNed 11058132. Machine H., Nakasone K., Takaki Y., Macho G., Sasaki R., Masui N., Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinde; Caiman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8, DB 16, Length 188;
Pred. No. 5.3;
9. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 4.1%; Score 8; DB 7; Length 254; Best Local Similarity 100.0%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTTE; PSO02/01: 16_MBC; DNKNOWN_L.
SEQUENCE: 253 AA; 28550 MW; D95EA5D9060E4325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       188 AA; 26473 MW; 4520RFC4AB045D47 CRC64,
                                              01-0CT_2000 (TrEMBLrel. 15, Created) 01-0CT_2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR 2001 (TERMELTE). 16, Last sequence update)
01 DE? 2001 (TERMELTE). 19, Last annotation update)
                                                                                                                                           Bacteria: Firmicutes, Bacillus/Clostridium group;
Bacilius/Staphylococcus group; Bacilius.
NYB: LaxIP-86665;
                  188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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SMART; SM00407; IGe1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%, Sc.
Local Similarity 100.0%; P
Tes 8; Conservative 9.
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InterPro; IPR003597; Iq_cl.
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                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047: iq: 1
                                                                                                                                Bacillus halodurans
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 COLETVIG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 ALITYLAI, 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 QULETVIG 14
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                                                                                               HH 1766 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                       SECTIONS
                              U*K663 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C96.JN1;
               15.6880
                                                                                                             HH 376.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GJN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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two new species.";
Submitted (SEP 1999) to the EMML/Genhank/LUBHJ databases.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT HKEAKAGE, PASSAGE AND KEJOINING
OF DOUBLE-STRANDED DNA
                                                                                                                                                                                                                                                                    STRAIN-IFO 16041;
Suzuki M., Yamagucki K.;
Phylogenetic analysis and taxonomic study of marine Cytophaga like
bacteria. Proposal of Haerentibaculum qen. nov. With Haerentihaculum
maritimum comb. nov. and Haerentibaculum ovolyticus comb. nov., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IFO 15056;
Suchly M., Yamaauchi K.;
Phylogenotic analysis and taxonomic study of matine Cytophaga Dike
bacteria, Proposal of Haerentibaculum qen. nov. with Haerentibaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TFEMBLECI. 16, Created)
01-MAR-2001 (TFEMBLECI. 15, Last sequence update)
01-PRC-2001 (TFEMBLECI. 19, Last annotation update)
DNA GYRASE B SUBUNIT (FRAGMENT)
                                                                                                                    01-MAR-2201 (TrEMBLrel. 16. Created)
01-MAR-2001 (TrEMBLrel. 16. Last sequence update)
01-DEC-2001 (TrEMBLrel. 19. Last annotation update)
                                                                                                                                                                                                        Bacteria, CFB Gloup, Flexibacter Gloup, Flexibacter
NCBI_FaxID+104662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; OFB group; Flexitacter group; Flexibacter
NCBL_Tax10-104663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1%; Score 8; DB 2;
100.0%; Pred. No. 12;
tive 0, Mismatches
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                                                                                          481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM60433; TOP2c; 1.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
ATP-binding; Isomerase; Topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; [PR00124]; UNA_topoisol].
InterPro; [PR003594; HATPase_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD000616; DNA_topo;soll; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002936; Toprin.
Plam; PF00204; DNA topoiso[1: 1.
Plam; PF00218; HATPase_c;
Ptam; PF01751; Toprim; 1.
PHINTS; PR00418; TP12FAMILY.
                                                                                                                                                                 DNA GYRASE B SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flexibacter filiformis.
                                                                                                                                                                                            Flexibacter japonensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P06982; 1AJ6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 SENDPEKC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 SENDPEKC 39
13 ALITVIAL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U9FAX0;
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                                                                                        09FAX2
                                                                                                     U9FAX2;
                                                           4
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                                                          RESULT
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                                                                        Q9FAX2
            <u>q</u>
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compagen Ltd.
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protein search, using sw model OM protein

Run on:

July 2, 2002, 16-18-32 , Search time 96-19 Seconds (without alignments) 350.702 Million cell updates/sec

US-09-603-665 5_CCFY_1956_2144

195 Perfect score:

PORT LOQUETVIGEPLOSYF 195 1 LPTI-PAGHLVK PEADULXQV Sequence:

Gapop 60 0 , Gapex! 60.0 oblao Scoring table:

562222 scqs, 172994929 residues Searched:

Word size :

1258 Total number of hits satisfying chosen parameters:

Minimum DB seq length, 0 Maximum DB seq length, 200000000

Post-processing: Listing first 45 summaries

SPTREMBL 19:* Database :

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertcbrate:* sp_mhc:*
sp_organelle:* sp_archea:*
sp_bacteria:* sp_rodent:* sp_rvirus:* sp_mammal:* sp_plant:* sp_virus:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_archeap:*

#### SUMMARIES

		ଷ							ນ		ņ		c		n	7
Description	gases home sapien	29k6q3 bacillus ha	Q9gjn1 caiman croc	09fax2 flexibacter	O9fax0 flexibacter	Q9faw9 flexibacter	Q9aq14 chitinophaq	Q44537 azotobacter	0912v5 arabidopsis	ygugig homo sapien	O9dOp3 mus muscul	070473 cricetulus	Q90wtl brachydanio	Q9jpe8 neisseria m	Q9ct53 mus musculu	ပ္9cgi5 mus musculu
9	LyneEx	Q9K6G3	Q9GJN1	Q9FAX2	COFAXO	O9FAW9	09AQL4	044537	Q91,2V5	940619	Q9D0P3	070473	Q90WT1	QGJPE8	Q9CT53	090015
	4	16	7	Č	C4	7	C4	a	10	4	11	11	13	7	Ξ	Ξ
% Ouery Match Length DB	14.4	188	253	481	481	481	481	72	165	205	214	228	232	238	252	7.57
% Ouery Match	1.5.1	4.1	4.1	4.1	4.1	4.1	4.1	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
Score	127	œ	30	30	80	8	œ	7	7	7	7	7	7	7	7	7
Result No.	. T	ଧ	3	₹*	5	y	7	œ	6	10	1.1	12	13	14	15	16

O99bhul rhizobium l O90045 macaca fasc U94au6 caulobacter O944cs errepromyce P91020 ceenorhabdi O94017 mus musculu O94017 mus musculu O94016 mus musculu O94018 mus musculu O95684 synechocyst O9789 arabidopsis O94017 brachydanio O9781 staphylococ U9786 staphylococ U9786 staphylococ U9786 staphylococ U9786 staphylococ U9786 staphylococ	996728 homo sapion 996728 homo sapion 999179 mus musculu 099179 mus musculu 028890 archaeoglob 588956 streptomyce 92108 drosophila 994313 drosophila 99451 streptomyc 99489 vibrio chol 994836 bacillus ha
50 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	34.2 4 0.966.28 34.3 11 0.040.904 35.3 17 0.28890 35.9 2 0.8863.5 37.4 1.0 0.945.42 37.4 1.0 0.945.83
	К к к к к к к к к к к к к к к к к к к к

# ALIGNMENTS

```
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Cianiata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC011983; AAH11983.1; -.
SEQUENCE 349 AA; 39921 MW; 3A355597FF7079EB CRC64;
                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10359.
                                                                                                                                349 AA.
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-OVARY, AND ADENOCARCINOMA;
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                            096FS5;
                                                                                                                                Q96ES5
RESULT
                                                                           096HS5
                                                                                                                                                                                                            ACCOCCOS SELECT ```

O: Gaps 65.1%, Score 127, DB 4, Length 349; 100.0%; Pred. No. 3e-122; Live 0. Mismatches 0; Indels Conservative Query Match Best Local Similarity Matchés 127. Conserval

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69. ALMMELVDIQLENKLIGGEEKFQEKVTKHLITPCTAQESVAMADDSTMKPLNYQTLLFKTRDSS 128 189 RPLQSYF 195

PESULT.

343 EPLQSYF 349

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MEDLINE 97494467; PubMed-9252185;
MEDLINE 977494467; PubMed-9252185;
MEDLINE 977494467; PubMed-9252185;
Tomb J. F., White o., Kerdavade A.R., Clayton R.A., Sutton G.G.,
Floischmann R.D., Ketchum K.A., Klenk H.-P., Gil S., Bougherty B.A.,
Nelson K., Quackenbush J., Zhon L., Kirkness B.F., Peterson S.,
Lofton R., Guackenbush J., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Filzdera d. L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gorayue J.D., Ulterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman T.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Horodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: HELONGS TO THE PHOSEHOLIPASE D'FAMILY. CARDIOLIPIN
SYNTHASE SUHFAMILLY: SIRONG, TO E.COLI YMOC.
                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guery Mātch (68) Score 7: DB 1: Length 502; Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C80911F2FB59C714 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori.":
Nature 888:539-547(1997).
-! SUBCELLHAR LEGATION: Membrane-bound (Potential).
                                                                                                                                                      01 NoV-1997 (Ref. 35, Created)
01 NoV-1997 (Ref. 35, Last sequence update)
01-MAK-2002 (Ref. 41, Last annotation update)
Hyporhetical protein #90190.
                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTENTIAL.
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502 AA: 58287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AE000539; AAD07257.1;
                                                                                   STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AEKLKEN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI Tax (D: 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter.
                                                                               Y190 HELPY
P56117;
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RESOLT 15
Y190_HELPY
                                                                               A PART A 
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Search completed: July 2, 2002, 16:19:39 Job time: 781 sec

44 AEKLKEN 50

0

Gaps

0

Length 444; 0; Indels

444 AA; 48792 MW; FORSOORCF241A4RF CRC64;

SECUENCE

SC

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Query Match 3.6%; Score 7; DB 1
Best Local Similarity 100 0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no testrictions on its use by non-profit institutions as long as its content, is in no way modified and this stalement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: FLAYS AN IMPORTANT ROLE IN THE DE NOVO FATHWAY OF PURINE NUCLEOTIDE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIAINE-97061201, PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nukamura Y.,
Miyajima N., Hirosawa M., Sudiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.;
Sequence analysis of the genome of the unicellular eyanobacterium
Synchocytis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.;
DNA Pes. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP + phosphate +
                                                                                                                                HYPOTHETICAL ABC TRANSPORTER
EXTRACELLULAR BINDING PROTEIN PH1214.
NACYL DIGLYCFRIDE (POTENTIAL).
558D963D816CA7EE CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE ADENYLOSUCCINATE SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NoV-1997 (Rel. 35, Created)
U-NoV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 46, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
                                                                                                                                                                                                                                                                                  .,0
                                                                         Hypothetical protein; Transport, Membrane, Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PR00709; Adenylsucc_synt; 1.
Probom; PH001188; Adenylsucc_synt; 1.
PROSITE; PS01266; ADENYLOSUCCIN_SYN_2; 1.
PROSITE; PS01266; ADENYLOSUCCIN_SYN_1; 1.
Purine blosynthesis; Liqase; GTP-binding; Complete proteome.
NP_BIND 13 19 GTP (POTENTIAL).
ACT_SITE 140 HY SIMILARITY.
ACT_SITE 147 147 HY SIMILARITY.
                                                                                                                                                                                                                                               DB 1; Length 441;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Symechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Symechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: GTP + IMP + L-aspartate
InterPro; iPR000567, 38P_bac_1.

Pfam; PF01547; SRP_bacterial_1; 1.

PROSITE; PS00013; PPOKAR_LIPOPROTEIN: 1.

PROSITE; PS01037; SBP_BACTERIAL_1; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 AA.
                                                                                                                                                                                                                                               3.6%; Score 7, DB 1;
100.0%; Pred. No. 21;
                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                  POTENT I AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001114; Adenylsucc_synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; p90905; BAA17318.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00709; Adenylsucc_synt;
                                                                                                                                                                      24 24 N 441 AA; 48896 MW;
                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                441
                                                                                                                  23
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                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADSS) (AMPSase).
PURA OR SLL1823.
                                                                                                                                                                                                                                                                                                                        143 AEKLKEN 149
                                                                                                                                                                                                                                                                                                                                                              191 AEKLKEN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1148;
                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P12283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PURA_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P73290;
                                                                                                                  SIGNAL
                                                                                                                                      CHAIN
                                                                                                                                                                        LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                   PURA_SYNY3
                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rurgos-Trinidad M., Ismail R., Ettinger R.A., Prahl J.M., Deluca H.F.; "Immunopuified 25 hydroxyvitamin D I alpha Hydroxyiase and 1,25-dihydroxyvitamin D 24-hydroxylase are closely related but distinct
                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniala, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Fhasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Hiol. Chem. 267:3498-3505(1992).
-!- FUNCTION: MAY HAVE A VITAMIN D3 HYDROXYLASE REGULATORY FUNCTION.
-!- SURPELIGILAY LOCATION: Mitgodical inter membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                   "cDNA cloning and characterization of a vitamin D3 hydroxylase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 7; DB 1; Length 463;
100 0%; Pred. No. 22;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W -> G (IN REF. 2).
68E7F5F48FB06497 CRC64;
                                                                                                                           Vitamin D3 hydroxylase-associated protein (VDHAP). Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I.W -> PS (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: KIDNEY.
-i- SIMILAPITY· RELONGS TO THE AMIDASE FAMILY.
                                                   090578;
01-Nnv-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               Ismail R., Deluca H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WHITE LEGHORN; TISSUE-Kidney;
                                                                                                                                                                                                                                                                               STRAIN=WHITE LEGHORN; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Mitochendrion; Membrane.
                                                                                                                                                                                                                                                                                           MEDLINE-94103206; PubMed-8276793;
Ettinger P.A., Ismail P., Deluca P
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92147714; PubMed=1310688;
                                                                                                                                                                                                                                                                                                                                                         associated protein.";
.r Biol. chom 269:176-182(1994)
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Local Similarity 100 0%; P
7. Conservative 0;
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Pfam; PF01425; Amidase; 1.
PROSITE; PS00571; AMIDASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 AA; 50760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U00694; AAC59645.1; -.
                                 STANDARD;
                                                                                                                                                                                                                                                           SECTIENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20
                                                                                                                                                                                                                       NCB1_Tax1D-9031;
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                                 VDHA_CHICK
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               VDHA_CHICK
RESULT
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Highlorematics and the SMI, outstation the European Highlights Institute of Highlorematics and the SMI, outstations on its use by non-profit, institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to lecense@isb-sib.ch/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Willis L.B., Walker G.D.: "Identification of the Philabium melihoti alvebable dehydrogenase gene (adha) and helerologous expression in Alcaligenes eutrophus."; Biochim. Biophys. Acta 1384:197-203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFATION: ZINT (HY SIMILARITY).
SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY: HIGH, WITH OTHER BACTERIAL ADH'S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAIALYIIC ACTIVITY: An alcohol . NAD(.) - an aldehyde or ketone
                                                                                                                                                                                                                                                                                                                                                           ACETYLATION (BY SIMILARITY).
HYDROGEN BOND DONOR (BY SIMILARITY).
A 18C5EA6F0F9C5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pSymA (megaplasmid 1).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnell M.J. Fisher R.F. Jones T., Komp C., Abola A.P., Barnell M.J. Fisher R.F. Jones T., Capela D., Galibert F., Gouzy J., Gurjal M., Honq A., Hubsar L., Capela D., Galibert F., Gouzy J., Gurjal M., Honq A., Hubsar L., Paper M.W., Sahryrki R., Wells, Yeh K., C., Davis K.W., Federspiel N.A., Long S.R.; "Nuclearlide Sequence and predicted lunctions of the entire Proct Natl Acad. Sci. U.S.A. 98.9883-9888 [2001].
! SIMILARITY: RELONGS TO THE ALDOZKETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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01-MAR 2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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fivo 0: Mismatches
                                                                                                                                                                                                           InterPro: IPR001495; Aldo_ket_red
Ptam; PF00248; aldo_ket_red; 1
PRINTS: PK00064; ALDKEHOTASE.
PROSTE: PS000645; ALDOKETO_REDUCTASE_2; 1
PROSTE: PS00064; ALDOKETO_REDUCTASE_3; 1.
PROSTE: PS00798; ALDOKETO_REDUCTASE_1; 1.
                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alcohol dehydrodenase (EC 1.1.1.1).
ADHA OR KAN704 0K SMA1296.
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                                                                                                                                                                                                                                                                                                                       exidereductase; NADP: Acetylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDI.INE-98323558; PubMod-9659380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                           324 AA; 34 474 MW;
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SEQUENCE
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ADMA_RHIME
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                                                                                                         entities requires a license derement (See http://www.isb sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Bata S.-I., Kosuqi H., Hosoyama A., Nauai Y., Sakai M., Ogura K., Orsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tataka T., Kedoh Y., Yamazaki J., Kushida M., Ohfuku Y., Aoli H. T., Tataka T., Nakamira V., Poth F.T., Horikoshi K., Masarchi Y., Shizuya H., Kikuchi H., Masarchi Y., Shizuya H., Kikuchi H., "Complete sequence and qene organization of the qenome of a hyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
-!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sdeep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40. Last annotation update)
Hypothetical ABC transporter extracellular binding protein PH1214
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                                                                                                                                                                                                                                                                                                    NAD) Plasmid: Complete profeome.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                             340 AA; 36235 MW; ClAO4B5FEE5095El CRC64;
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Pred. No.
                                                                                                                                                                                                         HSSP: P00325, 1DEH.
InterPro; TPP00238; ADH_zinc.
InterPro; IPR002085; Adh_zi_tamily.
Pfam: PF00107; adh_zinc; l.
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Local Similarity 100.0%; Pr
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(Rel. 37, Last sequ
                                                                                                                                                                  EMBL; AF031940; AAH87463.1; -. EMBL; AE007258; AAK65362.1; -.
                                                                                                                                                                                                                                                                                    PS00059; ADH_ZINC: 1.
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METAL 40 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 LALAEKI, 209
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Bohren K.M., Bullock B., Wermuth B., Gabbay K.H.;
"The aldo-keto reductase superfamily, cDNAs and deduced amino acid
                                                                                                                                                                                                                                                                                                               Interpro: IPR000385; ModA_NifB_PqqE.
Plam, PF01444; ModA_NifB_FqqE; 1.
PPOSITE; PS01405; MOAA_NIFB_PQQE; 1.
Molybdenum cofactor blosynthesis; Iron-sulfur: Complete proteome.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Croated)
01-APK-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last unmetation update)
Alcohol dehydrogenase [NADP+] (EC 1.1.1 2) (Aldehyde reductase).
AKRIAL OR ALDRI OR ALR.
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El-Kabbani C., Green N.C., Lin G., Carson M., Narayana S.V.L.,
Moore K.M., Flynn T.G., DeLucas L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87289801; PubMed-3615425; Wermuch B., Omat A., Forster A., di Francesco C., Wolf M., von Wartburg J.-P., Bullock B., Gabbay K.H.; "Primary structure of aldebyde reductase from human liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99417679; FubMed-10486210;
Barski O.A., Gabbay K.H., Bohren K.M.;
"Characterization of the human aldehyde reductase gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1, Length 316,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               27 IRON-SULFUR (POTENTIAL).
31 IRON-SULFUR (POTENTIAL).
34 IRON-SULFUR (POTENTIAL).
36975 MW. AZBOPT174702P5RC OPO64.
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J. Biol. Chem. 264-9547-9551(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%; Score 7, DB 1, 100.0%; Fred. No. 16; tive 0, Mismatches
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                                                                                                                                                                                                                                                                                           EMBL; AP000001; BAA29183.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 AA;
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALDX_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi M., Fujii J., Teshima T., Suzuki K., Shiba T., Taniquchi N.: "Identity of a major 3-deoxyglucosone-reducing enzyme with aldehyde reductase in rat liver established by amino acid sequencing and cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENXYGLUCASONE (3-DG).
112 HYDROGEN-BOND DONOR (BY SIMILARITY). 36442 MW: AC6B5006TA940FIF CFC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Pel. 39, Last annotation update)
Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c 127:249-253(1993). FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PSOU062; ALDOKETO_REDUCTASE_2; 1.
PROSITE; PSONO63; ALDOKETO_REDUCTASE_3; 1.
PROSITE: PSONO798; ALDOKETO_REDUCTASE_1; 1.
Oxidoreductase; NAPP; Acetylation; AP-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 7; DB 1;
100.0%, Pred. No. 16;
tive 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SHOURNCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF112485; AAF01260.1; -. AF112484; AAF01260.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF036682; AAB92369.1; JOINED. AF036682; AAB92369.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF036680; AAB92369.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project TPRO01395; Aldo_ket_red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney, and Liver;
MEDLINE=93273240, PubMed-8500767,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-2DPAGE; P14550; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J04794; AAA51711.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP036683; AAH92369.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (3-DG-reducing enzyme).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 VI.AI.AEK 239
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMPL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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use by non-profit institutions as lond as its content is in no Way
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                                                                                                                                                                                                                                                                                                                                    MEDLINE 99120557; PubMed-9924682;
Alm R.A., Ing L. S.L., Molt D.I., King H.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJooge B.L., Carmel G.,
Tommino P.J., Caruso A., Dria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
16-OCF 2001 (Ref. 40, last annotation update)
2 delydro 3 deoxyphosphosetonate aldelase (EC 4 1 2 16) (Phesphor2
dehydro 3 deoxyoctonate aldelase) (3 deoxy-D-manne-ocrullosenie acid
8 phosphore synthetase) (KEo-8-phesphore synthetase) (KEo 8-F
                                                                                                                                                                                                                                                                          "Genomic sequence comparison of two unrelated isolates of the human quartic pathogen Hellepbacter pylori.";
                                                                                                   Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klenk H. P., Clayton E.A., Tomb J.-F., White D., Nelson K.E., Kertchum K.A., Dodson E.J., Gwinn M., Hickey E.K., Peterson J.D., Glichardson D.L., Kerlavage A.R., Graham D.E., Kypides N.C., Flet schmann R.D., Ouadeckebush J., Lee N.H., Sutten G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.
                                                                                                                                                                                                                                                                                                                   : CATALYING ACTIVITY: 2-dehydro 3-deoxy-D-octomate 8-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001785: DAHP_synth_1.

Prain: PF00793: DAHP_synth_1: 1.

Lipopolyayacchaid= Signith_1: 1.

Elpopolyayacchaid= Signith_1: 1.

SEQUENCE 276 AA: 0.474 MM: EFETh97*ED4B5488 CR0544:
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Archaeoglobus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%: Score 7; DB 1; Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
16-oGT 2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransterase (EC 2 L 3 3) (OTCase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. m..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDL:INE~98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.JUL 1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001440; AAD05587.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                        Nature 197:176 180(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                            SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                             NCBI TAXID-85964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 LKTRDSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 LKIRBS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI TaxID-2234;
                                                                                      KDSA OR THP0003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGF OR AF1255.
                                                                                                                                Helicobacter.
                                                                                                                                                                                                                                                               Frust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFC_ARCEU
629013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTC_ARCEU
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Peterson S., Reich C.I., McNeil L.K., Hadger J.H., Glodek A., Zhou L., Owerbook B., Gwedyne J.D., Weidman J.E., Mchecald I., Utterback J., Cotton M.D., Spriggs T., Artiach P. P., Spring B. P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Eraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INVOLVED IN THE BLOSYNTHESIS OF MOLYBDOPTERIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                  -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine - phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea, Euryarchaeota, Thermocoecaies, Thermocoecaeeae, Egrocoecus.
                                                                                                                                                                                                                                         "the complete genome sequence of the hyperthermophilic, sulphate reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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-!- PATHWAY: MOLYHDENUM COFACTOR BIOSYNTHESIS (HY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MOAA / NIFB / PQUE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermophilic archaebacterium, Pyrococcus horikoshii 014.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.6%; Score 7; DH 1; Length 307; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase, Arginine biosynthesis, Complete proteome.
SEQUENCE 307 AA, 34913 NW, DB043BG5A40EBB5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLUIAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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PROSTIE; PS00097; CARBAMOYITRANSFERASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001017; AAH89987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piam; PF00185; Offace; 1.
Piam; PF02729; Offace_N: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            051742; IA1S.
                                                                                                                                                                                                                                                                                                                                                                                                       L-citrulline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformalics and the EMBL outstation the Puropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Praser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Floisrhmann R.D., Ploisrhmann J.D., Weidam J.F., Small R.V., Sandtosky M. Fuhrmann J.L., Weidam J.F., Saudok D.M., Phillips C.A., Morrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.M., Smith H.O., Hutchison C.A. Tit, Venter J.C., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE L9P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                               Length 141;
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%; Score 7; DB 1; Length 150; 100.0%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                       3 -> QE (IN REF. 3).
D7632905541C8266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; irrowners,
Pram; PF01281; Ribosomal_L9; 1.
PP04TTE: PANOK51; PIPOSOMAN_L9; FALSE_NEG.
Ribosomal protein; rkNA-binding, Cumplete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: BINDS TO THE 23S RRNA (BY SIMILARITY).
                                                                                                          Score 7; DB 1;
Pred No 8 2;
                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 33, Created)
01-FEB-1994 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AA.
BY SIMILARITY,
EH -> QE (IN F
                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000244; Pibesemal_L9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 33530 / G-37;
MEDLINE≐96026346; PabMed-7569993;
                                                                                                          3.55,
100.0%; Pre-
                                         15949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.6%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U39689; AAC71311.1; -.
                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                50S ribosomal protein 1.9.
RPLI OR RPL9 OR MG093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                     S'FANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma genitalium.
                                         141 AA;
                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                              148 ENYIVIJ, 154
                                                                                                                                                                                                                                          128 ENYIVLL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ALAEKLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E3GL_ADE05
P04494;
                                                                                                                                                                                                                                                                                                                                                     RL9 MYCGE
DISULFID
                                       SHOURNCE
                                                                                                          Query Match
                  CONFLICT
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                           RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chroboczek J., Bieber F., Jacrol B.;

The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2.";

With the genome of adenovirus type 2.";

Virology 186:280-285(1992).

--- FUNCTION: FORMS A COMPLEX WITH THE HEAVY CHAIN OF THE CLASS I TRANSPLANTATION ANTIGENS DURING AN ADENOVIRUS INFECTION, THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Farly R3 18.5 kba glycoprotein precursor (GP19K).
Human adenovirus type 5.
Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                    "DNA sequence of the early E3 transcription unit of adenovirus 5,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type I membrane protein Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLY E3 18.5 KDA GLYCOPROTEIN. LUMENAL, (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                           Wold W.S.M., Cladaras C., Deutscher S.L., Kapoor O.S.;
"The 19-kba glycoprotein coded by region E3 of adenovirus.
Purification, characterization, and structural analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 160; 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blrob2Ac4p6330E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDUCING CLASS I EXPRESSION ON THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early protein; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SIMILAKIIY: TO OTHER ADENOVIRUSES GP19K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An-MAY-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 7; 1
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purification, characterization, and J Biol. Chem. 260:2424-2431(1985).
                                                                                                                                                                                                                                             MEDLINE-85092388; PubMed-2981456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92087470; PubMed-1727603;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-85130985; PubMed=3882694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRPOZ MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                      Cladaras C., Wold W.S.M.;
                                                                                                                                                                                                                                                                                                                           Virology 140:28-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: M12406; AAA42492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: X03002; CAA26783.1;
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PIR; A22515; A22515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 LITVLAL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLETE GENOME
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Q92N55;
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                                                                                                                                                                                                                                                       2078 PYVEKAALITYLAEREKEKENYIVILLES PPELALMEDECSEVEHGCOKTTOOLITYLE 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Jashimoto K.;
                                                                                                                                                                                  2018 ALMMPLVDQIENRLAGEEKFQEKVTKHLIPCIAQESVAMAD5SLWKPLNYQILLKTRDSS 2077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 PKVRETALITZLALAEK. KENYTVLLDESTPETAB MEDEÇEPVEHOGOKTTOĞU ETVLG 188
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                                                                                                                                                                  69. ALIMMPLYDOLENRLOGPPPFPGPPVTKHLLPGLAÐISVAMADASLWKTSLNYÐILLKTRUSS 128
                                                                                                                                     O: Gars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macara fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota: Metares: Chordata; Craniata, Vertubrata, Eatuleostomi.
Mammalia; Eutheria; Primates: Catarrhin; Cerempitheeidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation of full-length cDNA clones from maraque brain cDNA libraries.";
Submitted (OCI-2000) to the EMHL/GenRank/MIHJ databases.
                                                                                                     Length 2144:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%; Score 64; DB 1; Length 958;
100.0%; Pred. No. 8.4e-58;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                             2114 AA: 212355 MW: D66816H78D8C9H7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3DBD95C3623CFB31 CRC64;
                                                                                                   65.1%; Score 127: DB 1; Le
170.0%; Pred. No. ..Ze-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                              /FTId-VAR_(0942.
/FTId-VAR_..0941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40, Last sequence update)
40, Last anactation (pdate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! SIMILARITY: HELONGS TO THE BAP2B FAMILY. I'SIMILARITY: CONTAINS I HEAT REPEAT.
                                                                                                                                   U; Mismatche,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AB049842: BAB16728.1; ALT_INIT.
InterPro; IPR000357: B:AT_repeat.
PROSITE: PS50077: BEAT_REPEAT: FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958 AA; 108644 MW;
                                                                                                                                Matches 127; Casservatize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein BAP28 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae: Macaca.
                2017 2017
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                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    2148 EPLOSYF 2144
                                                                                                                                                                                                                                                                                                      189 EPLUSYF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 GEPL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 - OCT - 2001
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                                              SECUENCE
                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amino acid sequence of an inducible cysteine profeinase inhibitor (cystatin) from submandibular glands of isoproterenol-treated rats."; Arch. Blochem. Blophys. 273:245-253(1989).
-!- FUNCTION: THIS PROFISH STRONGLY INHIBITS PAPAIN & FICIN, PARTIALLY INHIBITS STEM BROMELAIN & BOVINE CATHEDSIN C, BUT DOES NOT INHIBITED
POPETINE CATHEDSIN B OR CLOSTPIPAIN. PAPAIN IS INHIBITED
                                                                                                                                                      Rattus norvegicus (Rat).
Fukaryota: Motazoa; Chordata: Craniata: Vortebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                              "Structure, organization and regulation of a rat eysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :1- TISSUE SPECIFICITY: FOUND IN SALIVA, TEARS, URINE, AND SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                  Shaw P.A., Cox J.I., Barka I., Naito Y.;
"Clouded and sequencing of CDNA encoding a fat salicaty systeine proteinase inhibitor induced by beta adrenerate adonists.";
Riol. Chem. 264-1813-18137(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECONDARY AKEA OF CONTACT. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-Submandibular qland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    estitios requires a license paresment (See leff)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.
                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
01 MAR-2002 (Rel. 41, East annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSTALIN S.
REACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001231; Cystatin_C_M; 1.
                                                                                                                       Cystatin S precursor (LM protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003243; Cystatin_C_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUP-Submandibular gland;
MEDLINE-89334379; PubMed-27E7396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiol protease inhibitor; Signal. SIGNAL
                                                                                                                                                                                                                                                             MEDLINE-92165056; PubMed-1537554;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89053983; PubMed-3263967;
                                                                    01-NOV-1990 (Pel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000010; Cystatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYSTATIN; 1.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 10-141 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M75281; AAA41068.1; -. EMBL; J04206; AAB59703.1; -.
                                                                                                                                                                                                                                                                                                               inhibitor-encoding gene.";
Gene 110:175-180(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cystatin;
                                  STANDAPD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, S05252; S05252.
HSSP; P01038; 1CEW.
                                                                                                                                                                                                                                                                                Shaw P.A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A31891; A31891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHQUENCE OF 28-132.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                          NCB1_TaxID=10116;
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94
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                                                                                                                                      CST4 OR CYSS.
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                                 CYTS_RAT P19313;
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RESULT
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OM protein : protein search, using sw model

July 2, 2002, 16:19:08 ; Search time 30 19 Seconds (without alignments) 250.093 Million cell updates/sec Run on:

US-09 603 665-5\_COPY\_1950\_2144 195 1 LETLFAGHLVKPFADTLXQV................CCKTIQQLEIVLGEPLQSYF 195 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapert 60.0 Scoring table:

105224 seqs, 38719550 residues Searched:

340 Total number of hits satisfying chosen parameters. Word size .

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |       | ď      |              |            | SUMMARIOS   |                     |
|--------|-------|--------|--------------|------------|-------------|---------------------|
| Result |       | k Jeno |              |            |             |                     |
| No.    | Score | Match  | Match Length | 98         | (11)        | Description         |
|        | 127   | 65.3   | 2144         | _          | HP28_HIJMAI | O9h583 homo sapien  |
| · cs   | 64    | 32.8   | ಚಚಿತ         | -          | RP28_MACFF  | Q9qm44 marara tasc  |
| . ~    | 7     | er.    | 141          |            | CYTS_RAT    | P19313 rattus norv  |
| 4      | 7     | 9.1    | 150          | -          | RL9_MYCGE   | P47339 mycoplasma   |
| · 10   | 7     | 3.6    | 160          | -          | E3GL_ADE01  |                     |
| æ      | 7     | 3.6    | 276          |            | KDSA_HELP.  | 09zn55 helicobacte  |
| 7      | 7     | 3.6    | 307          | • -        | CTG_ARCFU   | O29013 archaeoglob  |
| · 00   | Ė     | 3.5    | 316          | e 4        | MOAA_PYRH   | O57854 pyrococcus   |
| · #    | 7     | (P)    | 324          | 17         | ALDX_HUMAN  | P14550 homo sapien  |
| 10     | 7     | 3.6    | 324          | ~          | ALDX_RAT    | P51635 rattus norv  |
| -      | 7     | 3.6    | 340          | _          | ADHA_RHIME  | O31186 rhizobium m  |
| 12     | 7     | 3.6    | 441          | <u>~</u> : | YC14_PYRHO  | O58969 pyrococcus   |
| 13     | 7     | 3.6    | 444          |            | PURA_SYNY3  | P73290 synechocyst  |
|        | 7     | 3.6    | 463          | -          | VDHA_CHICK  | •                   |
| 15     | 7     | 9      | 502          | 7          | Y190_HELPY  |                     |
| 16     | 7     | 3.6    | 556          | -          | PHR_CARAU   | P34205 carassius a  |
| 17     | 7     | 3.6    | 7.51         | _          | CATA_HALMA  |                     |
| 18     | 7     | 3.6    | 885          | -          | CHS3_EXODE  |                     |
| 9.0    | 7     | 3.6    | 911          | -          | CHSG_ASPFU  | P54267 aspergillus  |
| 20     | 7     | 9      | 916          | -4         | CHSB_EMENI  |                     |
| 21     | 7     | 9.     | 1045         |            | HMD2_YEAST  |                     |
| 101    | ŕ     | ٠.     | 1121         | -          | DDX8 ARATH  | O38953 arabidopsis  |
| 23     | 7     | 3.6    | 1122         | -          | ADP1_MYCGA  |                     |
| 24     | 7     | 3.6    | 1630         | _          | HP28_ARATH  |                     |
| 25     | . 9   | 3.1    | 7.3          | _          | RI.7_STAAU  |                     |
| 2.6    | 100   | 3.1    | 87           | r-1        | GLRX_HAEIN  |                     |
| 77     | 9     | 3.1    | 96           | -          | REV_SIVAM   | P36339 simian immu  |
| x:     | ت.    | 3.1    | 101          | - 1        | REV_SIVGB   |                     |
| 67.0   | 9     | 3.1    | 113          | -          | RL24_MICLII | P33174 microrogenus |
| ) C    | , c   | 3.1    | 114          | _          | GTH1_FUNHE  | P30971 tundulus he  |
| 3.1    | 9     | 3.1    | 118          |            | THIH_RICCO  |                     |
| 3.5    | 9     | 3.1    | 125          | Н          | MERR_STRLI  |                     |
| 1.60   | 0     | 3.1    | 132          | _          | YVGA_VACCC  | P20565 vaccinia vi  |

| P45928 bacillus su | P15135 human adeno | 800.000181 691860 | 4 -        | 059256 pyrocodeus | • •        | _          | 042425 gadus morhu | P16418 liophis mil | P54057 methanocoec | -          | Ū9jxz9 neisseria m |
|--------------------|--------------------|-------------------|------------|-------------------|------------|------------|--------------------|--------------------|--------------------|------------|--------------------|
| YQBL_BACSU         | E314_ADE07         | PEG7 DYPAR        | REG7_PYPFU | PEG7_PYPHO        | HBA4 ONCMY | PTA1_XENLA | HBA_GADMO          | HBB_LIOMI          | R19E_METUA         | Y645_NEIMA | YI16_NEIMB         |
| _                  | -                  | -                 | -          | _                 |            | -          | -                  | -                  | _                  | _          |                    |
| 134                | 135                | 141               | 141        | 14]               | 142        | 142        | 143                | 146                | 148                | 154        | 154                |
| 3.1                | 3.1                | ۲ ک               | 3.1        | ٦ ٢               | 3.1        | 3.1        | . T                | 3.1                | 3.1                | 3.1        | 3.1                |
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| 9                  | ş                  | ٤                 | 9          | •                 |            |            |                    |                    |                    |            |                    |

# ALIGNMENTS

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C. Species. Yersinia postis.
C. Date: O. Nov. 2001 Fasquence_restsion of Nov. 2001 Froz. Hunger 1 Febr. 2002
C. Accession: A10190
G. Marchill, J.: Wren, B.W.: Thomson, N.R.: Titball, R.W.: Holden, M.T.G.: Prentice, M.R. Berkhill, J.: Wren, B.W.: Thomson, N.R.: Titball, R.W.: Holden, M.T.G.: Prentice, M.R. Harterford, M.S.: Simmonds, M.: Skeiton, J.: Stevens, R., Whitehead, S., Harrell, Nature 413, 523-527, 2001
A. Mature 413, 523-527, 2001
A. A. Cression: A10190
A. A. Cression: A10190
A. Stafus: percliminary
A. Molecule type: UNA
A. Molecule type: UNA
A. Mesidens: 1-200 - KUR.
A. Residens: 1-200 - KUR.
A. Residens: 1-200 - KUR.
A. Cross-reterences: GB: ALSCOB42; PIDN: CAC90388.1: PID: 415979666; GSPDB: GN00175
.: Mazir, M.; Golfsman, E.; Selkov, F. Elver, P. H.; Hagins, S.; Comminghan, D.; Leress
Proc. Natl. Acad. Sci. U.S.A. 99, 441-448, 2002
A. Filler: the geneme sequence of the facultative intracellular pathogen Brucella melitens
A. Reference number: AD4252: PMID:11786688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rinceman, W.C.; Feldblyum, L.V.; Paulson, L.E.; Nelson, K.E.; Eison, J.; Heidclberg, J. B.; Laub, M.C.; Feldblyum, L.V.; Paulson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon of J.; Ermolaeva, M.; White, P.C.; Salaberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. J.; Ermolaeva, M.; White, P.C.; Parkette, Complete Genome Sequence of Caulobacter crescentus.

A.Retorence number: AA7249; MUD:21173698; PMID:11259647

A.Aecression: A87311

A.Status: proliminary

A.Molecule type: DNA

A.Residues: L.2%, S.E.;
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                                                                                                                                                                                                                                                                 A:Cross-references: GB:AE008917; PIDN:AAL51610.1; PID:g17982336; GSPDB:GN00190
A:Experimental source: strain 16M
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C:Date: Jo-Apr-2001 moquomoe_recision 20 Apr-2001 moxt_-bange 20 Apr-2001
C:Arcession: A87311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 27 Length 276,
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C.Superfamily: 2-hydroxyhopta-2,4-diene-1,7-dioate isomerase
C.KeyWords: inframolecular oxidoreductase; isomerase
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conscrvative U; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6%; Secto 7; DH 2
0.00.0%; Pred. No. 33;
.ve 0: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ":Keywords: methyltransterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           onery Match
Best Local Similarity
Matches 7, Conserv
                                                                                                                                                            A-status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 +KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LENKLOS 73
                                                                                                                                                                                                                                                                                                                                                               A;Gene: BMEI0429
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A87311
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EXTERN, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod .; Fleischmann, R.D.; Quarkenbush, J.; Lee, N.H.; Sutton, G.G.; Sill, S.; Kitkness, E. Giodden, E.; Stew, E.; Overbeek, R.; Gorayne, J.D.; Weidman, J.F.; Methodald, I. Nature 390, 364-370, 1997.
Alaure 390, 1864-370, 1997.
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woose, C.R.; Ventler, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch. A.Reference number: A69250; MU10:98049343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Accession: H71231
C.Accession: H71231
R.Kawarabayasi, Y.; Sawada, M.; Horikawa, Y.; Hino, Y.; Vamamoto, S.; Se.
M.; Ohluku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Fqu.
DNA Res. 5, 55-76, 1998
A.Title: Complete sequence and gene organization of the genome of a hyper thermophili
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A,Experimental source: strain 03
A:Note: this accession replaces an interim accession for a sequence replaced by GenHa
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ACCESSIFELECTER OF THE AEGISFITE NID GIRACETT, FILM AAKLEERS IS GSFELEGNOOTER
C.Genetics:
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C.Species: Pyrococcus borikoshi.
C.Date: 14 Aug.1998 *sequence_revision: 14-Aug-1998 *text_change 24 Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ornithine carbamogltransferase (argF) homolog. An haeoglobus fulcidus
C.Species: Archaeoglobus tulgidus
C.Date: 05-Dec-1997 #sequence_ravision 05-Dec-1997 #text_change 18 Jun-1999
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C.Keywords: molybdopterin biosynthesis
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                                                                                                                                                      Length 296;
                                                                                                                                                                                                       0; Indels
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                                                                                                                                                   DB 2,
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; Mismatches
                                                                                                                                                            100.0%; Pred. ac.
                                                                                                                                                Score 7, D
Pred. No.
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Best Local Similarity 100.u.
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Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LAEKLKE 148
                                                                                                                                                                                                                                                                                        1111111
240 LFILFAG 246
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                                                                                                                                                                                                                                                            1 1.FTI.FAG 7
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                                                               A; Gene: CC0498
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Aydriety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change OR-Oct-1999
C;Accession: B71985
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, H.L.; Hrown, E.D.; Doig, P.C.; Smith, D. Ives, C., Cikson, P.; Mortorg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
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C.Species: Brucella melitensis
C.Jain· (1-PBF-2002 #sequence_revision 01 Peb 2002 #Fext_change 01 Peb-2002
C.Agression· AG3308
R.DelVecchio, V.G., Kapatia!, V., Pedkar, P.J., Patra, G.: Mušer, C.: Les T.: Franov
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A;Reterence number: A71800; MUID:99120557
A;Accession: E71985
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.Chen, J.Y., Chang, R.F.; Chen, Y.H., Lin, G.J.F., Wu, J.L., Kuo, G.M. Blochem Brophys. Res. Commun. 285, 105-110. 2001
Affilia Molevular cloning, developmental expression, and hormonal regulation of zebr A.Reference number: JG7706; MUID:21331298; PMID:11437379
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                                                                                                                                                                                                                                                                                                                                                                C,Species: Brachydanic rerio (zebra fish)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #!ext_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Caps
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C.Comment: This protein is involved in regulation by growth factors.
C.Superfamily: beta crystallin
F.20-&/A-qion: artive prolline and alanime-rich motif #status predicted
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100.0%; Pred. No. 29;
Live 0; Mismatches
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Fost total Similarity 100.55
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A; Residues: 1-232 <CHE>
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                                         185 TVLGEPL 191
                                                                                                                    137 TVLGEPL 143
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P.Bevan, M., Peters, S.A., van Staveren, M., Dirkse, M.; Stickoma, W.; Bancroft, T.; Mew
submitted to the Protein Sequence Database, March 2000
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hypothetical protein T20135.180 · Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date. 20 Apr. 2000 #sequence_revision 20 Apr zouo #text_change 20 Apr. 2009
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C.bate. 28:Sep 1999 #sequence_revision 20:Sep·1999 #text_change 20-Sep-1999
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                                                                                                                                                         A;Molecule type: DNA A A Residual CONTROL OF THE STATE OF THE STATE OF STAT
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0
J. Biol. Chem. 260, 2424-2431, 1985
AFITIE: The 19-Kba glycoprotein coded by region E3 of adenovirus.
A/Reference number: A22515; MHID:85130985
A/Accession: A22515
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A; Residues: 1-165 <BEV>
A; Cross-relerences: EMBL:AL162351
A; Experimental source: cultivar Columbia; RAC clone T20115
C; Genetics:
A; Map position: 5
A; Introns: 99/3; 121/3
A; Note: T20115.180
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C;Genetics:
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э. 21;
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Matches 7, Conservative 0, Mismatches
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches
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Bost Local Similarity 100.0
Hearlas 7: Conservative
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A;Accession: T14745
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A:Molecule type: mRNA
A:Residues: 1-205 <DUE
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A; Status: preliminary
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RibelVecchin, V.G., Kapatral, V., Bodkar, B.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, M.; Mazur, M.; Coltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002.
A.Tille: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
A;Accession: AC3385
A;Accession: AC3385
A;Accession: Acad. Acad
B.Fraser, C.M.; Govayne, T.D.; White, O.; Adams, M.E.; Clayton, R.A., Fleischmenn, R.; Fuhrmann, T.; Nquyen, D.; Hiterback, T.P.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                         Asstatus: preliminary; nucleic acid sequence not shown; translation not shown
As Molecule type: DNA
As Residues: 1-150 <7138>
As Cross references: GB:U39688; GB:L43967; NID:q1045753; PID:q1045770; TICH:MC093
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C:Dato: 01-Peh-2002 *sequence_revision 91-Peh 2002 *text_change 31 Feb 2002
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C:Species: Mastadenovirus h5 (human adenovirus 5)
A;Note: host sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16.Jul 1999
C;Accession: A03822; A22515
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Virology 140, 28-43, 1985
A;Title: DNA sequence of the early E3 transcription unit of adenovirus A:Reterence number: A94335; MUID:85092388
A;Accession: A03822
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RyWold, W.S.M.; Cladaras, C.: Deutscher, S.L.: Kapvor, U.S.
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C,Superfamily. Escherichia coli ribosomal protein 1/9
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100.0%; Pred. No. 20;
ive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No.
Matches 7, Conservative 0; Mismatel
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A;Accession: C64210
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Matches 7; Conservative
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R:Redi. G.S.
Arch. Biochem. Biophys. 273, 245 253, 1989
A.Tile: Anino acid Sequence of an inducible cysteine preceinase inhibitor (cystatio) fr
A;Relerence number: 805252; MUID:89344379
A;Acression: 805252
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A;Kesidues: 28-113, 'OE', '116-141 - HED>
A;Kesidues: 28-113, 'OE', '116-141 - HED>
A;Koshiura, T.; Ishibashi, K.; Abe, K.
Biochim. Biophys. Acta 1077, 346-354, 1991
A;Title: Isolation of three forms of cystatin from submandibular saliva of isoproterenol A;Ketvience number: $15142; MUD:91240145
A;Accession: $15132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Residues: 29-38176-80 -810>
A:Note: torms RSC-1 - PSC-2 and PSC-3 with dittering amino-terminals were found; a form H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:III-le: Structure, organization and regulation of a rat cysteine proteinase inhibitor-c
A:Reference number: J@1470: MUID:92165056
A:Accession: J@1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K:Shaw, P.A.; Cox, J.L.; Harka, L.; Naito, Y. J. Hiol. Chem. 263, 1813-18137, 1988
J. Hiol. Chem. 263, 1813-18137, 1988
A:Tille: Cloning and sequencing ol cDNA encoding a rat salivary cysteine proteinase inhi A:Reterence number: A31891; MUID:89054983
A:Arcression: A31891
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                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Rattus norvegieus (Norway rat)
C.Dale: 17-Jul-1992 #sequence_revision 17-Jul-1992 #fext_change 16-Jul-1999
C.Acession: 191470: A4H941: S05252; S15132
Gene 110, 175-180, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species. Myroplasma genitalium
C.Date: 17 Nov. 1995 Esequence_Fevision 17 Nov. 1995 #Foxt_change 37.552-1999
C.Arcession: 064210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB:M75281; NID:q294537; PIDN:AAA41068.1; PID:g294538
         C.
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E)128/Pomain. signal sequence estatus predicted (SIS)
E)28 141/Product: Cystatin & #status experimental (MAT)
E)29-141/Product: Cystatin S. form RSC3 #status predicted (MAT)>
E)30-141/Product: Cystatin homology (CYS)
E)31 141/Eproduct: Cystatin bomology (CYS)
E)31 141/Eproduct: Cystatin S. form RSC2-1 #status predicted (MAT)>
E)31 141/Eproduct: Cystatin S. form RSC2-1 #status predicted (MAT)>
E)31 141/Eproduct: Cystatin S. form RSC2-1 #status predicted (MAT)>
E)31 141/Eproduct: Cystatin S. form RSC2-1 #status predicted (MAT)>
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141/Product cystatin S. torm PSC-1 #status predicted -MAT1>
104,118 138/Disullide bonds: #status experimental
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A:Residues: 'ISIDYLYISFEHEILSC',27-141 -SHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: DNA
A:Residues: 1-141 <COX+
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                                                                                        87 KPUERVI 93
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A; Introns:

Matches

RESULT

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Copyright (c) 1993 - 2000 Compagen Ltd
GenCore version 4.5
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OM protein - protein search, using sw model

501y 2, 2002, 10 15 41 , Search time 57,09 Seconds

(without alignments) 328 208 Million cell updates/sec

US 09 603 665 5\_COPY\_1950\_2144 Perfect score.

1 LETTERAGHLVKPEADTLXQV... Sequence

Gapop 60.0 , Gapext 60.0 Scoring table:

283138 seqs, 96089334 residues Searched:

Word size :

931 Total number of hits satisfying chosen parameters:

Minimum DH seq length: 0 Maximum DH seq length: 2000000000

Post-processing: Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAPIES

|            |       | æ              |                          |          |                 |                    |
|------------|-------|----------------|--------------------------|----------|-----------------|--------------------|
| Result     | Score | Query<br>Match | Query<br>Match Length DB | <u> </u> | 9               | Description        |
|            |       |                |                          | 1        |                 |                    |
| 1          | 8     | 4.1            | 188                      | ~        | F84120          | hypothetical prote |
| ~          | 7     | 3.6            | 98                       | C1       | S26914          | Ig heavy chain V r |
| ٣          | 7     | 3.6            | 141                      | ~        | J01470          | cystatin S precurs |
| 4          | 7     | 3.6            | 150                      | 7        | C64210          | _                  |
| 5          | 7     | 3.6            | 151                      | 7        | AC3385          | retroviruS-related |
| 9          | 7     | 3.6            | 160                      | _        | ERADA5          | early E3 18.5K gly |
| 7          | 7     | 3.6            | 165                      | C)       | T48212          | hypothetical prote |
| œ          | 7     | 3.6            | 205                      | C1       | T14745          |                    |
| 6          | 7     | 3.6            | 232                      | .~4      | JC7706          | $\rightarrow$      |
| 10         | 7     | 3.6            | 276                      | CI       | E71985          | 3-deoxy-d-manno-oc |
| 11         | 7     | 3.6            | 276                      | C 1      | AC3305          | 23S ribosomal RNA  |
| 15         | 7     | ~              | 580                      | C1       | A.(0190         | probable hydrolase |
| 13         | 7     | 3.6            | 396                      | €1       | A87311          | hypothetical profe |
| 14         | 7     | 3.6            | 307                      | ?        | FK940K          | ornithine carbamoy |
| 15         | 7     | 3.6            | 316                      | C a      | H71231          | molybdopterin bios |
| 16         | 7     | 3 E            | 317                      | C1       | 92,551          | hypotherical prote |
| 17         | 7     | 3.6            | 325                      | ٠.       | JN0629          | alcohol dehydrogen |
| 18         | 7     | 3.6            | 325                      | C 1      | A33851          | alcohol dehydrogen |
| 19         | 7     | 3.6            | 326                      | ?        | 876360          | hypothetical prote |
| C.         | 7     | ټ<br>ټ.        | 337                      | in u     | 120644          | hypothetical prote |
| 21         | 7     | 3.5            | 34.                      |          | 1195349         | alcohol dehydrogen |
| ::         | 7     | 3 6            | 453                      | e v      | 06.9472         | F420-nonreducing h |
| 23         | 7     | 3.6            | 359                      | 7        | 135179          | oxidoreductase alp |
| 54         | 7     | 3.6            | 359                      | Ci       | T22950          | hypothetical prote |
| uri-<br>Cu | 7     | 8              | 374                      | C 3      | B86457          | unknown protein, 1 |
| 36         | 7     | 3.6            | 391                      | C        | T36739          | hypothetical prote |
| 27         | 7     | 3.6            | 393                      | ?        | G837 <b>4</b> 9 | methionine gamma l |
| C1<br>an   | 7     | 3.5            | 400                      | - 1      | C82213          | conserved hypothet |
| 66         | 7     | ج<br>آ ک       | 4 ) 5                    | C        | 877471          | adenylesuccinate s |

| adenylosuccinate s | hypothetical prote | hypothetical prote | D-alanyl-D-alanine | probable cytoplasm | ABC transporter pe | vitamin D3 hydroxy | conserved hypothet | photolyase - goldt | 2', 3'-7yclic-nucle | mobilisation prote | kelch-like protein | iron (11) transpor | polyadenylate-bind | probable membrane- | hyperherical prote     |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------------|
| AH2403             | C83912             | D87550             | F81659             | H71064             | F86846             | A53101             | F6454 3            | A45098             | B71973              | 577647             | Т37322             | F69280             | T-06479            | 697213             | หล <sub>์</sub> คู่202 |
| Сŧ                 | C)                 | - 1                | 7                  | 7                  | 7                  | 7                  | C 1                | 2                  |                     | 2                  | c į                | _                  | ~                  | ?                  | C.                     |
| 419                | 419                | 422                | 438                | 441                | 453                | 464                | 505                | 556                | 5.R.                | 5R4                | 618                | 639                | 651                | 999                | 726                    |
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RESULT

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Appethetical protein BH3766 (imported) - Hacillus halodurans (strain C-125) C.Species: Bacillus halodurans C.Species: Bacillus halodurans C.Species: Bacillus halodurans C.Species: Bacillus halodurans C.Species: Director and the control of the control of the control of the complete complete genome sequence of the alkaliphilic bacterium Hacillus halodurans a A.Atcession: P84120 A.Accession: P84120 A.Accession: P84120 A.Status: preliminary A.Accession: P84120 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-188 <STO> A.Atcession: C.S. A.Beridues: 1-188 <STO> A.Beridues:
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A,Gene: BH3766 C;Superfamily: Racillus subtills hypothetical protein ywld

0; Gaps .. Length 188; ñ; indels UH 2; 0. 2.2; Ouery Match
4.1%; Scote 8; DB 2
Best Local Similarity 100.0%; Pred. No. 2.2
Maiches 8; Conservative 0; Mismatches

826914

1g heavy chain V region (DP-2) - human (fragment)

C,Speciës. Home sapiens (man) Cynate: 22:Nov-1947 #sequence\_revision lé∵Nov-1945 #text\_change 21 har 20n0

C;Arression: S26914

Pyrominison, T.M.: Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992. Affilie, The regettoire of formal germline V(H) sequences reveals about fifty groups o Affilie, The regettoire of MulD:93021117. A.Accession: S26914.

A; Molecule type: DNA A; Residues: 1 98 < TOM> A;Status: preliminary

Ajčross-references EMM: 2]2364; NII-932863; PILIN;7AA78174 1; PPI-932864

C, Superfamily, immunoglobulin V region, immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F, 15-98/Domain, inm.neglobulin homology < TMMS.

3.5%; Score 7; DB 2; Length 98; 100.0%; Pred. No. 14; Query Match Rest Local Similarity

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure dense expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ 1D NO; 30133.
                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microaffuy; cancer; leukaemia: lymphoma; mveloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO: 40133; 658pp · Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 8.6%; Score 7; DH 22; Longth 110; Bost Local Similarity 100.0%; Prod. No. 29; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in numan bone marrow
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                                                                                               AAM69827 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE .) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                   04 - FEH 2000; 20000S 0180312.
26 - MAY - 2000; 20000S - 0207456.
40 - JUN 2000; 20000S - 0.608408.
4 - AUG-2000; 20000S - 0.74286.
21 - SEP 2000; 20000S - 0.74687.
27 - SEP - 2000; 20000S - 0.74687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.SEP 2000; 20000S-0234687.
27-SEP-2000; 20000S-0236359,
04-901 2000; 20000S-0024263.
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W0200157276 A2.
                                                                                                                                                                                                                                                                                    Homo sapiens.
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Gaps

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Search completed: July 2, 2002, 16:06:95 Job time: 182 sec

140 LALAEKI. 146 82 Jalack | 88

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0;
                                                                                                                                                                                                                                                                                                                                                                                                           Protein #4004 encoded by probe for measuring heart ceil gene expression.
                                                            fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
         The invention relates to a single exon nucleic acid probe for measuring human que expression in a sample derived from human locatal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying quee expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                            0;
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                                                                                                                                                                                 DB 22; Length 110;
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                                                                                                                                                                                 3.6%; Score 7; DB 22
100.0%; Pred. No. 29;
ive 0; Mismatches
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2000US-0234687.
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                                                                                                                                                                                           Best Local Similarity
Matches 7, Conserv
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21 SEP 2000;
27 SEP 2000;
04-OCT-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEG ID NG: 29537.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at Itp.wipo.inL/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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microarray; Alzhoimor's disease; multiplo sclorosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                        DB 22; Length 110;
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                                                                                                                                                                                                                                                                                                                                        3.6%; Score 7; DH 2
100.0%; Fred. No. 29;
tive 0; Mismatches
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Best Local Similarity 100.9
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Best Local Similarity
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                                                                                                                                                                                                  110 AA;
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                       Sequence
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ARAZ1535-ARA41805). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying quene expression is samples derived from the human heart via mirrowarrays By measuring gene expression, the probes are useful for predicting, diagnosing, stading, stading, managing and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Claim 15, SEy ID No 23775, 530pp, English.

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27-SEP-.
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New spatially addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human broast, comprises number of single exon nucleic acid probes.
                                                                                                                            Producing human antitody polypeptide dimer specific for antigen
                                                                                                                                       comprises use of chain shuffling using phage expression, useful for reducing anti-globulin responses in humans for increased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human: microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                              The sequence is that of the pp.74 VHI gene heavy chain which may be used as part of a method of producing chimeric mouse-human antibodies or fragments which have the same binding specificity as a parent Ab but have increased human characteristics, preventing and all absents response in hamans.
                                                                                                                                                                                                                                                                                                                                    3.6%; Score 7; DB 14; Length 89;
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                                                                           Hoodenboom HRJM, Jespers LSAF.
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                                    (CAMB ) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                                        Example: Fig 11: 109pp: English
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2000US-0207456.
2000US-060840R
92GB-0006472.
             92WO-GB00883.
                                                  (MEDI-) MEDICAL RES COUNCIL.
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200008-0234687
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Matches 7; Conservative
                                                                                                                                                                  human characteristics
                                                                                                   WPI; 1993-117534/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                63 ktgervt 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; cancer
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SEP 2000-
         15-MAY 1992;
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                                                                                                                                                                                                                                                                                               Sequence
                                                                           Baier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB 11456;
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                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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The invention relates to a spatially-addressable set of sinule exon nucleic acid probes for measuring quee expression in a sample derived from human breast and HT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for genemic DNA predicted to encode proteins. They are useful for genemic by a force of the microarray of this invention predicting of chemical agents on cells, the microarray of this invention presents a far greater diversity of probes for measuring quee expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a peptide encoded by a single exon neglect acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ttp.Wipo.int/pub/lished_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O; Gabs
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Claim 27; SEQ ID NO 14424: 327pp · sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 7; DB 2
100.6%; Pred. No. 29;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABH36668 standard; Peptide; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20000S 0632356.
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ZUCUUS OZ36359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000CB 0024263,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZODOUIS-UBOR408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 LALAEKI, 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 lalaekl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157277-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4 FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10007
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Liu C, Drmanac RT;

Tang YT,

(HYSE-) HYSEQ INC.

26-FEB-2001; 2001Wn-US04927 28-PEB-2000; 200008-0515126 18-MAY-2000; 2000US-0577409

W0200164835-A2.

07-SEP-2001,

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the present invention relates to single exon nucleic acid probes (SENP) see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples delived from human placents. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy,
                                                     Poptide #8214 annualed by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine, peptide therapy, stem ceil growth factor, hacmatopolesis,
tissue growth factor, immunomodulatory, cancer, leukaemia,
nervous system disorders, arthritis; inllammation.
                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%, Score 7; DB 22; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                             Probe, microarray, human, placenta, antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                              analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SHQ ID No 34446; 654pp; English.
                                                                                                                                                                                                                                                                                                                      Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 15062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAOO1170 standard; Protein: 83 AA.
                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                               2000US-06084UB.
                                                                                                                                                                                                          04 FEB-2000; 2000us-0180312.
25-MAY-2000; 2000us-0207456
                                                                                                                                                                                    30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                     2000011S-02446A7
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                                                                                                                                                                                                                                                                            04-OCT-2000; 2000GH-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                    17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human genetic disorders.
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Best Local Similarity
Matches 7, Conserva
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GGEEKFO 89
                                                                                          genetic disorder
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                                                                                                                                       WO200157272-A2
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                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                 30-JUN-2000;
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27-SPP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
              AAM34177,
                                                                                                                                                                                                                                           03-AIIG
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The invention relates to human polymorteotides (AAI79941-AAI93841) and the encoded proteins (AAU00010-AAU13910) that exhibit activity elating to eytoxine, cell proliferation of cell differentiation or which may induce
                                                                                                                                                                                                                                                production of other cytokines in other cell pupulations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis requialing activity, issue growth factor activity, immunomedulatory activity and activity and may be useful in the diagnosis and/or transment of carrows.
                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_scquences.
                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SdeS
                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukacmia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                Claim 20; SEQ ID NG 15062; 1449pp + Sequence Listing, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; monocional antibody; anti-globulin response; chimeric; mouse-human antibodies; antibody; prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 6%, Score 7, DB 22;
100.0%, Fred. No. 22;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR34271 standard; Protein; 89 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp-74 VIII gene heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
WP1; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 7, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 NYVILLK 123
                     N-PSDB; AAI81101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 nyqillk 39
                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - MAR - 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1991,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9306213-A.
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                                                                                                                disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Query Match
Best Local Similarity
Thes 7; Conserva
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                                                               83 GCEEKFQ 89
                                                                                     4 ggeekfg 10
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                                                                                                                                                                                                                                                                                                                    W0200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000;
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30 - JUN - 2000;
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                                                                                                                                                                              AAM74002;
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                                                                                                                              RESULT
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                                                                                     qq
                                                                                                                                                                  probes which are derived from aenomic sequences expressed in the homan brain. They can be used to measure gene expression in brain cell samples, which may enable the diamonsis and improved freatment of nervous system diseases such as Alitheimet's disease, multiple selectoris, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 33384.
                                  measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleur acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exem nucleic acid probes for analyzing gene expression in human
            measuring human gene expression in a sample Acrived from human foetal
liver. The single exch nucleic acid probes may be used for predicting,
                                                                       Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                        Human: brain expressed exon- gene expression analysis; probe:
microarray: Alzheimer a disease- maltiple scienceis; schizaphienia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4: SEQ ID No: 3384; 650pp + Sequence Listing; English.
The invention relates to a single exon nucleic acid probe for
                                                                                                                                                               8.6%; Score 7; DB 22; Length 36; 100.0%; Pred. No. 10; ve. 0; Mismatches 0; Indels
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W, Bank DR;
                                                                                                                                                                                                                                                                                                     AAM61279 standard; Protein; 36 AA.
                                                                                                                                                                          100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE ) MOLECULAR DYNAMICS INC.
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2000US 0234687,
2000US 0234589,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 JAN 2001; 2001WO US00667
                                                                                                                                                                                                                                                                                                                                                       05-NOV 2001 (first entry)
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 2001-483446/52
                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                          36 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy: cancer
                                                                                                                                                                                                                 83 COREEKPO 89
                                                                                                                                                                                                                                          4 ggeekig 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200157275-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2,000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP 2000;
27 SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09 AUG-2001.
                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                               AAM61279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                               Unery Match
                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                   Scips)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed probe encoded protein SEQ ID NO: 34308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO: 34308; 658pp · Sequence Listing: English.
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5. 10;
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        DB 22; Length 46;
                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; cancer; leukaemia; lymphoma; myeloma.
3.5%; Score 7; DB 2
100.0%; Pred. No. 10;
ative 0; Mismatches
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100.0%; Pred. No. 10;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                               AAM74002 standard; Proteir; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM34177 standard; Protein; 36 AA
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200008-0207456.
200008-0608408.
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2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668.
                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001 (first entry)
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
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by detection of

26-MAR-1998

Baer R,

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Human; foetai Liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                            detection of a microbe, using the gyrase gene as the index. The method involves the use of PCR primers to amplify DNA from the microbe, which is then identified or detected depending on its base sequence. The method can be used to classify and identified an unidentified microbe strain rapidly and with high precision. The present sequence represents a gyrase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #7963 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                           the specification describes a method for the identification or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID No 33092; 639pp + Sequence listing: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 8; DB 20; Longth 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                Identification and detection of a microbe
                                                                          (MARI-) MARINE BIOTECHNOLOGY INST CO LTD
                                                                                             (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                         Example 3; Page 14-15; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB40457 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200003-0608408
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2000US-0234687
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                                      97JP-0343316
97JP-0343316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52.
                                                                                                                                       WPI; 1999-422615/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 sendpeke 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SENDPEKC 39
                                                                                                                                                              N-PSDB; AAX86000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157277-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27 SEP-2000;
12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FER-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                      12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                         gyrase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB40457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB40457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
    The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antiqen, BRCA1, binding preparation of the recombinant breast cancer antiqen, BRCA1, binding proteins BARD1, B123, BE14, BE14 or BE445, or a composition for the detection of a BARD1, B123, BE14, BE14 or BE445, or a remposition of a the sequence, specifically a wild type BARD1 composition for the detection of a purification of a BACA1, useful to identify a patient having, or at crisk of developing cancer. BARD1 can be used in the preparation of an anti-BARD1 antibody, and in the detection and purification of a BRCA1 or profein BARD1, B123, BE2, BE14, BE31 or BE445 can used in the preparation of an interpretation of a binding protein agonist or antagonist that alters denoting of BARD1, H123, BE2, BE14, BE31 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445, a specific anti-BARD1 antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 DESVAMADDSLIMKPLINYQILLIKTRDSSPKVRFAALITVLALAEKLKENYTVLLIPESTPFL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 qtsvamaddslwkplnyqillktrdsspkvrfaalitvlalaeklkenyivllpesipfl 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                       DNA sequence enroding BAPP1, B123, BE2, BE14, BE31 or BE445 - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification, detection; microbe; qyrase gene; gyrase protein
                                                                                                                                                                                                                                                                                                                                                            as breast cancer antigen, BRCAL, binding proteins are useful to identify patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 aclmedeceevehgegktiggletvlgeplgsyf 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AFLMEDECEEVEHOCOKTIOOLETVLGEPLOSYF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A gyrase protein of Chitinophaga pinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 287-288; 348pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23793 standard; Protein; 220 AA
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100.0%; Pr
                                                                                                                                                                    97US-0042611.
                                                                                    97WO-US16842.
                                                                                                                              97IIS-0042985
                                                                                                                                                    9603200-3096
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                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                     BOWCOCK AM;
                                                                                                                                                                                                                                                                                         1998 230317/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAV24135
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                                                                                        19-SEP-1997;
                                                                                                                              04 - APR - 1997;
                                                                                                                                                    20-SEP-1996;
                                                                                                                                                                       03-APR-1997;
            WO9812327-A2
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Sequence

Query Match

Matches

qq ò AAY23793;

0;

Gaps

0

Indels

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                                                                                                                                                                           The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and requiatory region located at the 3' and 5' ends of the HAP28 coding region. The BAP28 polypeptides can be expressed by standard recombinant methodology. HAP28 polymericectudes and polypeptides have been found to be over expressed in prostate tameur cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain prostate cancer. Antibodies specific for the BAP28 polypeptides are useful as dignostic regents. Bitalletic markers of the BAP28 gene are useful in genetic analysis. The present sequence represents a protein enroyed by a first cDNA sequence of the BAP28 gene consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FISKFPAXALMMPLVPQLENPLAGEEKFQERVTKHLIPGIAQFSVAMADDSLWKPLNYQI 120
                                                                                     New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumous, e.g. by hybridization or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyman; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LETLEAGHLVKPPADTLXQVNISKTDRAFFDSENDPRKGCLLLQFTLNGLYKTFLFDTQH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                              99.0%; Score 193; DB 22; Length 2144;
100.0%; Pred. No. 3.9e-192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
              Chumakov I, Cohen-Akenine A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                     Tlaim 14; Page 297-304; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEO ID NO:11159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB92729 standard; Protein; 349 AA
                                                                                                                    polymerase chain reaction assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0*; F
ive 0;
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2000JP-0183767.
                                                          N-PSDR: AAFR3909, AAFR3910
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              Bouqueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2130 qq1ctv1qep1qsyf 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                           WP1; 2001-367042/38.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loral Similarity
                                                                                                                                                                                                                                                                                                                                                     exons 1 to 45.
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02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-301,-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB92729;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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92
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Sequence and an oligonuclectide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence, is elected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or flagnosis of the primers are also useful for the confection and/or the primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs castly without any specialised methods. AAH03163 to AAH18628 and AAH18631 to AAH18722 represent human cDNA sequences, and AAH18632 to AAH18632 represent bugges all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises, (a) an oliqo-dT primer and an oliqonucleotide complementary to the complementary strand of a polynucleotide which comprises one of oliqonucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                     Primer sets for synthusizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abrormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69. ALMMPLVDÖLENKLÖGEEKFÖCKVÆKHLIPCTAQFSVAMADDSIJMKPLNYOTLLIKTKDSS-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 PKVRFAALJTVLALAEKLKENYIVLLPESTPFLAELIMEDECEEVEHOCOKTTOOLETVLG 188
                                                                                          Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BARD1, ring protein, BRCA1, breast cancer; risk; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Short 127, 158 22, 1
Pred. No. 5.26-124;
                                                                                                                                                                                                                                                                                                                           Claim 8, SEQ ID 11159, 2537pp + CD ROM; English.
                                                                                       Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakematsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW54099 standard; Protein; 515 AA.
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Matches 127; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens BAP28 sequence.
194-188-2000; 20001P-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention.
                                              (HELLI - ) HELLIX RES INST.
                                                                                                                                                            WFI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 349 AA;
                                                                                                                                                                                                                                                                            full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 EPLQSYF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 epigsyf 349
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                                                                                                                  ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW54099;
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                                                                                          Ota T,
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 2, 2002, 16:06:04 ; Search time 117 59 seconds (without alignments) 184.194 Million cell updates/sec Run on:

US-09-603-665-5\_13-PY\_1950\_2144

Perfect score:

1 LETLEAGHLVKPFADTLXQV Sequence:

Gapop 60 0 - Gapext 60 0 Scoring table:

747574 segs, 111073796 residues Searched:

Word size :

669 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: zumünunünön

Post-processing. Listing first 45 summaries

Database :

|   |       | ام     | A_Geneseq_032802:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|---|-------|--------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|   | 1     |        | /SIDS1/qcqdata/hold-qeneseq/qeneseqp-embl/AA1980.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | E.A.  | 2      | /SIDS1/gradata/hold geneseg/genesegp-embl/AA1981 DAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|   | m     | <br>~  | /SIDS1/gcgdata/hold-genesed/qeneseqp-embl/AA1982.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | 4     | ··     | /SIDS1/gcgdata/hold-geneseq/genesegp-emb1/AA1983.DA1:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | S.    |        | /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1984.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | 9     |        | /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1985.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | 7     | ٠.     | /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1986.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | œ     |        | /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1987.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | 57    |        | /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1988.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | ,     | 0      | /SiDS1/gegdata/hold-geneseq/genesegp-emb1/AA1989.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | 1     |        | /SIDS1/gegdata/hold-geneseq/geneseqp-emb1/AA1990.DAF:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | -     | 12:    | /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1991.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   |       | 3:     | /SIDS1/qcqdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | -     |        | /SIDS1/gcgdata/hold-geneseg/genesegp-embl/AA1993.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   |       | 2      | /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA1994.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   |       | غو     | /Sitis1/grgdata/hold-geneser/genesergp_embl/AA1995_DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|   |       | 7      | /SIDS1/gegdata/hold-geneseq/genesegp-cmb1/AA1996.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | _     | 18:    | /SIDS1/qcqdata/hold-qeneseq/geneseqp-embl/AA1997.DAT.*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | _     | 19:    | /SIDS1/gradata/hold-geneseq/geneseqp-embl/AA1998 DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | CA    | C      | /SIDS1/qrqdata/brld-qeneseq/qeneseqp-emb1/AA1999.DAT-*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | (4    |        | /SIDS1/gcgdata/hold geneseg/genesegp embl/AA2000.DAT:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|   | C-1   | <br>Ci | /Sibsi/gegdata/bold-geneseq/geneseqp_embi/AA2001.DAT.*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 7 | <br>9 | ,      | M. M. Company of Company of the Comp |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| ı I   | ID           | *************************************** | AABSOOTS | AAB92729 | AAW54099 |
|-------|--------------|-----------------------------------------|----------|----------|----------|
|       | EG :         |                                         |          | C1       | 9        |
| Query | Match Length | 7144                                    |          | 345      | 515      |
| Query | Match        |                                         | 0.6      | 65.1     | 48.2     |
|       | ore          |                                         |          | 153      | 46       |

| Description                 | Protein encoded by | Human protein sequ | Homo sapiens BAP28 | A gyrasê protein o | Peptide #7963 enco | Human brain expres | Human bone marrow | Peptide #8214 enco | Human polypoptide | Dp-74 VH1 gene hea | Peptide #4107 enco |
|-----------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|
| ID                          | AAB85029           | AAB92729           | AAW54099           | AAY23793           | ABB40457           | AAM61279           | AAM74002          | AAM34177           | AA001170          | AAP34271           | ABB31456           |
| DB                          | C1                 | 싆                  | 19                 | 00                 | 22                 | C)                 | 22                | (1)<br>(1)         | C1                | 14                 | 22                 |
| Query<br>Match Length DB ID | 2144               | 349                | 515                | 220                | 36                 | ¥.                 | 36                | 36                 | яз                | ଫ                  | 110                |
|                             | 0.66               | 65.1               | 48.2               | 4.1                | 3.6                | ب<br>ج             | 3.6               | 3.6                | 3                 | у<br>Ж             | 3.6                |
| Score                       | 193                | 127                | 46                 | 8                  | 7                  | 7                  | 7                 | 7                  | 7                 | 7                  | 7                  |
| Result<br>No.               | 1                  | C1                 | 3                  | 4                  | เก                 | ¥                  | 7                 | ω                  | 5                 | 10                 | 11                 |

| Peptide #4174 enco<br>Protein #4504 enco<br>Human brain expres<br>Human bonc marrow<br>Peptide #4085 enco<br>Pebtide #4206 enco | Peptide #3991 enco<br>Human immunaglobul<br>Novel human sectet<br>Mutant Aspergillus<br>A. oryzac P7-14.1<br>Novel human secret.<br>Zea mays protein 1 | pylári<br>pylári<br>an ORF<br>an can<br>an can<br>an col                                              | PRO189 (phila mel sapiens B polypept polypept acid seq | Rice poly (A) bind<br>Houns sapiens BRCA1<br>Yeast HMG-COA redu<br>Cytadhesin protein<br>Streptococcus pneu<br>Streptococcus pneu |
|---------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------|--------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| 22 ARR36668<br>22 ABB22005<br>22 AAM57432<br>22 AAM69827<br>22 AAM17651                                                         |                                                                                                                                                        | 18 AAW55542<br>18 AAW55142<br>18 AAW56142<br>22 AAW66297<br>21 AAB43736<br>22 AAX36267<br>21 AAY86633 | . , , . ,                                              | 2 AAE13001<br>9 AAW47538<br>6 AAE58611<br>6 AAE4927<br>11 AAY8512<br>22 AAU47719                                                  |
|                                                                                                                                 | 110<br>1110<br>1128<br>1138<br>1138<br>1138<br>1134<br>1134<br>1135<br>1135<br>1135<br>1135<br>1135<br>1135                                            |                                                                                                       |                                                        | 655 2<br>729 1<br>1045 1<br>1144 1<br>1138 2                                                                                      |
| w w w w w w<br>k k m b b b k                                                                                                    |                                                                                                                                                        | ယယ္သည္ သည္ သည္။<br>ကိုက်တဲ့ ဧက်လ်က်တဲ့                                                                |                                                        | မယ္ထန္ထန္<br>စဲတဲ့လုံဆိုင္                                                                                                        |
| <i></i>                                                                                                                         | ~~~~~                                                                                                                                                  | ~~~~~~                                                                                                | rr                                                     | ~~~~                                                                                                                              |
| 12<br>14<br>15<br>16                                                                                                            | 118<br>120<br>120<br>140<br>140                                                                                                                        | 00000000000000000000000000000000000000                                                                | <br>@ T @ B B B B B B<br># 4 N O C B B B               | 0 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                           |

#### ALIGNMENTS

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BAP28; prostate; tumour; cancer; diagnostic; genetic analysis.
                                                              Protein encoded by BAP28 obNA consisting of exons 1 to 45.
             AAB85029 standard; Protein; 2144 AA.
                                                                                                               Location/Qualifiers
                                                                                                                          /label- Ser or Asn
Misc-difference 1854
                                                                                                                                         /labcl= Ala or Val
Misc-difference 1967
                                                                                                                                                               /label= Asp or Asn
                                                                                                                                                                               /label- Gly or Glu
                                              U6-AUG-2001 (first entry)
                                                                                                                      Misc-difference 1694
                                                                                                                                                                        Misc-difference 2017
                                                                                               Homo sapiens.
                              AAB85029;
       AAH85029
RESULT
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WO200100669 A2.

04-JAN-2001.

23 JUN 2000, 2000WO-IB01183

25-JUN-1999, 99US 0141323. 18-JAN-2000, 2000US-0176880.

(GEST ) GENSET.

DB 16; Length 673;

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RESULT 15
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      Lin X., Kaul S., Popnsley S.D., Shea T.P., Henito M.-T., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Baruslead M.E., Feldfilyum T.V., Buell C.R., Ketchum K.A., Lee T.T., Bonning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.F., Imagyam L., Tallon L.J., Gill J.E., Cadams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Fisen J.A., Salzberg S.L., Praser C.M., Venter J.C., "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21359325; PubMed-11466286; MEDLINE-21359325; PubMed-11466286; MEDLINE-21359325; PubMed-11466286; Mociling J., Bircton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qibin D., Hitti J., Wolf Y.L., Tatusov K.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Liam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Liam B., Southwick B., Jones T., Hanb J., Chen H., Cheuk R.,
Churq M.K., Kim C., Lin J., Liu S.X., Pham P.K., Sakano H., Shinn P.
Yamada K., Becker J., Theologis A., Davis R.W.;
Submitted (APR-2001) to the EMBL/GenRank/DDBJ databases.
EMBL, ACUG2332, AAMBUD75.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae,
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                                                                                                                                                                                                                             submitted (MAR 2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PFGAA69, pkinase, l.
PRASTIE: PSSOULL; PKATEIN_KINASE_50.M. 1.
ATP-binding; Hypothetical protein; Transferase.
SEQUINCE: 604 AA, 7250.9 MW, 41FULI4FB18H97E6 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-07T-2001 (TiEMBLrel. 18, Created)
01-07T-2001 (TrEMBLrel. 18, Last sequence update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 AA.
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Best Local Similarity 100 0%; Prod No 10;
Sectional Similarity 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR002513; Transposase_7.
Piam; PF01226; Transposase_7; 1.
Plasmid; Complete proteome.
SEQUENCE 673 AA; 76570 MW; C8073
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MEDIANE-20083487; PubMed-10617197;
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InterPro; IPROUU719; Euk_pklidse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :-2001 (TrEMBLrel: 19, Las TRANSPOSASE (3' SEGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001438; AAK76839.1;
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                                                                                                                                                    Nature 402:761-768(1999).
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                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567 KKKEGEEE 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 КККЕСЕЕЕ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_Tax1D-1488;
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                                                                   O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LaPlante I., O'Rourke F A., Du X., Matthews E., Olsen A., Choi J.S. Rose E., Feinstein M.B.;
Submitted (cdr-2000) to the EMBL/GemBank/DDBJ databases.
EMBL; U94836; AAB53327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Graniata, Vortebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homo.
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                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00443; G-patch; 1.
SEQUENCE 884 AA; 100015 MW; 51BBFF371HA132D9 CKC64;
                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TTEMBLEEL. 04, Created)
01-JUL-1997 (TTEMBLEEL. 04, Last sequence update)
01-DEC-2001 (TTEMBLEEL. 19, Last annotation update)
ERPROT 213-21.
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                     4.0%; Score 8; DB 16
100.0%; Pred. No. 30;
Live 0; Mismatches
                                                                                                                                                                                                                                                                           884 AA
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                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20256781; PubMed-10794731;
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Interpro; IPR000061; Surp.
Pfam; PF01885; G-patch; 1.
Plam; PF01805; Surp; 1.
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Best Local Similarity 100....
8; Conservative
Ouery Match
Bost Local Similarity 100.0
For B: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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                                                                                                                                           207 LDLLINKL 214
                                                                                                                 27 LDLLNNKL 34
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Ouery Match
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Galibert F., Finan F.M., Long S.R., Puchler A., Abola P., Ampe F.,

Galibert F., Barnett M.J., Becker A., Boisrard P., Rothe G.,

Boutry M., Bowser L., Bahrmester A., Gadieu E., Gapela D., Chain P.,

Cowie A., Davis R.W., Dreamo S., Federspiel N.A., Fisher R.F.,

Gloux S., Godfro E., Goffeau A., Golding B., Gouzy J., Gurjal M.,

Hernandez-Lucas I., Hong A., Halzer L., Hyman R.W., Jones I., Kahn D.,

Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Leiaure V.,

Masuy D., Palm C., Peck M.C., Pohl T.M., Portelelle D., Purnelle B.,

Ramsperger H., Waldier S., Wells D.H., Wondenbol M.,

Vorhoeller F.J., Waldier S., Wells D.H., Wong K., Yeh K.-C., Babut J.,

"The composite groups of the Legume symbiont Sinchirobium meilloti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Import G. Sandon F. Yverf G. hovys D. Trettier V., Garnier J.M., Weber C., Mandel J.L., Cancel G., Abbas N., Duerr A., Didier]ean O., Stevanin G., And Y., Brice A., "Cloning of the gene Lir spinocerebellar ataxia 2 reveals a locus with high sensitivity to expended CAC/glutamine repeats."; Mat. Genet. 14.285 201(1996)

Mat. Genet. 14.285 201(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                     2.7.7.23).
Rhizobium meliloti (S norhizobium meliloti).
Hactoria: Proteobatteria: alpha subdivision: Khizobiareae gloup;
Rhizobiaceae: Sinorhizobium.
                                                                                                           01-080-2001 (FFBMH.rel. 19, Created)
01-087-2001 (FFBMH.rel. 19, Frest sequence update)
01-08C 2001 (FFBMH.rel. 19, Last annotation update)
PROBABLE HDP-N-ACFTYLGHTCOSAMINE PYROPHOSPHORYLASE PROTEIN (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15: Length 456;
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SEQUENCE 456 AA; 47775 MW: 784F04BAC9CF1C41 CRC64;
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01-MAY-1997 (TrEMBLE). 03, Last sequence update)
01-DEC-2001 (TrEMBLE). 19, Last annotation update)
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EMBL: AL591788; CAC46236.1:
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Best Local Similarity 100.
Matches 8: Conservative
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID-382;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-1021
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Spermatophyta, Magnoliophyta, cudicotyledons; core cudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Liu S.X., Chan A., Yu G., Lee J.M., Lenz C., Pham P., Sakano H.,
Toriumi M., Vysotskaia V.S., Chin C., Chio L., Choi E., Chung M.,
Toriumi M., Vysotskaia V.S., Chin C., Chio L., China M.,
Buchiel E., Chao C., Conn. Conway A.B., Hansen N.F.,
Johnson-Hopson C., Khan S. Kim C., Lam B., Miranda M., Nquyen M.,
Palm C.J., Shinn P., Southwick A., Davis B.W., Erker J.R.,
Theologia N.A., Theologia A.,
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Length 459;
                                                                                                 0; Indels
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Submitted (JUL-2000) to the EMBL/SenBank/LVBJ dalabases.
EMBL; AC007767; AAF81343.1, ...
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-JAN-1998 (TrEMBLiel, 05, Last sequence update)
01-DEC-2001 (TrEMBLiel, 19, Last annotation update)
4.08; Score 8; DB 4;
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                                                                                            8; Conservative
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Best Local Similarity
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                                                                                                                                                                                             168 LAALOKVV 175
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                                                                                                                                                                                                                                                                                    244 LAALOKVV 251
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Gaps

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100.0%; Pred. No. 17; tive 0; Mismatches

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Best Local Similarity 100.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                    O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetales; Streptomyces.
                                                                                     01-DEC-2001 (TTEMBLIE) 19, Last sequence update)
01-DEC-2001 (TEMBLIE) 19, Last annotation update)
HYPOTHETICAL 34.9 KDA PROTEIN.
HOMO Saplemes (Human).
Eukaryota: Metazoa: Chordata; Craniata; Vertubiata, Euteleostomi;
Mammalia; Futheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Rieser H.M., Denapaite D., Diehner A., Cullum J., Kinashi H., Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-2000) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                          .cngth 307,
                                                                                                                                                                                                                     Submitted (NOV-2001) to the EMBL/Genbark/Drubs databases.
EMBL; BC017168; AAH17168.1; ".
Hypothetical protein.
SEQUENCE 307 AA, aqaan MW; Bagaraar72r60448D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2),
Oliver K., Harris D.;
Submitted (JMN-2000) to the EMBL/GemBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpres | IPRODOT92: HTH_LUXR.
SMART; SMO0421; HTH_LUXR: 1.
SEQUENCE 343 AA; 36355 MW; F18ABCEAD31AD499 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996)
EMBL: A1359949; CAH95810 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-2000 (TrEMBLrel, 15, Created)
01-007-2000 (TrEMBLrel, 15, Last sequence update)
01-10N-2001 (TrEMBLrel 17, Last annotation update)
                                                                                                                                                                                                                                                                                         Ouery Match 4.0%, Score 8, DB 4,
Best Local Similarity 100 0%; Prod No. 15,
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                343 AA.
                                                   307 AA.
                                                                           01-DEC-2001 (TremBirel, 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                   PRT;
                                                                                                                                                                                     SEQUENCE FROM N.A.
IISSUE-UTERUS, AND LEIOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN+A3(2),
MHDLINH-97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO02197, HTH_Fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            27 LDLLNNKL 34
                                                                                                                                                                                                                                                                                                                                                            90 LDLLNNKL 97
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                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
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                                                                 USPAG4;
                                                   Q96AG4
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4.0%; Score 8; DB 2; Length 343;

Query Match

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                                                                                                                                                                                                                                                                                                           Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mnwes H W., Mannhaupt G.;
Submitted (DEC-2000) to the EMRI/SenHank/NNBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Melazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                          Eckaryota, Füngi, Ascomycota: Perinomycotina, Serdariomynches,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 439;
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Local Similarity 100 0%; Pred No 19;
les 8; Conservative 0: Mismatcher ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APP-2001) to the EMML/GenHank/DDRL databases.
EMBL: BC006751; AAHU8751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDHJ databases.
EMBL, A4451019; CAD11358.1; --
Hypothetical protein.
SEQUENCE 394 AA: 45742 MW; SD2FCD4792146D3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 AA; 50054 MW; AFBENBED1D34605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Öl-DEC-2001 (TremHirel 19, Created)
01-DEC-2001 (TremHirel 19, Task Sequence update)
01-DEC-2001 (TremHirel 19, Lask annotation update)
SEP/ARC-PEDATED MICLEAP MATRIX PROTEIN.
                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel 19, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 0%, Score 8, DB 11
100.0%, Pred. No. 21,
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 AA.
                                                                                                                                                                                                            Sordafiales, Sordariaccae, Neurospora.
NCBI_TaxID=5141;
                                              01 DEC-2001 (TrEMBLirel: 19, Created)
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PRT;
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PRELIMINARY;
                                                                   01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSHE-BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Lucal Similarity
                                                                                                                                                                        Neurospora crassa.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RKKKEGEE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matrix protein.
SEQUENCE 439
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Mitochondrion.
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                                                                                                                                        Mitochondrion
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                                                        0950F5;
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                                           Q950F5
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                 RESULT
                               0950F5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawarahayasi Y. Sawara M. Horikawa H. Haikawa Y., Hino Y., Yamamoro S., Sokino M., Haba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ostuka B., Nakazawa H., Itakaiya M., Ostuka Y., Panahasi T., Tanaka T., Kaibi Y., Shida M., Ostuka Y., Aoki K. I., Yoshizawa T., Polbi Y., Pobb F.T., Horikoshi K., Masuchi Y., Shiouya H., Kikuchi H.; Mongleto sequence and gene organization of the genome of a hyporthermophilic archaebacterium, Pyrococcus horikoshii Qin T.
                                                                                                                                       White P., Elsen J.A., Heidelberg J.F., Hirkey E.K., Peterson J.D., Dodson R.J., Hatt D.H., Gwinn M.E., Nelson W.C., Richardson D.L., Mottat K.S., Qin H., Clang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McConaid L., Hittback T., Zalewski C., Makarova K.S., Aravinu L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archara; Euryarchacota; Thermorecales; Thermoreceace; Pyroceccus.
NCH.[tax10-53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                        Bacteria: Thermus/Deirococcus group: Deinococcales: Deinococcus.
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                                                                                                                                                                                                                                    "Genome Sequence of the radioresistant bacterium Deinococous radiodurans RL",
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Srore 8; DB 17; Length 123; 100.0%; Pred. No. 6.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 8; DB 16; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: APROCOCO: BAA-1110.1;
Hypothetical protein: Complete proteome.
SEQUENCE: 123 AA: 14212 MW: 1771906136G00A18 CRC64;
                                                                                                                                                                                                                                                                                                                           3B93E87030B3081C CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (IFEMBLECL. 07, Created)
10-AUG-1998 (IFEMBLECL. 07, Last sequence update)
01-JUN-2000 (IFEMBLEL. 14, Last annotation update)
HYPOTHELICAL 14.2 KDA PROTEIN PH1983.
01 MAR 2001 (Tremblrel. 16, Last annotation update) HYPOTHETICAL 12.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6.6;
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                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. no.
                                                                                                                                                                                                                                                                                             IIGK: DRO207: -.
Hypothetical protein: Complete proteome.
                                                                                                                         MFDLINF-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE-98344137; PubMed-9679194;
                                                                                                                                                                                                                                                                                                                           123 AA: 12733 MW;
                                                                                                                                                                                                                                                                                 EMBL; AE001883; AAF09E01.1;
                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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                                           Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 5:55-76(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrocecus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
hes H; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   Hest Local Similarity
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                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           164 LLSALAMI 171
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                                                                    NCB1_TaxID-1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 KKKEGEEE 84
                                                                                                                                                                                                                          Frasor C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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MEDLINE-21306528; PubMcd-14412371;
Bos D.H., Sites J.W. Jr.;
"Phylogeography and conservation genetics of the Columbia Spotted From
(Rana luteiventris).";
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Bos D.H., Sites J.W. Jr.;
"Phylogeograph, and conservation genetics of the Columbia Spotted Frod
(Rana luteiventris).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                 Eukaryota; Metazoa; Chorda a; Craniata; Vertebrata; Euteleostomi;
Amphibia, Batrachia, Anura Neobatrachia; Ranoidea; Ranidae; Rana,
NCBL_TaxID-58176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura, Neobatrachia; Kanoidea; Kanidae; Kana
NCBL_TaxID=58176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 400;
15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AA; 33574 MW; 212A26A6CAB6BBB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA: 33505 MW; 552AZ6BH7DHF5CA3 CRC54;
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Last annotation update)
                                                              Last sequence update)
Last annotation update)
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100.0%; Pred. No.
ative 0; Mismatch
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BEMBI. AY016649; AAK54395.1,
EMBI. AY016652: AAK54391.1.
EMBI. AY016654; AAK54401.1.
                                                                                                                                                                                                                                                                                                                                                                   Mol. Ecol. 10:1499-1513(2001).
EMBL: AY016673; AAK54420.1 -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel, 19. 01-DEC-2001 (TrEMBLrel, 19. 01-DEC-2001 (TrEMBLrel, 19. CYTOCHROME B (FRAGMENT).
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PRELIMINARY;
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8: Conserv
                                                                                                                            Rana lutciventris.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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US-09-603-665-5\_COPY\_1594\_1794

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562222 seqs, 172994929 residues Searched:

Word size .

2567 Total number of hits satisfying chosen parameters:

Minimum DH seq length: 0 Maximum DH seq length: 2000000000

Post-processing: Listing first 45 summaries

SPTREMBL\_19:\* Database :

sp\_human:\*
sp\_invertebrate:\* sp\_organelie:\* sp\_archea:\* sp\_bacteria:\* sp\_rodent:\* sp\_mammal:\* sp\_plant·\* sp\_fungi:\* sp\_phage:\* sp\_mhr.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp\_rvirus:\*
sp\_bacteriap:\* sp\_archeap:\*

sp\_unclassified.\*

sp\_vertebrate:\*

sp\_virus.\*

#### SUMMARIES

|            | Description     | O9uxul pyrococcus | Ogrxu9 deinococus | 057720 pyrococcus | Q950f5 rana luteiv | Q94ph4 rana luteiv | บุษ์กัลสุ4 homo sapien | Q9k3yl streptomyce | U96ty7 neurospora | Q91w08 mus musculu | Q92ps3 rhizobium m | O99492 homo sapie⊓ | Q91q12 arabidopsis | OLZWUM arabidopsis | Q97tk7 clostridium | COUSUZ homo sapies |  |
|------------|-----------------|-------------------|-------------------|-------------------|--------------------|--------------------|------------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
|            | <u></u>         | Q90X01            | O9RXII9           | Ō57720            | 540560             | 094РН4             | Q96Act4                | Q9K3Y1             | U96TY7            | Q91w08             | 0921/53            | Ca40405            | 2101Pg             |                    |                    | 000302             |  |
|            | EH :            | 17                | 9                 | 1.7               | æ                  | œ                  | 4                      | 7                  | *                 | 11                 | 9.                 | 4                  | $1 \circ$          | Ξ                  | 16                 | 4                  |  |
|            | Match Length DB | 108               | 123               | 123               | 300                | 300                | 407                    | 343                | 394               | 439                | 456                | 45.4               | 6.06               | 5 P P P            | 673                | 484                |  |
| %<br>Query | Match           | 4.0               | <b>4</b>          | 4.0               | 4.0                | 4                  | . t                    | 4.0                | 4.0               | 4.0                | 4.0                | 4                  | 4                  | ं. क               | 4.0                | 4.0                |  |
|            | Score           | æ                 | œ                 | 8                 | œ                  | œ                  | œ                      | œ                  | œ                 | 90                 | œ                  | æ                  | α                  | æ                  | œ                  | 30                 |  |
| Result     | No.             | 1                 | 2                 | 33                | 4                  | <i>ن</i> ۲.        | œ                      | 7                  | œ                 | on.                | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 |  |

| O86472 rhodobacter<br>O8307 rhodobacter<br>O92)14 rickettsia<br>O9btq2 homo sapien<br>O9vq36 aeropyum p | 99793 seropyrum p<br>99xfd2 oryna sativ<br>94xfd2 oryna sativ<br>94xfd2 oryna sativ | 09yca6 aeropyrum p<br>09)z54 neisseria m<br>09)z47 neisseria m<br>093er3 photorhabdu |                                                  | Q9c2b2 human immun<br>Q9vby7 drosophila<br>Q9vu25 drosophila<br>Q912q2 streptiomyce<br>Q9789 qossypium h | Q39763 gossypium b<br>P96320 crwinia amy<br>O85662 proteus mir<br>O9m3r3 pinus sylve<br>Q9pln0 homo sapien<br>Q99yb2 streptococc<br>Q90dt8 chimpanzee |
|---------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|--------------------------------------------------|----------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2 086472<br>2 083021<br>16 09231.4<br>4 09BTG2<br>17 09YB36                                             | 7.<br>10<br>10<br>5                                                                 | 17<br>16<br>15<br>2                                                                  | 4041                                             | 25<br>50<br>10<br>00                                                                                     | 10 039763<br>2 095320<br>10 09M3R3<br>4 09PINO<br>16 04YEE<br>15 090DT8                                                                               |
| 7 3.5 57<br>7 3.5 72<br>7 3.5 95<br>7 3.5 95                                                            | 7 3.5 135<br>7 3.5 136<br>7 3.5 143<br>7 3.5 143                                    | 7 3.5 143<br>7 3.5 146<br>7 4.5 14b<br>7 3.5 153                                     | 7 3.5 164<br>7 3.5 164<br>7 3.5 180<br>7 3.5 192 | 7 3.5 192<br>7 3.5 195<br>7 3.5 200<br>7 3.5 209<br>7 3.5 209                                            | 2.55                                                                                                                                                  |
| 17<br>19<br>20<br>21                                                                                    | I디디디                                                                                | 2                                                                                    | 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3            | 34<br>35<br>37<br>38                                                                                     | w 4 4 4 4 4 4<br>© O − 13 10 4 10                                                                                                                     |

#### ALT GNMEN'TS

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"Pyrococous abyssi genome sequence insights into archaeal chromosome
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                                                                                                                                                Archaea; Euryarchaeota; Thermococcales, Thermococcase, Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                          DB 17, Length 108, 5.9;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                   structure and evolution ";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248288; CAB50672.1; -.
                                                                                                                                                                                                                                                                                                             170274A4A8A659C1 CRC64;
                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL, 12 & KIDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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4 005, ..... 70, 5.9;
Best Local Similarity 180.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches
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                             108 AA
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SPOUENCE 108 AA; 12527 MW; 176274A4A
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                             PPELIMINARY;
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                                                                                                                                  Pyrocecus abyssi
                                                                                                                                                              NCBI_TaxID=29292;
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                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: GUANINE NUCLECTIDE-BINDING PROTEINS (G PROTEINS) ARE PROVINCED AS MODIFICATORS OF TRANSDUCIES IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THIS PROTEIN MAY BE INVOLVED IN THE DETERMINATION OF THE CAMP LEVEL ACCORDING TO NUTRITIONAL. SOUTH THOUS, MOST PROHABLY AS A REGULATOR OF ADMINITY. CYCLASE, SUBJUNITS OF PROHABLY AS A REGULATOR OF ADMINITY OF CHARSE.

THE ALPHA CHAIN CUNTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R->H: DECREASE IN MATING AND SPORULATION BEFILLENCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U->L: DECREASE IN MATING AND SPORULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.,
                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCY FROM N A . AND MUTAGENESIS OF ARG-176 AND GLN-202. MEDLINE-44040710: Pubmed-1340462. ISSIN'S I . . MOCHICLKI N., Maeda I., Yamamoto M.; ISSIN'S I . . Mochicki N., Maeda I., Yamamoto M.; Issin's Peast gene, gpa2, that encodes a Galpha subunit involve, in the monitoring of nutrition.";
                                                                                                                                                                                                                                                                                                                                Off-don's 1994 (Rel. 29, Created)
Off-don's 1994 (Rel. 29, Last sequence update)
Lever 1 2001 (Rel. 40, Last annotation update)
Ondrine nucleonide-binding protein alpha-2 subunit (GP2-alpha),
GPA2 ok SPAC24H3.13C.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                         4.5%; Score 7; DB 1; Length 320;
.00.0%; Pred. No. 30;
                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP 1997) to the EMBL/GenBank ZDDBJ databases
                 420 4A: 47202 MW; FD404B]BE86A0EED CRC64;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                             Best Local Similarity ..00.0%; Pred. No. 30;
Matches 7; Conservat, ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       offP binding; Transducer; Multigene tamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to licensedisb-sib,ch).
POLY GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPRU61019; Gprotein_alpha.
                                                                                                                                                                                                                                                                                                      ..
24
2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev. 6:2455-2462(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: D14365; BAA02630.1;
EMBL: 299163; CAB16244.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMARI; SM00275; G-alpha; 1
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272
176
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HSSP; PI0824; IAS4.
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                                                                                                                                                                     128 VISHER 134
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Q04665;
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SHOUSINGE
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                                                                                                                                                                                                                                                                RESULT 15
GBAZ_SCHPQ
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EFFICIENCY.

SQ SEQUENCE 354 AA; 40522 MW; A0042174C1389BBA CRC54.

Query Match
Best Local Similarity 100.0%; Pred. No. 43:
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 6 TFIPVIR 12

HILLII
Db 69 FFIPVIR 25
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Search completed: July 2, 2002, 16:19:05 Job time: 777 sec

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                                                                                                                             ALKYLATING AGENTS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: Bydrolysis of DNA containing ring-opened N7-nethylquanine residues, releasing 2,6-diamino 4 hydroxy 5 (N-methylloromanidopyrimide.

-!- COPACTOR: BINDS 1 ZING TOW (BY SIMILARITY).
                                                            May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V., "Complete genomic sequence of Fascheurella m.H.b. dad Spiro", proc. Natl Acad Soci in S.A. 98.3460.3465(2001).
-1- FUNCTION: THIS ENTYME MAY PLAY A SIGNIFICANT ROLE IN PROCESSES LEADING TO RECOVERY FROM MUTAGENESIS AND/OR CELL DEATH BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Enkaryota, Fungi: Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two new genes, PHO86 and PHO87, involved in inorganic phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bun-Ya M., Shikata K., Nakade S., Yompakdee C., Harashima S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Indeis
                                                                                                                                                                                                                                                                                                                                                                                                       DNA repair; Hydrolase; Glycosidase; Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                            30612 MW; B44C3BDFDD968734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C / FV1679;
MEDLINE-97103775; PubMed-8948161,
Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obery Match 3.5%; Score 7; DB 1;
Hest Local Similarity 100 0%; Prod No. 26;
Matches 7; Conservative 6; Mismatches
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Interpro, 1PR000191; Papy_DNA_91yco.
Interpro, 1PR000214; Papy_DNAg1yco_rn,
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uptake in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF01149, Fapy_DNA_giyco, î.
ProDom, PD603680, Fapy_DNA_giyco, l.
PROSITE, PS01242; FPG; l.
                                                   MEDLINE 21145866, Pubmed-11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96171517; PubMed-8598055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Genet. 29:344-351(1996).
                                                                                                                                                                                                                                                                                                                              EMBL, AE006155; AAK03229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA;
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                           SEQUENCE FROM N.A.
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P46956;
                                         STRAIN-PM70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SHOURNCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb.sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of Bioinformatics are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb sib.ch).
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96077112; PubMed-7477378;
E.I. X.-J., E.I. S.-H., Sharp A.H., Nuclfora F.C. Jr., Schilling G.,
Lanahan A., Worley P., Snyder S.H., Ross C.A.;
"A huntingtin-associated profein enriched in brain with implications
"Sequencing analysis of a 40 2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2, SPT10, GCD14, RPR1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon."; Yeast 12:1471-1474(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                 -!- SUBCELLULAP LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: IN CONTRAST TO HAPL, DOES NOT SEEM TO BIND TO HUNTINGTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR 1; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1CB19C9184BF1C48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Transmembrane.
)1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00T-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%; Score 7; P
100.0%; Pred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: STEGNG, TO HAP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAP1-like protein 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D64817; BAAU9885.1; -.
EMBL; 249392; CAA89412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U38371: AACS0297 1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quory Match
Best Loral Similarity lue
7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
55
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; SONO3653; PHO86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphate transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
200
311 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.I.SSUE-Caudate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 OPKKKPG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QRKKKEG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLF1_HUMAN
P54257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECHENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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Caps

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0: Indels

DB 1; Length 218

3.5%; Score 7; DB 1; 100.0%; Pred. No. 21;

Owery Match Best Local Similarity 100.0 7; Conservative

25 KALDLLN 31

ò

0; Mismatches

218 AA; 24137 WW; 39CB897HA9FBA94A CRC64;

InterPro; IPR003034; SAP. Piam; PF02037; SAP; 1. SMART; SM00513; SAP; 1.

SEQUENCE

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modified and this statement is not removed. Usage by and for commercial
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MEDLINE-9847276; Pubmed-9707445;
Piriat J.L., Annihera A.:
"A novel yeast gene, 1802, is involved in RNA pol II transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STPAIN STREET ARGOLD TO THE METHOD BY ALL ALL AND BY AND B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: UNKNOWN; SUPPRESSOR OF THE TRANSCRIPTIONAL DEFECT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fynai: Ascomyceta: Saccharomycetica: Saccharomycetes.
Saccharomycetales: Saccharomycetaceae: Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provides new evidence for transcriptional elongation-associated
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                             Hypothetical profein; Transmembrane: Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9E148F0FC267@CH6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ol-FFB 1995 (Rel. 4), Last sequence update)
16-071-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%; Score 7; DB 1
100.0%; Pred, No. 21;
11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  FOTENTIAL.
FOTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                Prof ENTIAL.
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                                                                                                                                                                                              EMBL; AE001094; AAB91063.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                    214
2.847 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17:4859 4872(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 LLSALAA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1 Lax110-4942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THOLOR YEROFAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 LLSALAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombination
                                                                                                                                                                                                                        AF0172:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOURING
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                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
     Sauddda Mae Mae ee ee ee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                           Submitted (IAN-1949) to the EMHL Chenty Depth databases.
-!- FUNCTION: NOI KNOWN: PROBABLY INVOLVED IN PROSPHALE IMANSFORE AND/OR METABOLISM (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYLOpiasmic (By Similarity).
-!- SIMILARITY: BELONGS TO THE PHOU FAMILY.
                                                                                                                                                                                                                                        Bacteria; Proteobacteria, alpha subdivision. Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellareae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
91-MAR-2002 (Rel. 41, Last annotation update)
Formamidepyrimidise DNA 4lyposylase (ET 3.2.2.23) (Fup./ DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DH 1; Longth 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 AA; 26270 NW, 54549310E48D8C2B CRC64;
                                                                                                                          16-ocr-2001 (Rel. 40, created)
16-ocr 2001 (Rel. 40, last sequence update)
16-ocr-2001 (Rel. 40, last annotation update)
Phosphate transport system protein phou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20cry Match 3.5%; Srcrc 7; 38 1;
Best Local Similarity 100.0%; Pred, No. 23;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.K.1 :
                                                                                                                                                                                                                                                                                                                            STRAIN-AICC 31821 / ZM4 / CP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF124757; AAD29648.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTM OR FPG OR PM1145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                 Lee H.J., Kang H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphate transport.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 TSTLEAL 135
 128 KALDLLN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 TSTLEAL 43
                                                                                                                                                                                                                                                                        NCB1_1dx1D=542;
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                                                                                            PHOU_ZYMMO
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P57910;
                                                                                                                                                                                                                                                             Zymomonas.
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                                                                                                             Q9X5E1;
                                                         RESULT 11
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EMBL: 018814: AAB64599.1; -.

SGD: SOCOOR865; YEROFAM

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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RCSB IS A MEMBER OF THE TWO-COMPONENT FEGULATORY SYSTEM, PROBAPCSC, WHICH REGHTALES THE EXPRESSION OF REMESS INVOLVED IN COLANIC ACID CAPSULE SYNTHESIS. RCSB ACTS AS THE EFFECTOR. ADDITIONAL CONTROL IS PROVIDED BY THE DEPENDENCE ON THE ALTERNATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClefland M., Sanderson K.E., Spieth J., Clifton S.W., Latrcille F., Courtney L., Porwellik S., Ali J., Danie M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
-!- FUNCTION: ALSO STIMULATES FTSZ EXPRESSION, THIS SUGGEST THAT RCSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                      SIMILARITY: BELONGS TO THE LUXP/UNDA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, gamma subdivision, Esterobacteriaceae,
               IS A REGULATOR IMPLICATED IN THE REGULATION OF MORE THAN ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00622; HTH_LUXR_FAMILY: 1.
PROSITE, PS50110: RESPONSE_RESILTATORY: 1.
Sensory Liausduction: Phospharylalion: Transcription regulation, PNA-binding. Activator: Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESPONSE REGULATORY, PHOSPHORYLATION (BY SIMILARITY). H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D35CE2AB2B1DC0E4 CRC64;
                                                                                         -!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o. mar-2002 (Rel. 41, last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Capsular synthesis requiator component B.
RCSB OR STM2270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 7; DB 1
ilarity 100.0%; Pred. No. 21;
Conservative 0; Mismatches
                                     CELLULAR FUNCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LTZ / SCSC1412 / AICC /00725,
MEDITAL:21534948; FUBMEd=:15/7609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                            EMBL; AB000683; BAA19163.1; -. MBML; AL627274; -. CAD07501.1; -. InterProj. 1PR001792; HTH luxe InterProj. 1PR001789; Kusponse_teg.
                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00196, GerE, 1.
Pfam; PF00072; response_req, 1.
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01-MAR-2002 (Pcl 41, Croated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23728 MW;
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SMAPT; SMOO421; HTHEIJIXR; 1.
SMART; SMOO448; REC; 1.
                                                                                                                                                                                                                                                                           EMBL; X87830; CAA61094 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413-852-856(2001).
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nes 7; Conserv
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                                                                            REGULATORS
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                               THIS SUGGEST THAT RUSH
SIGMA FACTOR, RPON, FOR THE SYNTHESIS OF RCSH. RCSA AND RCSH FORM A COMPLEX TO PROMOTE TRANSCRIPTION OF THE GENES FOR CAPSULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                        -1 - SIMILAPITY - RELONGS TO THE LUXRZUHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                  IN THE REGULATION OF MORE THAN ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sensory transduction, Phosphorylation, Transcription regulation;
DNA-binding, Activator, Complete proteome.
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C
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H-T-H MOTIF (BY SIMILARITY).
A63D1ECF704E0680 CR064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 7; DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0: Indels
                                                                                                                                                              -!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESPONSE REGULATORY.
                                                             -!- FHNCTION: ALSO STIMULATES FTSZ EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reducing archaeon Archaeoglobus fulgidus.".
Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                                                 Styčene, SC27377; rosB.
PPOSITE; PSOO622; HTH_LUXP_FAMILY; 1.
PROSITE; PS[©]0110; PESPONSE_PROHLATOPY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN VC-16 / DSM 4304 / ATCC 49558;
                                                                                                     CELLULAR FUNCTION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23714 MW,
                                                                                  IS A REGILLATOR IMPLICATED
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Matches 7; Conserv
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DNA_BIND
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Haydshi I., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C. G., Ohtsubb B., Nakayama K., Marata T., Tanaka M., Tobe T., Lida T., Takami H., Benda T., Sasakawa C., Oqasawara N., Yasunaqa T., Kuhara S., Shiba T., Hattori M., Shimaaawa H., Tobe T., Tope T., Shiba T., Hattori M., Shimaaawa H., Shimaaawa G., Oqasawara O., Tasunaqa T., Kohara S., Shiba T., Hattori M., Shimaaawa H., Shimaaawa G., Oqasawara C., Olific A., Shiba T., Battori M., Shimaaawa H., Shimaaawa K., Shiba T., Shimaaawa H., Shimaaa H., Shimaaawa H., Shimaaawa H., Shimaaawa H., Shimaaawa H., Shimaaa H., Shimaaa H., Sh
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Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iroh I., Alba H., Haba I., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimita S., Kitakawa M., Kitaqawa M., Kitaqawa M., Makino K., Miki I., Mizobuchi K., Mori H., Mori T., Motomura K., Nakadue S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Salto N., Sampei G., Seki Y., Sivasundaram S., Taqami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; A 460 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1 50.0 min region on the linkage map.";
Gregor J., Davis N.W. Kirkpatrick B.A., Goeden M.A., Rose D.J.,
                                                                                           Man B., Shao Y.;
"The complete denome sequence of Eschetichia col: K-12.";
Science 277:1453-1474:1997).
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MEDLINE-21074935; PubMed-11206551;
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MEDLINE-21156241; PubMed-11258796;
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DIMA MCS. 8:11 22(2001).

FUNDTIONS MCSH ENGLATEN THE EXPRESSION OF GENER TWOTYED IN COLANIC ACID CAPSULE SYNTHESTS FOR ACTS AS THE PEPTOP ADDITIONAL CONTROL IS PROVIDED BY PHE DEPROPRIEMED ADDITIONAL CONTROL IS PROVIDED BY THE DEPROPRIEMED ADDITIONAL CONTROL IS PROVIDED BY THE DEPROPRIEMED ADDITIONAL CONTROL FOR THE SYNTHESTS OF MCSH. RCSA AND MCSH FORM A COMPLEX TO PROMOTE THANSCRIPTION OF THE GENES FOR CAPSULE SYNTHESTS.

FUNCTION: ALSO STIMULATES FISZ EXPRESSION, THIS SUGGEST THAT ROSB IS A REGULATOR IMPLICATED IN THE REGULATION OF MORE THAN ONE CELLULAR FUNCTION.

SIMILARITY: BELONGS TO THE LUXRZUBDA FAMILY OF TRANSCRIPTIONAL PECTUATORS

SIMILLARITY: CONTAINS LEESPONSE REGULATORY DOMAIN.

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Ecodenc: BG10821; resB.
InterPro; IPR000792; BTH_LuxR.
InterPro; IPR001789; Response_req.
                                                                                                                                                                                                                      AE002453; AAG57452.1; -.
AP002550; BAB36529.1; -.
                                                                                                                                                                                                             AE000310; AAC75277.1; -.
                                                                                                                                                                                                               D90850: BAA15000.1; -.
                                                                                                                                                                                                      EMBL: M28242; AAA24504.1;
                                                                                                                                                                                                          1.11272; AAA24506.1;
                                                                                                                                                                                                                   BAA16008.1,
                                                                                                                                                                                                                             JV0068; BVECCB.
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EMBL:
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MEDLINE-21534947; PubMed-11677608;
MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungali K.L., Hentley S.D., Holden M.I.G., Sebaiha M.,
Baker S., Hasham D., Brooks K., Chillingworth I., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Peltwal T., Hamlin N., Hacue A., Bies T.T., Holloyd S., Jaachs K.,
Kroqh A., Lasten T.S., Leather S., Moule S., Caoza P., Parry C.,
Ouall M., Putherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCSB/RCSC, WHICH REGULATES THE EXPRESSION OF GENES INVOLVED IN
COLANIC ACID CAFSULE SYNTHESIS. RCSH ACTS AS THE EFFECTOR.
ADDITIONAL CONTROL IS PROVIDED BY THE DEPENDENCE ON THE ALTERNATE
SIGMA PACTOR, RPON, FOR THE SYNTHESIS OF RCSH, RCSA AND RCSH FORM
A COMPLEX TO PROMOTE TRANSCRIPTION OF THE GENES FOR CAPSULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:848-852(2001).
-:- FUNCTION: RCSE IS A MEMBER OF THE IWO-COMPONENT REGULATORY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virlogeux I., Waxin H., Ecobichon C., Lee J.O., Popoll M.Y.; "Characterization of the resh and resh senses item Salmouella typhicres through tyla is involved in regulation of Vi antiqen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         whitehead S. Marrell B.G. "Complete growing R., Shevens R., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTIB.";
                                                                                           PROSITE: PSG0622; HTH_LUXR_FAMILY; 1.
PROSITE: PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction: Phosphorylation; Transcription regulation;
DNA-binding; Activator; Complete profession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, gamma subdivision, Enterobacteriageae;
                                                                                                                                                                                           56 56 PHOSPHORPLATION (HY SIMILARITY).
168 187 H-T-H MOTIT (BY SIMILARITY).
216 AA: 23670 MH; A78DIBD3004E0680 CRC64;
                                                                                                                                                                                                                                                                                       3.5%: Score 7; DB 1; Length 216; 100.0%; Pred, No. 21; Live 0; Mismatches 0; Indels tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FER-1997) to the PMRL/GenBank/DDBJ databases.
                                                                                                                                                                         RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Capsular synthesis regulator component B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis.";
J. Bacteriol. 178:1691-1698(1996).
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Ptam; PF00196; GerE; 1.
Ptam; PF00072; response_rea; 1.
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                                      PRINTS: PROGU48; HTHIJJXR.
SMART; SMO0421; HTH_JJJXR; 1.
SMART; SMO0448; REC; 1.
                                                                                                                                                                                                                                                                                                            Local Similarity 100.0
les 7: Conservative
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Q56127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-KI / MG1655; MEDLINE-974563; MEDLINE-97426617; Dubmod-9278503; MEDLINE-97426617; Dubmod-9278503; MEDLINE-97426617; Punkett G. III, Bloch C.A., Petha N.T., Builand V., Rijtey M., Collado-Vides J., Glasher I D., Rede C R., Mayhew G.F., Gregor J., Davis N.W., Kirkpairick H A., Goeden M.A., Fose D J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein: Transport, Transmendrame, Complete professe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macteria, Proteobacteria, gamma subdivision, Enterobacteriaceae;
Escherichia.
                         EUNCTION: MAY PLAY A ROLE IN L-LACTATE TRANSPORT.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE LLDP PAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
Submitted (AHG-1996) to the EMML/GenBank/DDEJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E3B0983059BlyB08 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (kel. 40, Last annotation update)
Hypothetical protein ybaw.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Subtinist; BG11875; yvfH.
InterPro; IPR003804; Lactate_perm.
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100.0%; PT.
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59761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF02652, Lactate_Perm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                              EMBL; 234643, CAB08002.1; ·
                                                                                                                                                                                                                                                                                                                                                                             271928; CAA96486.1;
299121; CAB15424.1;
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93
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269
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157
194
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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MEDLINE-9742617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Pilay M., Collado-Vides J., Glasner J P., Rode C K., Mayhaw G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of resB and resC from Dscherichia coli 09:K30:H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shout V_{\star\star} Gottesman S ; "ResB and ResC: a two-component regulator of capsule synthesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macteria, Proteubacteria, gamma subdivision, Enterobacteriaceae,
Lew H., Lin D., Namath A., Oefner F., Schramm S., Davis R.W.:
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE 93374832; PubMed-8366025;
Jayaratne P., Keenleyside W.J., Maclachlan P.R., Dodqson C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and examination of the role of the rcs regulatory system in expression of aroup I capsular polysaccharides."; J. Bacteriol, 175:5384-5394(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Longth 132;
; Pred No 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                           Us)
SRQUENCE FROM N.A.
STRAIN-KIZ / W3110;
Hatada E , obmort H , ciac Y., Isuii M , Fukuda P.;
Hatada E , obmort H , ciac Y., Isuii M , Fukuda P.;
Submitted (OCT-1946) to the EMBL/GenBank/PDBH databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBB3539149A37383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAP-2002 (Rel. 41, Last annotation update)
Forganiar synthesis requiator component B.
PRESE OF F2217 OF 23476 OP PES3106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome
SEQUENCE 132 AA; 15088 MW; EBB35391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene: EG13251: ybaw.
InterPro; IPR000365; 4HBcoA_thioestrse.
Pfam: PF03061; 4HBr; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000150; AAC73546.1; -.
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100 0%;
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Best Local Similarity 100 ...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID+562, 83334;
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P14374;
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                                                                                                                                                                                       Osada N., Hida M., Kosada J., Tanuma P., Isek' K., Hirai M., Terao K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LIPTETFIPVIRGLYGNPLPSVRRKALDLENNKLQQNISWKKTIVTRFLKLVPDLLAIVQ 60
                                                                                                                                     O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 I PSVPRKAIDII NNKLODNISWKKTIVTPFLKLVPDLLAIVQREKKEGEEEQAINRQTAL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mocara Lascionlaris (Grab ealing macaque) (Synomolaus monkey).
Eukaryota: Metarous Chordatus Graniata, Vettebrata, Eutelsostomis,
Emmalia: Eutheria: Primatos: Catarrhini; Cercopithecidae;
Cerropithecimaes: Macara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki Y., Suqano S., Hashamoto K.; "Isolation of full-length cDNA clones from manague brain cDNA libraries.";
                                                                                                 Score 100; DH 1; Tength 2144;
Pred. No. 3.4e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82: DB 1; Length 958;
Pred. No. 1,5e-73;
                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o, Indels
                              ZETIG VAR_010942.
W: D66815EE78D899B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (Off 2000) to the EMHL/Connabal/FDRI databases of SIMILARITY: HELONGS to THE BAP28 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 958 AA: 108644 MW; 3DBD95036230FB31 CRC64;
                                                                                                                                                                                                                                                       1654 RKKKEGEEEGAINRQTALYLLKLL/KNFGAENPDFFVFVL 1693
                                                                                                                                                                                                                                   61 RKKKEGEEEQAINRQTALYTLKLLCKNFGAENPDPFVPVL 100
/FTId-VAR_010941.
                                                                                                                                                                                                                                                                                                                                                                                   in ext 2001 (Rei. 40, Greated)
16 ext-2001 (Rei. 40, East Sequence update)
16 ext-2001 (Rei. 40, Last annotation update)
                                                                                                        100.0%; Pred. ....
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PROSITE: PS50077; HEAT_REPEAT; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license (isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS I HEAT REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: AB049842: BAB16728.1: ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                 2144 AA: 242355 MW:
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                2013
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                                                                                                                Rest Local Similarity
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                2017
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                                                                                                                                                                                                                                                                                                                                                     BPZB MATFA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bininformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence analysis of the denome of the bacterium Mycoplasma pneumoniae.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fabret C., Quentin Y., Chapal N., Guiseppi A., Haiech J., Denizot F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacilus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL LIPOPROTEIN MPN097.
N-ACYL DIGLYCERIDE (POTENTIAL).
AD2FCB2B826B1E9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%, Score 8; DH 1; Length 541;
100.0%; Pred. No. 4.8;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                           16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MPN097 precursor (R02_orf541).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria: Firmicutes: Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCI-2001 (Rel. 40, Last annotation update)
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                                        541 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nurleic Acids Res. 24:4420-4449(1996),
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                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-AICC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative L-lactate permease YVFH.
                                                                                          16-OCI-2001 (Rel. 40, Crealed)
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SEQUENCE 541 AA, 59153 NW,
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                                                                                                                                                                                                                                                                                                                       Mycoplasmataceae, Mycoplasma.
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                                    STANDARD;
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541
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                                 YA97_MYCPN
P75595:
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P71067;
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Gendore version 4.5 Copyright (c) 1993 - 2000 Fompugen Etd

OM protein - protein search, using sw model

July 7, 2002, 16 06:08 ; Search time 30 19 Seconds

(without alignments) 257.788 Million cell updates/sec

: US-09-603-665-5_COPY_1594_1794

Perfect score: 201 Sequence, 1 LLPTETFIPVIRGLYGNPIP , , ISPYLEGILSQVIHLEKITS 201

Scoring table: OLIGO

Gapop 60.0 , Gapext b0.0

Searched: 105224 seqs, 38719550 residues

Word size : 6

Total number of hits satisfying chosen parameters: 514

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing. Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 1 1 1 1	March	Match Length	Di	ID	d :
100	49.8	2144	-4	BP28_HUMAN	homo sa
င္မ		958		BI 28_MACEA	വ്ഴദ്ന⊀4 സാദാദദ †കാടാ
œ	4.0	541	_	YA97_MYCPN	P75595 mycoplasma
30		563	-	YVFH_BACSU	_
7	3.5	132	Н	YBAW_ECOLI	P77712 escherichia
	3.5	215	-1	ROSB_BCOLI	P14374 escherichia
7	3.5	216	4	RCSB_SALTI	Q56127 salmonella
7	3.5	216	_	RCSH_SALTY	P58663 salmonella
7	3.5	217	7	Y172_ARCFU	030065 archaeoglob
7	3.5	218	-	THO1_YEASI	P40040 saccharomyc
7	Lin Oro	233		PHOU_2YMMO	Q9x5el :ymomonas
۲.	υ, υ,	270	Н	FPG_PASMU	P57910 pasteurella
7	3.5	311	-	PH86_YEAST	P46956 saccharomyc
7	3.5	320	-	HI.P.1 HUMAN	P54257 home sapien
7	3.5	354	_	GBA2_SCHPO	
7	3.5	385	_	YB01_MYCTU	U53449 mycobacter
7	3.5	425	-4	SYH_STREQ	P30053 streptococc
7	ج. ج.	449	٦	STPK_STPGP	
7	3.5	478	П	IFT1_HUMAN	
7	3.5	478	-	NRFA_ECOL!	P32050 escherichia
7	3.5	510	-	ENP1_P1G	Q9myu4 sus scrofa
7	3.5	579	-	HMDH_MA!2E	
7	ر ا		1	MUTA_POPG1	gse676 porphyromon
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7	3.5	883	_	CAPP_ECOL.1	P00864 escherichia
7	ς.	986	-	DSC1_MOUSE	P55849 mus musculu
7		1453	_	Y373_BOVIN	hos t
7	•	1539	Н	Y373_HUMAN	homo
7		4289	~	TENX_HUMAN	homo
9	3.0	52	_	RL40_TRYBB	P21899 trypanosoma
9	3.0	3.0	-	KL.40_1KYCK	P14795 trypanosoma

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### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai F., Oda T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wadalama M., Husoiri T., Kaku Y., Kadaiza H., Kanda H., Sugawara M., Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiquchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Naqahari K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGORNCE FROM N.A., AND VARIANTS S 1694; A-1854; D-1967 AND C-2017 Bougueletel L., Chumakov L., Barry C., Cohen-Akenine A.; An ovel BAP28 gene and protein."; An ovel BAP28 gene and protein."; Patent number wonlon669, 04-1AN-2001.
                                                                                                                                                                                                                                                                                                                                                                     Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metaloa, Chordata, Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2000) to the EMBL/GenBank/NUBJ databases.
-!- SIMILAPITY: RELOWS TO THE BAP28 FAMILY.
-!- SIMILAPITY: CONTAINS 1 HEAT REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2006) to the EMBL/GenBank/DDBJ databases.
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                                                                     | BP28_HUMAN | STANDARD; | PRT; | 2144 AA. | 69H583; | Q9M23; | 16-OCT-2001 (Rel. 40, Created) | 16-OCT-2001 (Rel. 40, Last sequence update) | 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
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Interpre; IPRO00357: HEAT_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1534-2144 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism.
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Search completed: July
Job time: 755 sec
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 LAALUKV 116
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                                                                                                                                                                                                                                                                                                                                                                                A;Gene: APE1292
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E88541
hypothetical protein ybaw [imported] - Escherichia coli (strain 0.157:H7, substrain EDL.93
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16 Feb-2001 Escquence_revision 16 Feb-2001 #text_change 14 Sep-2001
C;Acression: E85541
E:Perna, L.; Gioubert, E.J.; Davis, N.W.; L.M., A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                K:Blattner, F.K.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
.A.; Rose, D.J.; Mau, B.; Shao, Y
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                     A FITTE: The complete geneme sequence of Escherichia coli K-12.

A. Reference nomber: A64720: MUID:97426617

A. Reversalius: nuclear and sequence not shown: translation not shown

A. Molecule type: DNA

A. Residues: List HLDA

A. Residues: List HLDA

A. CLOSS-TOTO-CONCOS: GH:ABG00150: GH:U000966; NID:91786639; PIDN:AAC73546.1; PID:91786647;

A. Experimental Sequence: Strain K-12, Substrain M31655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross references: GB:AE005174; NID:412513305; PDDN:AAG54793.1; GSPDB:GN00145; UWGP:205
A:Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                      Cispecies: Escherichia coli
Cibate: 12-Sep-1997 #sequence_remision 17-sep-1997 #fext_change 24-Nov-1999
CiAccession: C64774
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                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:ITTLE: Genome sequence of enterohemorrhagic Escherichia coli 6157:H7.
A:Reference number: A85480; MUID:21074945; PMID:11205551
A:Accession: E85541
A:Status: pre-liminary
A:Molecule Type: DNA
A:Residues: 1-132 <SP$>
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C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 132;
                          U: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascene: ybaW
C:Supertamily: 15.5K protein (tolAB operon 5' region)
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Cisupertamily: 15.5K protein (todAP operom 5' region)
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  00.0%; Pred. No. 31;
                          Mismatches
                          3
                                                                                                                                                                                                                                                      Escherichia coli
                       7; Conservat ve
Best Local Similarity
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                                                                       188 GILSQVI 194
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                                                                                                                 44 CHISOVE 93
                                                                                                                                                                                                                                                   ybaw protein
                     Matches
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                                                                                                                                                                                                 RESULT
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A;Pesidues: 1/132 *KAM>
A;Cross-references: PPBJ:AP900033; NIB:g5101821, FTFN.BAA80283.1; PID:d1044069; PID:d
A;Experimental source: strain Ki
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M. submitted to the Protein Sequence Database, February 2000
A;Reference number: 224475
A;Accession: [47845]
C)Species: Aeropyrum pernix
C)Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change zo Aug 1999
C)Ancession: E72603
E;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kod-h, Y.; Jin no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kod-h, Y.; Vamazaki, J. DNA kes 6, 83-101, 1999
A;Altile: Complete genome sequence of an aerobic hypor-thormophilic Cremarchaeon, Acro A;Reference number: A72450; MUI):99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :
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C.Dute: 20-Apr-2000 #sequence_tevision 29 Apr 2009 #text_change 29 Apr 2000
C.Accession: T47845
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100.0%; Pred, No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: cultivar Columbia, BAC clone 1209 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T209.190 - Arabidopsis thaliana
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100.0%; Pred. No. 31;
tive 0; Mismatches
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A;Introns: 31/1; 50/3; 67/3; 89/3; 105/3; 115/3
A;Note: F209.190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Host Local Similarity Toury
7; Conservative
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2, 2002, 16:15:38

RESULT

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C;Species: Escherichia coli
C;Date, 18-Jui-2001 #sequence_revision 18 Jul 2001 #text_change 03 Aug 2001
C;Date, 18-Jui-2001 #sequence_revision 18 Jul 2001 #text_change 03 Aug 2001
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res: 8, 11-22, 2001
A;Title: Complete genome sequence of entetohomourhagic Escherichia coli 0157.H7 and g
A;Reference number. A99629; MgID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Species: Aeropyrum pernix
C;Date. 20.Aug 1999 #sequence_revision 20.Aug-1999 #text_change 20 Aug-1999
C,Accession: E72707
R;KawaraLayasi, Y., Hinc, Y.; Horikawa, H.; Yamacaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamacaki, J.
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of an aerobic hyper thermophilic Cremarchaesh, Aero
A;Reference number: A72450; MUID:99310339
A;Accession: E72707
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AyTitle: Mechanisms of Evolution in Rickettsia conorii and Pickettsia prowazokii.
A,Reference number: A97730; Mulb:21442074; PMID:11557893
A,Accession: E97706
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-72 -KBR>
A;Cresidues: 1-72 -KBR>
A;Cresiderches: GR:ARGO6914; P!DN:AA!Q2591-1; D!D+g15619089; GSPDH-GND0173
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Caps
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C:Superfamily: 15.5K protein (folAB operom 5' region)
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illarity 100.0%; Pred. No. 25;
Conservative 0; Mismatches
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100.0%; Pred. No. 18;
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Best Local Similarity 100.0%; Pred. No. 10,
Matches 7; Censervative 5; Mismatches
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C,Genetics:
A,Gene APR1076
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-105 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                                                                   A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 KUTALYT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PLPSVPR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 ROTALYT 35
                                                                                                                                                                                                                                                                                          A; Gene: RC0053
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C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #fext_change 30-Sep-2001
A.Accession: E97706
R.Ogata, H., Addic, S., Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rd
Science 294, 2094-2098, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kanoko, F.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A., Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
A;Tille: Complete Geomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number, AB1807, MUID:21595285, PMID:11759840
                                                                                                                                                                                                                                                                                                                      Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Sheu, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
cuss, D.; Nierman, W.C., White, O., Eisen, J.A., Salaberg, S.L., Flaser, C.M.; Vonter, J.
Nature 402, 761-768, 1999
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A.Note. Anabaena sp. (Strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C.Date: 14 Dec-2001 #sequence_revision 14-Dec-2001 #Fext_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aritle, Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. Asheerence number: A84420; MHTD:20083487
Asheession: C84747
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A)Cross-reterences: GB.BA000619, FIDN.BAB76799.L; PID:917134238; GSPDB;GN00179
A)Experimental source: strain PCC 7120
C)Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE002093; NID:g2459440; PIDN:AABB06/5.1; GSPDH:GNG0139
                                                                                                                                                                                             probable protein kinase [imported] · Arabidopsis thaliana
C;Species, Arabidopsis thaliana (mouse car cross)
C;Date. 02: Feb.2001 #sequence_revision 02:Feb.2001 #text_change 02 Feb.2001
C;Accession: C84747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%, Score 8; DB 2, 100.0%; Pred. No. 13; Live 0, Mismatches
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Best Local Similarity
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A:Residues: 1-664 <STO>
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567 KKKHGEEE 574
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                                     5 KKKEGEER 12
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C;Genetics:

Matches

6

A; Gene: all5100

RESULT E97706

qq

8; Conservative

Matches

62 KKKEGERE 49

77 KKKEGEEE 84

Local Similarity

Onery Match

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Asauthors: Sov. 249-250, 1997.

Asauthors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galicch, J.; Harwood, C. R.; Honaut, A.; Hilbert, H.; Holsappel, S.; Hosone, S.; Huile, M. Koetler, P.; Koningstein, G.; Knoph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laidudo, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, Y. M.; Gawa, K.; Galwara, A.; Gudega, B.; Park, S.H.; Parco, V.; Pohl, T.M.; Portere Rieger, M.; Rivolta, C.; Rucha, E.; Roche, H.; Rose, M.; Saddie, Y.; Sato, T.; Scand A, Authors. Schleich, S.; Schroezer, R.; Scoffone, F.; Scklaguchi, J.; Sckowska, A.; Schandarthors. Schleich, S.; Schroezer, R.; Scoffone, F.; Scklaguchi, J.; Sckowska, A.; Schandarthi, M.; Tamakoshi, A.; Tamaka, H.; Pamane, K.; Yasumoto, L.; Yasumoto, R.; Yasumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cydecession G8449

C. Theologis, A. Ecker, J.R., Palm, C.J., Federspiel, N.A., Kaul, S.; White, P.; Alon Chin, C.W.; Chura, M.R.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, anser, N.F.; Hughes, B.; Hulzar, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, anser, N.F.; Hughes, B.; Hulzar, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, A.B.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, A.B.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, B.; Klm, C.J.; Matthers; Hugher, J.C.; Chanter, J.C.; Khan, S.; Khaykin, B.; Klm, P.; Elzo, M.; Rocney, T.; Rowley, D.; Sakano, H.
A.A. Hu, G.H.; Conway, T.; Rowley, D.; Sakano, H.
A.A. Mu, Du, D.; Conway, C.; Fasher, J.C.; Davis, R.W.
A.H.; His Sequence and analysis of Chromosome I of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArResidues: 1-563 <KUN>
Arcross-references: GR-299121; GR-AL099126; NIU-92695827, FIDNERABIE424.1; FID.426499
ArExperimental source: strain 168
                                                                                                                                                                                                     B.Kinel, F.; ogasawara, N.; Moster, I.; Albertini, A.M.; Alloni, G.; Azevodo, V.; Her
C.; Broom, S.; Broudlett, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errinqton, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-606 -<3TO>
A;Cross-references: GB:AE005172; NID:g8920621; PIDN:AAF81343.1; GSFDH:GNC0141
C;Genetics:
L-lactate permease homolog yvfH - Bacillus subrilis
C,Species: Bacillus subtilis
C,Date. OS Dec 1997 #sequence_revision OS Dec 1997 #text_change 20-Jun-2000
C,Accession: A70038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species. Arabidopsis thaliana (mouse eat chess)
C.Date: 02-Mar_2001 #sequence_revision 02 Mar 2001 #foxt_char.c 09 Nov 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 4.0%, Score 8; D
Best Local Similarity 100.0%; Pred. No.
Matches 8; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F5D14.23 protein Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: L lactate permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 LLSALAAL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KKKEGEEE 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: G86449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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C.Species: Mycoplasma preumoniae
A.VATIETY: AICC 29342
C.Date: 26.Feb-1997 Rasquence_revision 25.Apr-1997 #text_change 07 Dec 1999
C.Accession: S73484
R.Himmelreich, R.: Hilbert, H.) Plaqens, H.: Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A.Fithler Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A.Reference number: 873484
A.Accession: 873484
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Aptross references: EMBL:AF000007; GR:U000089; NID:q1673704; PIDN:AAB95705.1; PID:q167370
A;Note: the nucleotide sequence was submitted to the PMBL Data Library, Nevember 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GH: AEOC1883; GH: AEO00513; NID: 45457878; PIDN: AAF09801.1; PID: 4645788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RjWhite, G.; Eisen, J.A.; Feidelberg, J.F.; Hickey, F.K.; Peterson, J.D.; Dodson, P. M.; Shen, M.; Vandarhevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. Science 286, 1571-1577, 1969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Litle: denome Segarnée of the radioresistant bacterium incinocuçus radiodurans Pl. A; Meterence number: A75250; MJD:20036896
A: Meterence number: B7546
A: Mataus: preliminary
A: Malecule type: DNA
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A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BySoluetical protein Defronces radiodurans (strain Pl)
Cisperies. Definocoreus radiodurans
Cisperies. Definocoreus radiodurans
Cisperies. Definocoreus radiodurans
Cistate: Usinec-1999 Esequeice_revision 03 Dec 1999 #text_change 31 Mar 2000
Citate: Usinec-1999 Esequeice_revision 03 Dec 1999 #text_change 31 Mar 2000
Citate: Usinec-1999 Esequeice_revision 03 Dec 1999 #text_change 31 Dec 1900
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100.0%; Pred. No. 11;
ive 0; Mismatches 0; Indels
                         Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 123,
                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8, DH 2,
Pred, No. 2.8;
               Score 8; DB 1;
Pred. No. 2.8;
               4.0%; Score 8; DB 1
100.0%; Pred. No. 2.8
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. ....
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A; Experimental source: strain R1

A: Map position: 1 Ardene: DR0207

A.Residues: 1 123 · WHI.

8; Conservative

164 LESALAAL 171

5 11.SALAAL 12

RESULT

Best Local Similarity

Matches

Onery Match

Best Local Similarity 100.9Matches 8: Conservative

Query Match

A;Genetic code: SGC3

Coenetics:

169 AALUKVVE 176

50 AALOKVVE 57

RESULT

```
GenCore version 4.5
Copyright (F) 1993 - 2001 - Chapugen Ltd
```

protein search, using sw model eM protein

July 2, 2002, 16.03:03; Search time 57.09 Seconds

Kun on:

(without alignments) 338.307 Million cell updates/sec

US 09:603:665 5\_COPY\_1594\_1794

ISPYLEGIUSEV; RURKITS 201 1 LIPTETFIPVIRGINGNPLP... Perfect score. Sequence.

Gapop 60 0 , Gapext 60.0 OFIGO Scoring table:

283138 seqs, 96089334 residues Searched:

Word size :

1351 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR\_71:\* Database :

pir1:\* pir2:\* pir4:\* Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | hypothetical prote | hypothetical prote | hypothetical prote | probable lipoprote | L-lactate permease | +5D14.23 protein - | probable protein k | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | ybaw protein Esc | hypothetical prote | hypothetical prote | _      | hypothetical prote | hypothetical prote | hypothetical prote | interleukin-10 pre | hypothetical prote | extensin-like cell |          | colanic acid biesy | hypothetical prote |            | colanic acid biosy | hypothetical prote | -       | hypothetical prote |
|-----------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|------------|--------------------|--------------------|---------|--------------------|
| SUMMARIES | 911            | B75029             | G71214             | B75546             | 573383             | A70038             | 1386449            | C84747             | AD2443             | E9770A             | 1.72707            | A90691             | C64774           | E85541             | E72503             | 14/845 | H72610             | HB1840             | C81100             | JN0475             | 136827             | T10/3/             | 709854   | RVECCH             | D85891             | AC0790     | B91017             | D69271             | Ar.0149 | S50566             |
|           | D. H.          | a                  | 7                  | C‡                 | 7                  | 7                  | 7                  | ~                  | ೧೩                 | C+                 | ~1                 | C1                 | C1               | C 3                | C1                 | 7      | 7                  | -1                 | 20 <b>4</b>        | ?                  | C1                 | CI                 |          |                    | C↑                 | 2.4        | ~1                 | C1                 | c-1     | CI.                |
|           | Length         | 108                | 123                | 123                | 541                | 563                | e û û              | 664                | 1906               | 7.3                | 105                | 132                | 132              | 132                | 132                | 138    | 143                | 146                | 146                | 178                | 180                | 214                | 214      | 216                | 216                | 917        | 316                | 217                | 217     | 218                |
| æ         | Query<br>Match | 4.0                | 4.0                | 4.0                | 4.0                | 4.0                | 4.0                | 4.0                | 0.4                | .e.                | 3.5                | 3.5                | 3.5              | 3.5                | 3.5                | 3.5    | •                  | 3.5                | 3.5                |                    | 3.5                |                    | 3.5      | 3.5                |                    | ξ.)<br>Γ., |                    | 3.5                |         | 3.5                |
|           | Score          | œ                  | æ                  | æ                  | 80                 | œ                  | œ                  | œ                  | æ                  | 7                  | 7                  | 7                  | 7                | 7                  | 7                  | 7      | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7        | Ĺ                  | Ĺ                  | ۲.         | ,                  | 7                  | 7       | 7                  |
|           | Result<br>No.  |                    | a                  | 8                  | 4                  | ſ                  | 9                  | 7                  | 8                  | 6                  | 10                 | 11                 | C                | 13                 | 14                 | 15     | 16                 | 1.7                | 18                 | 19                 | 0.7                | 21                 | CI<br>CI | í.                 | 57                 | uh<br>na   | ទំព                | 27                 | 3B C1   | 62                 |

|         | 3.5 240 2 F82790 CMP synthase XPOP6 | 7 T20258 hypotherical | 2 F90102 | 3.5 303 2 T36509 probable molybdopt | 3.5 306 2 G97457 hypothetical prote | 2 AH2675 | 3 5 311 2 \$56898 PHORE protein 1 ye | 3.5 317 2 S67493 huntingtin-associa | 8.5 320 2 872555 huntingtin-associa | 3.5 324 2 G98326 c4-dicarboxylate-b | 3.5 324 2 AC2956 hypothetical prote | 2 C83264 hypothetical | 3.5 330 2 851426 hypothetical prote | 3.5 330 2 T35360 probable membrane | 3.5 336 2 690421 |
|---------|-------------------------------------|-----------------------|----------|-------------------------------------|-------------------------------------|----------|--------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-----------------------|-------------------------------------|------------------------------------|------------------|
| ~~~~~~~ | W                                   | ) !~<br>) R           | 3.5      | 3.5                                 | 3.5                                 | 3.5      | د.<br>ت_                             | 3.5                                 | £.5                                 | 3.5                                 | 3.5                                 | 3.5                   | .5                                  | 3.5                                | 3,5              |
|         |                                     | , _                   | 7        | 7                                   | 7                                   | 7        | 7                                    | 7                                   | ./.                                 | 7                                   | 7                                   | 7                     | 7                                   | 7                                  | 7                |

### AL I GNMENTS

|   | RESULT 1<br>B/5029                                                                     |
|---|----------------------------------------------------------------------------------------|
|   | hypothetical protein PAB1179 - Pyrococcus abyssi (strain Orsay)                        |
|   | C;Species: Pyrococcus abyssi                                                           |
|   | C.foate10.Aug.1347 #Srquence_revision_26.Aug.1999 #fextPang28_200.2000                 |
| _ | C; Accession: B75029                                                                   |
|   | R;anonymous, Genoscope                                                                 |
|   | submitted to the EMBL Data Library, July 1999                                          |
|   | Appropription: Pyrococcus abyssi genome sequence, insights into archaeal chromosome s  |
|   | A, Reference number, A75001                                                            |
|   | A,Andession: R75029                                                                    |
|   | A;Status: preliminary                                                                  |
|   | A; Molecule type: DNA                                                                  |
|   | A;Residues: 1 108 kKAW>                                                                |
|   | A, Cross references: CR:AJ248288; CR:AI006836; NIP:G5458960; PIDN:GAR-0672 1: PID:G545 |
|   | A; Experimental source: strain Orsay                                                   |
|   | C.Genetics:                                                                            |

A)Gene: PAB1179 C,Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0223

0 Gaps ... 4.0%; Score 8: DH 2; Length 108; 100.0%; Pred. No. 2.5; olive 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches

62 KKKEGEEE 69 Š qq

RESULT

hypothetical protein PH1983 · Pyresoccus borikoshii

C,Species: Pyrococcus horikoshii C,Datu. 10-Sepi1999 #sequence\_revision 10-Sepi1999 #revt\_change 21 ml 2000

C;Accession: G71214

P.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hoikawa, Y.; Hino, Y.; Yamamoto, S.; Se M., Ohfuku, Y.; Fundhashi, F.; Tanaku, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oqu DNA Pos. S. 55-76, 1998
A.Filler Complete sequence and gene organization of the gene of a hyper thermophili A. Reference number A71000: MUID-98344137
A. Reference number A71014
A. Stafus: preliminary; nucleic acid sequence not shown: translation not shown

A,Molecule Lype: DNA A, Rosiducs: 1 123 - XAMY-A,Crosiducs: 1 123 - XAMY-A,Crosiduction of the control of the

AjGene: PH1983 CjSuperfamily - Methangepreus jannaschii sonservod hypothotica! protein M40223

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 3.0%; Score 6; DB 4; Length 46; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 6; Conservative 0, Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                              NAME/KEY: Other
LOGATION: 1...1
CTHER INFORMATION: Residue 1 methoxy pegylated
NAME/KEY: Other
LOGATION: 22...22
CTHER INFORMATION: Disulfide linkage to SEQ ID NO: 7
US-09-391-799-8
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
HEBERNACTOCKER NUMHER: P31169
TELECOMMUNICATION INFORMATION:
TELEPRA: 610-270-5096
TELEPRA: 610-270-5090
                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 46 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 KTIVTR 47
|||||||
|2 KTIVTR 17
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Search completed: July 2, 2002, 16:03:57 Job time: 54 sec

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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Biologically Active Peptide TITLE OF INVENTION: Fragments of Ob Protein NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
SOFTWARE: FESTEM: DOS
SOFTWARE: FESTEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/A9/291,799
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: PESSEED FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
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709 Swedeland Read
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Patent No. 6187751
                                                                                                                                                                                                                        33,833
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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IBM Compatible
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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APPLICANI: Beeley, Lee
                                                                                                                                                                                                                                                                             610-270-5096
                                                                                                                                                                                                                                                                                                                                                                          46 amino acids
                                                                                                                                                                                                      Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                             TELEPHONE: 610-270-509
TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                         SS: single
linear
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                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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NAME/KEY: Other
CCCATION: 22..."
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                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                            CLASSIFICATION: 514
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; OTHER INFORMATION:
US-09-391-799-5
                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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||2 KTIVTR ||7
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                                                                                                                                                                 FILING DATE:
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                                                                                                                                       APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houdston, Raymond L.
IIIILE OF INVENTION: COMPOUNDS AND METHODS FOR THE PETECTION AND PREVENTION OF I
CORRESPONDENCES: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3C
                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fiith Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Smith, Richard
APPLICANT: Beeley, Lee
IIILE OF INVENITION: BLOIGHIGALLY ACTIVE PERTIDE
IIILE OF INVENITION: Broadments of Ob Protein
NUMBER OF SEGUENCES: 3
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100.0%; Pred. No. 85;
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King of Prussia
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Tob.0%: Pred. No. .
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TELECOMMUNICATION INFORMATION:
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                                                                    Sequence 66, Application US/08557309B
Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application U3/89391799
Patent No. 6187751
                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRALION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
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Matches 6; Conservative
                                                                                                                            Reed, Steven G.
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Washington
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US-08-557-3098-66
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                                                                                                          GENERAL INFORMATION:
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                               RESULT 13
08:08-557-3098-66
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Gaps

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STATE: NEW JERSEY
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AIDPESSEY: MAMY A APPOLLINA - MERCK & CO., INC.
STREET, 126 EAST LINCOLN AVENUE - F O BOX 2000
                                                                                           APPLICANT: Smith, Richard
APPLICANT: Bealey, Lee
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Pragments of Ob Protein
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                        SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/391,799
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APPLICANT: CASCIERL, MARGARET A.
APPLICANT: MACINITYRE, EUAN
APPLICANT: MACINITYRE, EUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7, Application US/08961749
; Patent No. 5908830
                                      // Sequence 1, Application HS/09391799
// Patent No. 6187751
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                                                                                                                                                                                                                                                                                                                                   Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Baumeister, Kirk
REGISTRATION NUMBER: 3
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                 NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
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                       US-09-391-799-1
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APPLICANT: Barney, Shawn
APPLICANT: Harney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Euranam, Kasturi
APPLICANT: Matt. Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DISCHOSING
TITLE OF INVENTION: CELL DEATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                     SOPTWAPE. Patentin Pelease #1 0, Version #1 30 CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Srore 6, DB 4;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3 0%, Score 6, DB 2, Best Local Similarity 100.0%; Pred. No. 53, Matches 6, Conservative 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.0%, Score 6, DB 4 Best Local Similarity 100.0%; Pred. No. 80; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENTE. 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASLENG FOR WINDOWS VERSION 4.0
                                                                                                                                                                           US/08/961,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 281, Application US/09461697
; Patent No. 6277974
                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE, TON NUMBER: 19822
TELEPHONE: (732) 544-3462
TELEPHONE: (732) 544-3462
TELERAX: (732) 544-3462
TELERAX: (732) 544-3462
                                                                                    IBM PC compatible
                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                        CLASSIFICATION: 514
                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                  07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 LQKVVE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LOKVVE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 KTIVTR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 KTIVTR 20
                                                                    MEDIUM TYPE:
                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-461-697-281
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                                                                                         COMPITER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-961-749-7
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TITLE OF INVENTION: MUTANT PHOSPHOFNOLPYRUVATE CARBOXYLASE,
TITLE OF INVENTION: ITS GENE, AND PROJUCTION METHOD OF AMINO ACID
NUMBER OF SEQUENCES: IS
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C
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ADDRESSEE: P.C.
                                                                                                                                                                            Length 883;
                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/967,104
                                                                                                                                                                        3.5%; Score 7; DB 2; Ler
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                              Ouery Match
Hest toral Similarity 100.0%; Pred. No. 1.74
Metches 7; Conservative 0; Mismatches
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PRIOR APPLICATION NORBER: US 08/596, 466
FILING DATE: 29-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 5 269775
FILING DAFE: 24 AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 5-209776
FILING DATE: Z4-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08967104
Patent No. 5919694
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUGIMOTO, Masakazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELEEAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUZUKI, Tomoko
MATSUI, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE, TOWNET NUMBER -
                                       : 883 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883 amino acids
                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: OBLON, NORMAN F.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : MOLEGULE TYPE: protein US-08-967-104-2
                                                                                              : MOLEGULE TYPE: protein as 08 596-466-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM FYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear
                                                                              Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                    170 ALQKVVE 176
                                                                                                                                                                                                                                                                                       737 ALUKVVE 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                           POPULOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     US-08-967-104-2
                                       L.F.N.C.T.H.:
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STATE:
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0
                     Length 883;
                                                        0; Indels
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3.0%, Score 6; DH 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: Uses
                  3.5%; Score 7; DH 2; Ler 100.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/159,339A
29-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/926,666
FILLING IATE: 07-ANG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US (08/103, 396 FILLING DATE: 06-AUG-199.)
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     Sequence 312, Application US/08159339A, Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIF, 94111-3834
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Diskettu
Ouery Match
Best Local Similarity
7, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                  170 ALQKVVE 176
                                                                                                                                      737 ALQKVVE 743
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                                                                                                                                                                                                   RESULT 9
US-08-159-339A-312
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DB 1; Length 315;
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/770,035
 3.5%; Score 7, DB 1;
100.0%; Pred. No. 69;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                          APPLICANT, Pasamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                              1. Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-556-419-25
; Sequence 25, Application US/08556419C
; Patent No. 6093549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER- 07/729,099
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ...,
100 0%; Pre
                                                                                                                                                                                                   ; Sequence 1, Application US/08770035; Patent No. 6008342
                                                                                                                                                                                                                                                       APPLICANT: Binger, Mary-Helen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Roseman, Catherine R
RECISTRATION NUMBER: 34,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT Ross, Christopher
APPLICANT: Li, Xiao-Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Hest Local Similarity Tures
Lea 7; Conservative
                   Best Local Similarity 100. Matches 7, Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
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STREET: A...
""Y: Nutley
                                                                        164 LLSALAA 170
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56 LLSALAA 62
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                                                                                                                                                                                US-08-770-035-1
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 Query Match
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Gaps
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11S GENE, AND PRODUCTION METHOD OF AMINO ACID: 12
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                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 7; DB 3; Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentln Release #1.0, Version #1.30
                                                     APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107,52271
CURRENT APPLICATION NUMBER: US/08/556,419C
CURRENT PILING DATE: 1995-11-09
NUMBER OF SEQ 1D NOS: 25
                                                                                                                                                                                                                                                                                                                                                                      Best Loral Similarity 100.0%; Pred. No. 723
Matches 7, Conservative 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10-784-0 PCT TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11S/08/596,366
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APPLICATION NOW!
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 5-209776
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-153876
FILING DATE: 05-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08596366; Patent No. 5876983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SUGIMOTO, Masakazu
APPLICANT: SUZUKI, Tomoko
APPLICANT: MATSUI, Hiroshi
APPLICANT: 120I, Katsura
ITLE OF INVENTION: MITANT PHO
ITLE OF INVENTION: 115 GENE,
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: (703) 413 2220
248855 OPAT UR
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                                     APPLICANT: Lanahan, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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ADDRESSEE: OBLON, SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES;
APPLICANT: Li, Shi-Hua
APPLICANT: Sharp, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRGINIA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VTSTLEA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 VTSTLEA 313
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                                                                                                                                                                                                                                                                                               US-08-556-419-25
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                                                                                                                                                                                                               SEQ ID NO 25
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/729,099
FILING DATE: 19910712
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pasamontes, Luis
FITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOLLMann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                        1122990831
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 15-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              APPELICATION NUMBER: US/08/217,327
Filling date:
                                                                                                                                                MEDIUM IYPE: Floppy disk
COMPUTER: HM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07729099 Patent No. 5403581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34.240
REFERENCE/DOCKET NUMBER: 8514
                ADDRESSEE: Quarles and Brady STREET: P.O. BOX 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKESSEE: HOLIMann ... ADDRESSEE: HOLIMann ... CTMPET: 340 Kingsland Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Binger, Mary-Helen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPACTABLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J
PEGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . MOLEGULE TYPE: protein
US-08-217-327-4
CORRESPONDENCE ADDRESS:
                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                      4.35
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CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                            54701-2113
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                        Madison
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                                                                                            USA
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                                                                            SIATE: WI
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US-07-729-099-1
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH
                                                      C11Y:
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Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTWM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Passamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..or.
...eR: US/UB/257,392
09-JUN-1994
N: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729,099
FILING DATE: 12-UU-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Hoffmann La Foche Inc.
340 Kingsland Street
                                                                                                                                                                                                                  ) ORGANISM: Elmeria tenella
) DEVELOPMENTAL STAGE: merozolte
HS 07 729-099-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08257392
Patent No. 5688513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
TELEPHONE: (201) 235-5208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
IENGTH: 315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Eimeria tenel.a
DEVELOPMENTAL STAGE: metol
                                                                                    : 315 amino acids
AMINO ACID
                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                             TOPOLOGY: linear
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| 4.5         | Computation |
| version 4.5 | - 2000      |
| GenCore     | (c) 1993    |
|             | Copyright.  |

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Title: Perfect score:

Sequence:

Scoring table:

Gapop 60 0 , Gapext 60 0

231628 scqs, 24425594 residues Scarched:

Word size :

387 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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/cgn2\_6/ptodata/2/iaa/ftt.coMB prp.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Length DB ID  829 4 US 69-413-814-105  214 1 US 08-217-327 4  315 1 US-07-29 099 1  315 1 US-08-257-392 1  315 3 US-08-257-392 1  315 3 US-08-556-419-25  883 2 US-08-556-419-25  883 2 US-08-957-104 2  10 3 US-08-957-104 2  10 3 US-08-957-394-312  20 2 US-08-957-394-312  46 4 US-09-391-799-8  46 4 US-09-391-799-8  48 3 US-08-488-214A-23  48 3 US-08-488-214A-23  48 3 US-08-488-214A-23  48 3 US-08-488-214A-23  48 4 US-08-488-21A-23  48 3 US-08-488-21A-23  48 4 US-08-488-21A-23  48 4 US-08-488-21A-23  48 1 US-08-488-21A-23  49 1 US-08-488-21A-23  71 4 US-08-488-22-A-23  63 5 ECT-US-08-56-07820  72 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     |     | *<br>Ouery         |        |           |                    |                   |
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| 829 4 US 09-413-814-105 315 1 US-07-229 092 1 315 1 US-07-229 092 1 315 1 US-07-229 092 1 315 3 US-08-257-392 1 315 3 US-08-556-419-25 883 2 US-08-556-419-25 883 2 US-08-159-39A-312 10 4 US-07-391-79-3 2 US-08-159-39A-312 34 2 US-08-159-39A-312 35 2 US-08-159-39A-312 36 4 US-08-341-799-8 46 4 US-08-341-799-8 47 US-08-341-799-8 48 3 US-08-488-214A-23 48 4 US-08-488-214A-23 49 US-08-483-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Scc | ore | Match              | Length | DE        | QI                 | Description       |
| 214 1 US 08-217-327 4 315 1 US-08-257-392 1 315 3 US-08-257-392 1 315 3 US-08-557-492 1 318 3 US-08-556-419-25 883 2 US-08-565-356-2 883 2 US-08-967-104 2 10 4 US-08-1947-104 2 20 2 US-08-197-9-1 32 4 US-08-391-799-8 46 4 US-08-391-799-8 48 3 US-08-391-799-8 48 3 US-08-391-799-8 48 3 US-08-381-298-8 48 4 US-08-381-298-8 48 4 US-08-381-298-8 48 4 US-08-381-298-8 48 4 US-08-488-2176-23 49 4 US-08-488-2176-8 79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     | œ   | 0.4                | 829    | 4         | .413-814           | Sequence 105, App |
| 315 1 US-08-27-192 1 315 3 US-08-27-192 1 315 3 US-08-27-192 1 318 3 US-08-556-419-25 883 2 US-08-556-419-25 883 2 US-08-556-2 883 2 US-08-956-104 2 US-08-159-339A-312 10 3 US-08-159-339A-312 2 US-08-159-339A-312 3 US-08-159-339A-312 4 US-08-159-339A-312 4 US-08-159-339A-312 4 US-08-159-339A-312 4 US-08-159-339A-313 4 US-08-159-339A-313 4 US-08-317-759-8 4 US-08-317-759-8 4 US-08-317-759-8 4 US-08-317-759-8 4 US-08-318-213A-23 4 US-08-318-213A-23 4 US-08-318-213A-23 4 US-08-318-213A-23 4 US-08-318-213A-23 4 US-08-318-313A-23 5 US-08-483-213A-23 79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     | 7   | u':<br>(*:         | 23.4   | ۲.        | 08-217-            | 4, Ap             |
| 315 1 US-08-257-392 1 331 3 US-08-70-035-1 331 3 US-08-70-035-1 883 2 US-08-76-10-25 883 2 US-08-956-419-25 883 2 US-08-95-7-10-4 10 3 US-08-95-7-10-4 18 4 US-08-91-7-394-312 2 US-08-91-7-394-312 34 2 US-08-91-7-39-7 48 3 US-08-857-3098-66 48 4 US-09-857-3098-66 48 4 US-09-857-3098-66 48 4 US-09-857-3098-66 48 4 US-08-888-214A-23 48 4 US-08-488-214A-23 49 1 US-08-488-214A-23 79 2 US-08-488-214A-49 75 4 US-08-483-21A-23 79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     | 7   | 3.5                | 315    | _         | -07-729            | _                 |
| 315 3 US-08-770-035-1 3 US-08-56-419-25 883 2 US-08-56-419-25 883 2 US-08-56-419-25 10 4 US-08-196-104-2 10 7 US-08-197-104-2 10 7 US-08-197-104-2 10 7 US-08-197-104-2 10 7 US-08-197-104-2 10 7 US-08-197-29-8 10 8-08-197-29-8 10 8-08-198-214A-23 10 8-08-488-214A-23 10 US-08-488-214A-23 10 US-08-488-214A-23 10 US-08-488-214A-23 10 US-08-488-214A-23 10 US-08-488-214A-23 10 US-08-488-211A-23 10 US-08-488-227-4 10 US-08-488-207-4 10 US-08-488-227-4 10 US-08-488-207-4 10 US-08-488-207-4 10 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |     | 7   | 3.5                | 315    |           | -08-257-           | ٦,                |
| 331 3 US-08-556-419-25<br>883 2 US-08-596-36-2<br>883 2 US-08-596-36-2<br>883 2 US-08-596-36-2<br>10 3 US-08-391-104-1<br>20 2 US-08-31-29-1<br>32 4 US-08-31-290-6<br>44 4 US-08-31-799-8<br>46 4 US-09-391-799-8<br>47 4 US-08-345-309-66<br>48 3 US-08-345-347-23<br>48 3 US-08-348-214A-23<br>48 4 US-08-348-214A-23<br>48 4 US-08-38-38-38<br>48 4 US-08-38-38-38<br>48 4 US-08-38-38-38<br>48 4 US-08-38-38-38<br>48 4 US-08-488-214A-23<br>48 4 US-08-38-38-38<br>53 US-08-488-214A-23<br>54 US-08-488-214A-23<br>55 US-08-488-214A-23<br>56 US-08-488-214A-23<br>57 US-08-488-214A-23<br>58 US-08-488-214A-23<br>59 US-08-488-214A-23<br>50 US-08-488-214A-23 |     | 7   | 3.5                | 315    | e         | - 80-              | 1,                |
| 883 2 US-08-596 166-2<br>883 2 US-08-967-104 2<br>10 3 US-08-967-104 2<br>18 4 US-08-919-7394-312<br>20 4 US-08-191-7394-312<br>34 2 US-08-191-799-8<br>46 4 US-09-391-799-8<br>48 2 US-08-371-799-8<br>48 3 US-08-385-942A-23<br>48 4 US-08-488-214A-23<br>48 4 US-08-488-214A-23<br>50 US-08-488-214A-23<br>79 2 US-08-488-401-6<br>79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     | 7   | 3,5                | 331    | ~         | - 80-              | 25                |
| 883 2 US-08-967-104 2 10 4 IIS-09-339A-312 18 4 IIS-09-339A-312 20 7 IIS-09-4391-799-1 34 2 US-08-15-73098-66 46 4 US-09-391-799-8 48 3 US-08-487-563A-23 48 3 US-08-487-563A-23 48 4 US-08-488-214A-23 48 4 US-08-488-214A-23 49 1 US-08-488-214A-23 49 1 US-08-488-214A-23 49 1 US-08-488-214A-23 49 1 US-08-488-20-8 73 US-08-488-20-8 73 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     | 7   | 3.5                | 883    | CI        | -08-596            | ci                |
| 10 3 US-08-159-339A-312<br>20 2 US-08-391-391-391-391-391-391-392 4 US-08-557-3098-66<br>46 4 US-08-557-3098-66<br>46 4 US-08-391-799-8<br>46 4 US-08-391-799-8<br>48 3 US-08-391-799-8<br>48 3 US-08-488-34A-23<br>48 3 US-08-488-31AA-23<br>48 4 US-08-488-21AA-23<br>48 4 US-08-488-21AA-23<br>48 4 US-08-488-21AA-23<br>48 4 US-08-488-21A-23<br>48 4 US-08-488-21A-23<br>48 4 US-08-488-21A-23<br>48 4 US-08-488-21A-23<br>48 4 US-08-488-21A-23<br>59 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | 7   | 3.5                | 883    | -1        | -198-80-           | ci.               |
| 18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     | ¢,  | 3.0                | 10     | ٣,        | -159-339A-31       | 312               |
| 20 2 RS 08 961 749-7 34 2 US-00-461 697-281 34 2 US-00-461 697-281 46 4 US-09-391-799-8 46 4 US-09-391-799-8 48 3 US-08-485-942A-23 48 4 US-08-488-942A-23 49 4 US-08-488-21A-23 49 4 US-08-483-211A-23 49 4 US-08-488-22-A-23 49 4 US-08-488-22-A-23 49 4 US-08-488-23-A-23 49 4 US-08-488-23-A-23 49 4 US-08-488-23-A-23 49 4 US-08-488-23-A-23 59 2 US-08-48-411-6 79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     | 9   | 3.0                | æ.     | 4         | - 1                | Έ,                |
| 32 4 08 09 461 697 281<br>34 4 08 -857 3098 -66<br>46 4 08 -897 3098 -66<br>46 4 08 -08 -391 799 -8<br>48 3 08 -08 -347 563 A 23<br>48 3 08 -08 -348 5942 A -23<br>48 4 08 -08 -488 5942 A -23<br>48 4 08 -08 -488 5942 A -23<br>48 4 08 -08 -488 212 A 23<br>48 4 08 -08 -488 223 A 23<br>48 4 08 -08 -488 223 A 23<br>59 5 08 -08 -88 -88 -88 -88<br>63 5 62 -68 -88 -88 -88 -88 -88 -88 -88 -88 -88                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     | v   | C ~                | 20     | 2         | 08 961             | , ,               |
| 34 2 US-08-557-3098-66 46 4 US-09-391-799-8 48 2 US-08-347-553A-23 48 3 US-08-488-214A-23 48 4 US-08-488-21A-23 48 4 US-08-488-21A-23 5 PCZ-0S9-466-583-8 63 5 PCZ-0S95-07820-8 73 4 US-08-884-88-8 73 2 US-08-884-88-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |     | œ   | ∪ . <del>.</del> . | 32     | 4         | 09-461             | 60                |
| 46 A US-09-391-799-8<br>48 2 US-08-347-563A 23<br>48 3 US-08-485-942A-23<br>48 4 US-08-485-942A-23<br>48 4 US-08-485-942A-23<br>48 4 US-08-483-214A-23<br>49 4 US-08-483-213A-23<br>48 4 US-08-483-213A-23<br>48 4 US-08-483-213A-23<br>63 5 PCT-US-08-68<br>63 5 PCT-US-08-46-581-8<br>73 4 US-08-485-709-8<br>73 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     | و   | 3.0                | 34     | 7         | -08-557-           |                   |
| 46 4 US-09-391-799-8<br>48 2 US-08-347-563A 23<br>48 3 US-08-485-942A-23<br>48 4 US-08-488-214A-23<br>48 4 US-08-488-214A-23<br>48 4 US-08-488-213A 23<br>48 4 US-08-483-213A 23<br>48 4 US-08-483-213A 23<br>53 5 PCT-0895-0780-8<br>73 4 US-08-839-709-3<br>79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |     | 9   | 3.0                | 46     | 4         | 09-391             |                   |
| 48 2 US-08-347-563A 23<br>48 3 US-08-488-242A-23<br>48 4 US-08-488-214A-23<br>48 4 US-08-488-204A-23<br>49 4 US-98-488-204A-23<br>49 4 US-98-488-204A-23<br>63 5 PCT-US95-07820-8<br>63 5 PCT-US95-07820-8<br>73 4 US-08-454-404<br>75 2 US-08-839-709-3<br>79 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     | 9   | 3.0                | 46     | 4         | US-09-391-799-8    | 8                 |
| 48 3 US-08-485-942A-23<br>48 4 US-08-488-214A-23<br>48 4 US-08-488-214A-23<br>49 4 US-08-483-217A-23<br>48 4 US-08-483-217A-23<br>63 5 US-08-48-23A-8<br>63 5 PCT-0895-07820-8<br>73 4 US-08-88-404<br>75 2 US-08-839-709-3<br>79 2 US-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |     | 9   | 3.0                | *      | <u>~1</u> | 90                 | 23,               |
| 48 4 105-08-488-214A-23<br>49 4 105-08-408-234<br>49 4 05-08-103-23<br>48 4 05-08-103-23-4<br>53 5 68-498-8<br>63 5 FCT-0595-078-0-8<br>73 4 05-08-858-8<br>73 4 05-08-858-8<br>79 2 05-08-839-709-3<br>79 2 05-08-839-709-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     | 9   | 3.0                | 4      | m         | US-08-485-942A-23  | 23,               |
| 48 4 15:08-488-208A-23<br>48 4 15:08-48; 21:A 23<br>48 4 15:08-48; 22:A 23<br>63 2 15:08-466-583-8<br>63 5 FCT-0595-07800-8<br>73 4 18:08-858-207-409<br>75 2 05:08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     | ٥   | 3.0                | 48     | ~         | 214A-              | 23,               |
| 48 4 US-98-483-217A-23<br>43 2 US-98-466-583-8<br>63 5 PCT-6295-07820-8<br>73 4 US-08-85-07820-8<br>74 4 US-08-85-4401-5<br>79 2 US-98-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     | 9   | 3.0                | 48     | ~         | -488-208A-         | 23,               |
| 48 4 1 12 08 - 488 - 223 A 23<br>63 2 105 - 08 - 466 - 583 - 8<br>63 5 PCT - USSS - 078 0 - 8<br>73 4 105 - 08 - 858 - 20 A 40 9<br>75 2 05 08 839 709 - 3<br>79 2 05 08 - 839 - 709 - 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     | اي  | 3 0                | a t    | 4         | 08-483             | 23,               |
| 63 2 18-08-466-583-8<br>63 5 18-27-0835-078:0-8<br>73 4 118-08-8-8-401-7<br>75 4 118-08-8-8-401-5<br>79 2 05 08 839-709-3<br>79 2 05-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     | 4   | 0<br>د             | α ∵    | ς:        | 08 - 488 -         | 23,               |
| 63 5 PCT-US95-07820-8<br>73 4 IS-08-858-207A-409<br>75 4 IS-08-688-800-5<br>79 2 US-08-839-709-4<br>79 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     | 9   | 3.0                | 63     | ?         | 115-08-466-583-8   | 8, 4              |
| 73 4 IIS-08 - 858-201/A-409<br>74 4 IIS-08-08-08-400-5<br>79 2 US-08-839-709-3<br>79 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     | ç   | 3.0                | 63     | S         | PCT-US95-07820-8   | œ                 |
| 75 4 HS-09-60-6<br>79 2 US 08 839 709-3<br>79 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     | ç   | 3.0                | 1 +    | 4         | US-08-858-2010-409 | 409               |
| 79 2 US 08 839 709-3<br>79 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     | 9   | 3.0                | 72     | 4         | US-08-909-480-8    |                   |
| 2 US-08-839-709-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |     | ø   | 3.0                | 19     | C 1       | . 618 80           | ~                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     | 9   | 3.0                | 79     | ~1        | -08                | 4                 |

| -3 Sequence 3.  | -4 Sequence 4   | -32 Sequence 32, App. | Sequence      |                 |               |                 |                |               |               | (14       | Sequence        |                |               | Sequence      |                   | Sequence         |                 |
|-----------------|-----------------|-----------------------|---------------|-----------------|---------------|-----------------|----------------|---------------|---------------|-----------|-----------------|----------------|---------------|---------------|-------------------|------------------|-----------------|
| US-09-204-859-3 | US-09 204-859-4 | US-08-965-762         | US-08-398-021 | US-08-383-631-1 | US-08-383-639 | US-08-384-183-1 | EDS 1557 80-80 | US-08-834-306 | US-08-993-674 | 5229115 2 | US-08-466-583-5 | PCT-US95-07820 | US 08-383-650 | US-08-384-292 | US-09-024-020B-12 | US-09-425-043 12 | US-08-383-632-3 |
| C1              | C4              | 4                     | Н             | ٦               | 7             | _               | - 1            | 3             | 4             | Œ.        | C4              | 2              | _             | ٦             | ٠٠.               | 4                | _               |
| 79              | 79              | G<br>G                | 9.0           | 100             | 119           | 128             | 2              | 128           | 128           | 150       | 131             | 131            | 1.35          | 138           | 138               | ÷                | 141             |
| 0.8             | 3.0             | 3.0                   | 3.0           | 3.0             | 3.0           | 3.0             | 3.0            | 3.0           | ٠ <u>.</u>    | ر<br>د.   | 3.0             | 3.0            | 3.0           | 3.0           | 3.0               | T ¥.             | 3.0             |
| 9               | ō.              | ٤                     | اک            | 9               | 9             | 9               | ۵              | 9             | v             | ¥         | 9               | 9              | 9             | Ų:            | ع                 | ç                | 9               |
| 20              | 56              | U                     | 31            | 32              | 33            | 34              | 55             | 36            | 17            | 38        | 39              | 10             |               | 12            | 13                | 14               | 5               |

# ALIGNMENTS

| orschung mbH | synthesis of polyketide or                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | .cagth 829;<br>0, Indels 0, Gaps 0;                                                                  | tton Fiber                                                                                                                                                                                                                                       |
|--------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| i in vojič   | APPLICANT: Grino, Paul M APPLICANT: Cino, Paul M APPLICANT: Gridberty, Brian A APPLICANT: Goldberty, Steven L APPLICANT: Goldberty, Steven L APPLICANT: Mueiler, Joachim APPLICANT: Mueiler, Joachim APPLICANT: Reichebach, Hans TITLE OF INVENTION: DNA sequences for enzymalic: TITLE OF INVENTION: DNA sequences for enzymalic: TITLE OF INVENTION: DNA sequences for enzymalic: TITLE OF INVENTION: DNA sequences TITLE OF STENENCE: POTVIOS 99/23335 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07 SAPILER FILING: DATE: 1999-10-07 NUMBER OF SEQ ID NOS: 107 SSEYIND NO 105 SSEYIND NO 105 | pranglum cellulosum  105  108; Scorc 8; DB 4;  100.0%; Pred. No. 19;  100.0%; Pred. No. 19;  101.071 | Db 309 LESALAAL 316  RESULT 2 US-08-217 327-4  Sequence 4, Application US/08217327  Patent No. 5474225  GENERAL INFORMATION.  APPLICANT: John, Maliyakal E APPLICANT: John, Maliyakal E TITLE OF INVENTION. immobilized Proteins in Cotton Fiber |

NUMBER OF SEC ID NOS: 2460

US-h0-046-404-20694

0; Gaps

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Query Match 5.03 Score 10; DB 26; Length 241; Best Local Similarity 100.03; Pred. No. 0.86; Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: PCT/ISO1/08631
CURRENT FILING DATE: 2001-0:-30
PRIOR APPLICATION NUMBER: 09/540,217
FECK FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                       : Sequence 32819, Application Pt/TUS0108631
: GENERAL INFORMATION:
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PCr-US01-08631-32819
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Job time: 691 sec
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GENERAL INFORMATION:
APPLICAN: KCHICK C. a.d.
APPLICAN: KCHICK C. a.d.
ITHE CF INVENTION: NGCHEC ACLD AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN ITHE CF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196_132
COHRENT APPLICATION UNDER: US/09/248,796
CORRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 28206
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APPLICANT: Keith Weinstork et al.
TITLE OF INVENTION: NOUGHER ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GIA 0169
CORRENT APPLICATION NUMBER: US/60/096,409A
CORRENT FILING DATE: 1998-08-13
NUMBER OF SEQ. ID NOS: 28206
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-THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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100.0%; Pred. No. 0.86;
tize 0; Mismatches 0; Indels
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106.8%.
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Hest Local Similarity 106 8
Matches 27: Conservative
SOFFWARE: Patentin Ver. 2.0
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IIS-09-248-796-20694
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Best Local Similarity 190.0
Matches 10; Conservative
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                                                                                   ORCANISM: Homo sapiens
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IIS+09+248+795-20594
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                  SEQ ID No 2541
LENGTH: 105
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                LOCATION. (436)..(427)
OTHER INFORMATION Caseins alpha/beta proteins domain identified by eMAIRIX,
OTHER INFORMATION acression number REGUINDEB, p-value-7.303e-09, raw score of 8.28
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OFHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                30.8%; Score 62; DB 1; Length 1569;
                                                                                                                                                                                   Query Match 30.8%; Score 62; DB 1; Length 1569
Best Local Similarity ludium, Fred. No. 2.66°51,
Matches 62; Conservative 0; Mismatches 0; Indels
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CURPENT FILING DATE 2001-01-09
PRIOR APPLICATION NUMBER: 60/779,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 2000
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Matches 53; Conservative
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; GENERAL INFORMATION.
NAME/KEY: DOMAIN
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LOCATION: (166)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-449-1058
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CURRENT APPLICATION NUMBER: US/09/757,028
FILE REFERENCE: PM026
CURRENT APPLICATION NUMBER: US/09/758,449
CEPPENT FILTING DATE: 2001-01-11
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                                     PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1478
SOFTWARE PATENTIN VOT: 2-0
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PRIOP FILING DATE 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
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NUMBER OF SEO 1D NOS: 2660
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo saptens
US-09 757-028-2590
                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Best Local Similarity
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IIS-09-757-028-2590
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                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                           LOCATION: (80)
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                                                                                                                                                                                                    SEQ ID NO 1058
                                                                                                                                                                                                                            LENGTH: 164
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                                                                                                                      0; Gaps
                                                                                 Score 75: DB 13: Length 515;
Pred. No. 1.4e-65;
0: Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods Comprising TITLE OF INVENTION: BARDI and other BRCAL Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%; Smare 75; DR 25; 100.0%; Pred. No. 1.4e-65;
                                                                                            100.0%; Pred. w...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/60,042 633
                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/60042611
General information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hibler, David W. REGISTRAFION NUMBER: P-41,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE TOOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NJ: 52: SEQUENCE CHARACTERISTIES:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOWCOCK, Anne M. APPLICANT: Baer, Richard
                                                                                    . 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 amino asids
                                                                                                   Best Local Similarity 100.0
Matches 76; Conservative
                                                                                                                                                                                                                       186 LEGILSQVIHLEKITS 201
                                                                                                                                                                                                                                            150 LEGILSOVIHLEKIIS 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arrold, WE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 77210
COMPUTER READABLE FORM:
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              ; ToPoLoGY: linear
US 08 936 487-52
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Best Local Similarity
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77210
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08 60 042-611 52
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                                                                                    Query Match
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RESULT

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APPLICANT: Bowcock, Anne M.
APPLICANT: Bacr, Richard
TITLE OF INVENTION: Compositions and Methods Comprising
TITLE OF INVENTION: BARDI and Other BRCAI Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 915;
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                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%; Sucre 76, DH 26, 100.0%; Pred. No. 1.40-65; Live 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/JOCKET NUMBER: UTSD:499PZ3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                Concurrently Herewith
                                                                                                                                                                   Arnold, White & Durkee
D. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                US/(0/042,985
                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
US-50-042-985-52
; Sequence 52, Application US/60042985
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hibler, David W. REGISTRATION NUMBER: P-41,071
                                                                                                                                                                                                                                                                                                  4: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICH FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 amino acids
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                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                   NUMBER OF SEQUENCES:
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Best Local Similarity
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                                                                                                                                                                                                           CITY: Houston
                                                                                                                                                                       ADDRESSEE: ADSTREET: P.O.
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PCT-US01-08631-45591
                                                                                                                                                                                                                               Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LEPTETFIPVIRGEVGNPLPSVRRKALDLLNNKLQQNISWKKTIVTFFLKLVPPALLAIVQ 60
                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: potential leucine zipper pattern, BLA Program US-60-141-323-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100, DB 25, Length 2144;
Pred. No. 1 20088,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      49.8%, Scott 100.0%, Pred, No. 100.0%, Pred, No. 100.0%, Pred, No. 100.000, No. 100.0000, No. 100.000, No. 10
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRIOR FILING LATE: 2001-07-25
PRIOR FILING LATE: 2001-07-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-02-26
PRIOR PILING DATE: 2001-03-40
PRIOR PILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-03-19
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
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FRIOR FILLING DATE: 2000 12-22
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PRIOR FILLING DATE: 2000-08-23
PRIOR APPLICATION UNBER: PCT/US01/08631
PRIOR FILLING DATE: 2001-03-30
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PPIOP APPLICATION NUMBER: US 09/488,725
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PRIOR APPLICATION NUMBER: US 09/552,317
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PRIOR APPLICATION NUMBER- US 04/491,404
PRIOR FILLING DATE: 2000-01-25
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Matches 100; Conservative
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APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Jian-Rui
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                                                                                                                                                                               NAME/KEY: SITE
LOCATION: 1750..1771
                                         1987..2007
NAME/KEY: TRANSMEM
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                                         1.0CAT 1.0N:
                                                                                                                                           FEATURE
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102 TAVKLIAPERKEEKNVLGSALI.CIAHVTSTLEALADDLPSLMPSLLTTMKNTSELVSSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1149;
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FITLE OF INVENTION: BARD1 and Other BRCA1 Binding Proteins
NUMBER OF SEQUENCES: 130
                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                           45.3%; Score 91; DB 26; I
100 0%; Pred No 4 Re-80;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION NUMBER OF 04/552,929 PRICE FILING DATE: 2000-04-18 PRICE PRICE PRICE DATE: 2000-04-18 PRICE PLICATION NUMBER OF 04/770,160 PRICE FILING DATE: 2001-01-26 PRICE TOTAL NUMBER POT/ISO1/08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, While & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPIOP APPLICATION DATA: APPLICATION NUMBEP: IIS 60/042,611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 52, Application US/08936487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-41,071
                                                                                                   PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 412
SOFTWARE: Pt_FI_genes Version 6.0
SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER UTS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRM Pr compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bowcock, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALDE AFFERMANTMEPP - US AD COLUMN DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATH: 04-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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INF-ZEEPAX: 10 FOF SEE: SEQUENCE CHAPATTEPISTICS: LENGTH: 515 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURPENT APPLICATION DATA
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                                                                                                                                                                                                          TYPE: PPT
ORGAN:SM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                        LENGTH: 1149
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Wed Jul

1594 LLPTETFIPVIPGLVGNPLPSVPPKALDILNNKLQQNISWKKTIVTRFLKLVPDLLAIVQ 1653

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                                                                                                                                                                                                                                                                                                                                                               121 ALLCIAEVTSTLEALAIPQLPSLMPSLLTTMKNTSFLVSSEVYLLSALAALQKVVETLDH 180
                                                                                                                                                                                  Caps
                                                                                                                                                                                                                1 LLPTETFIPVIRGLVGNPLPSVRRKALDLLNNKLQQNISWKKTIVTRFLKLVPDLLAIVQ 60
                                                                                                                                              Length 2144;
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                                                                                                                                              Score 200; DB 20; L
Pred. No. 2.7e-187;
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APPLICANT: BougueTeret, Lydie
APPLICANT: Choumakov, Ilya
TITLE, OF INVENTION: A NCYEL BAP28 GENE AND PROTEIN
FILE REFERENCE: 67,US2.FRO
                                                                                                                                 99,5%; sec. 100.0%; Pred. No. - 100.0%; Pred. No. - 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/An/174, RRA
CURRENT FILING DATE: 2000-01-18
EARLIER FULING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 12
LOCATION: 1967
OTHER INFORMATION: Xaa-ASP OF ASD
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: X43-G)y of G(u) US-60-176-880-4
                                                                      2 OTHER INFORMATION: Xaa-Gly of Glu US-09-603-665-5
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GENERAL INFORMATION:
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Hest Local Similarity
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                                                     LOCALION: 2017
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                                                                                                                                                                                Matches 201;
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1654 RKKKEGFFFQAINPQTALYTIFLLCKNFGAENPDPFVPVLXTAVKLIAPERKEEKNVLGS 1713
                                                                                                                    LOCATION: 91.,111
OTHER INFORMATION: Potential membrane-spanning segment, TopPred Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCATION: 212 232 OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potentia) membrane-spanning segment, TopPred Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 884..904
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHEP INFORMATION pedential membrane spanning segment, TopPred Program
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«THEK INPORMATION: potential membrane spanning segment, Toppined Program
61 PKKKEGEERQAINRQTALYTLETLEKNEGAFNPINFVPLXTAVKLJAPEREERNVLGS 129
                                                                                             121 ALLCIAEVTSTLEALAIPQLPSLMPSLLTIMKNTSELVSSEVYLLSALAALQKVVETLPH
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barry, Caroline
APPLICANT: Bougueleret, hydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: A MOVEL HAP28 GENE AND PROTEIN
FILLE REFERENCE: GENSET OFAPPE
CUPRENT APPLICATION NUMBEP: 11S/60/141,323
UUMBER OF SEC ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/60141323 GENERAL INFORMATION:
                                                                                                                                                                                                                      1774 FISPYLEGILSQVIHLEKITS 1794
                                                                                                                                                                                           181 FISPYLECILSOVIHLEKITS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                               RESULT 3
US-60-141-323-3
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Length 2144,

99.5%, Shorm 200, DR 26, I 100.0%; Pred. No. 2.7c 187; Flyo 0, Mismatches 0;

Matches 201; Conservative

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Hest Local Similarity

Query Match

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Copyright (c) 1993 - 2000 Compugen Ltd.
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July 2, 2002, 16 03 03 / Scared time 565 3 Seconds Run on:

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3502263 segs. 351980561 residues Searched:

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Post-processing: Listing first 45 summaries

Database

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| c. |              |                |                                            |                |                                           |                                            |   |                              |                          |                             |                                     |                           |                                |                         |  |                   |                    |                                           |                              |                                            |                    |       |            |                                           |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   |        | Description |                                         | Sequence 5, Appli | Sequence 4, Appli | Sequence 3, Appli | Sequence 167, App | Sequence 52, Appl | Sequence 52, Appl | Sequence 52, Appl |
|---|--------|-------------|-----------------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
|   |        | ID          |                                         | US-U9-603-665 5   | US-60-176 880 4   | US-60-141-323-3   | US-60-339-453-167 | US-08-936-487-52  | US 60 042 611-52  | US-60-042 985 52  |
|   |        | ЭВ          | 1 1 1                                   | 0,7               | 30                | 97                | 92                | *                 | Ç                 | 4.                |
|   | Query  | Length 1    | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 2144              | 2144              | 2144              | 1149              | 715               | 515               | 515               |
| æ | Query  | Match       | 1 1 1 1 1 1 1                           | 96.5              | 99.5              | 49.8              | 45.3              | 3.7 B             | 37.8              | 37.8              |
|   |        | Score       | 1 1 1 1 1 1 1                           | 200               | 200               | 100               | 91                | 76                | 76                | 97                |
|   | Result | Q           |                                         | -                 | C4                | m                 | 4                 | Ŋ                 | 9                 | 7                 |

| 45591, |                   | Sequence 1058, Ap | quence 2541.      | 20694             | 20694, | 32819,           | 31,               | 1836,            | 1836,              | e 40,            | 1271              | 579, | 1271              | 58077              | e 158,           | Sequence 865, App | 31113,               | c 16178           | 16177              | 11.17               | equence 105,     | ~             |                   | 12248           | 82158           | 82164           | 8217     | 82189           | 83034           | 83033              | 83047              | 83055               | 3940                 | 34              | 406              | Scycence 841487,        |  |
|--------|-------------------|-------------------|-------------------|-------------------|--------|------------------|-------------------|------------------|--------------------|------------------|-------------------|------|-------------------|--------------------|------------------|-------------------|----------------------|-------------------|--------------------|---------------------|------------------|---------------|-------------------|-----------------|-----------------|-----------------|----------|-----------------|-----------------|--------------------|--------------------|---------------------|----------------------|-----------------|------------------|-------------------------|--|
| Ž,     | 1 05.05 /5/ 60.50 | T.6## 06/ 60-8    | 1 US-09 757 028-2 | 6 US-U9-248-796 2 | í 9    | 197-0301-08531-3 | 6 US-60-187-382-3 | PCT-US01-16450-1 | PCT-US01-16450A-18 | 4 US-09-001 403- | PCT-US00-05882-12 | S    | US-09 925-301 127 | PCT-US01-08631-580 | US-60 243-742-15 | US-60 243 468-86  | PCT-+HS91+98631 3111 | US-09-708-427-161 | US U9-708-427 1617 | TIS 69 708-427 1617 | US-04-416-145-10 | US-09-252-691 | US-09-252 691C-87 | US-09-489-039A~ | HS-04-724-059-9 | US-09-724 059-8 | TS-08-15 | HS-09-724 059 8 | US 09-7-4-059 8 | US 09 744-059-8303 | US-09 724 059-8304 | US 09-724 059-83055 | 11S 014 724-059-8394 | US-09-724 059 8 | 104-774 054-8406 | 21 US-09-724 059 841487 |  |
| 1564   | 164               | 135               | 105               | 74.               | 241    | 53               | 88                | 307              | 307                | 307              | 363               | 363  | 363               | 435                | 486              | 487               | u"<br>12:<br>u"      | 208               | ÷                  | 6.6.4               | 7<br>X           | 688           | $\alpha$          | . Th            | 10              | -               | σ:<br>Π  | <u>-</u>        | 2               | 5                  | 1.5                | 13                  | <u>.</u>             | را              | <u>.</u>         | 16                      |  |
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| တင     | n C               | 11                | 12                | <u>۳</u>          | 14     | <i>ن</i> د.      | 16                | 17               | 18                 | 19               | 20                |      | <del>.</del> .    | 23                 | 54               | 25                | 44                   | 27                | 82                 | o<br>Ci             | 30               | 31            | 32                | 33              | 34              | ج.<br>ج.        | 36       | 3.7             | 38              | £.                 | 40                 | 41                  | .1                   | 43              | 44               | φ:<br>•:                |  |

### ALIGNMENTS

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APPLICANT. Barry, Caroline
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Cohen-Akenine, Annick
TITLE OF INVENTION: A N'VEL BAPER AND PPOTEIN
FILE PEFEPENCE: GENSEI.063AUS
                                                                                                                                                                                                     CURKENT APPLICATION NUMBER: US/US/603,065
CURKENT FILING CAIE. 2000 US 23
FRICH AFFLICATION NUMBER: US 60/141,323
PRICH FILING DATE: 1999-06-25
PRICH APPLICATION NUMBER: US 60/176,880
PPICE FILING DATE: 2000-01-18
                 Sequence 5, Application US/09603665 GENERAL INFORMATION:
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OTHER INFORMATION: Xaa-Ser or Asn
NAME/KEY: VARIANT
LOCATION, 1854
OTHER INFORMATION: Xaa-Ala or Val
NAME/KEY. VARIANT
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent.pm
SEQ ID NO 5
LENGTH: 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY. VARIANT
US-09-603-665-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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12-0CT-2001 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human bone matrow. They can be used to measure gene expression in bone matrow samples, which may enable the improved diagnosis and treatment of cancers such as iymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
              Caps
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                                                                                                                                                                                                                                             Human: bono marrow expressed exer; gene expression analysis; probo; microarray, cancer, loukaemia; lymphema; myelema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4: SEQ ID No: 27407: 658pp + Sequence Listing; English.
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             J; Mismatches
Told man pred No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM14962 standard; Protein: 42 AA
                                                                                                                                   AAM67101 standard; Prutein; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE ) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                               26 MAY - 2000; 2000US 0207456.

30 JUN - 2000; 2000US - 06.08408.

03 AUG - 2000; 2000US - 06.2366.

21 SEP 2000; 2000US 02.44697.

04 mt 2000; 2000US 02.4563.
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             7; Conservative
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Best Local Similarity
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                                       61 PREKEUE 67
                                                                18 rkkkege 24
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                                                                                                                                                             AAM67101;
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Search completed: July 2, 2002, 16:06:91

Job time: 178 sec

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(SENT) see AA110068 AA1284 9) The present sequence is a peptide encoded by one such probe. The SENUs are derived from human Hela cells. The SENUs can be used to produce a single exon microarray, which can be used for measuring human qene expression in a sample derived from human erivinal epithelial cells. By measuring one expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPo at Ltp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to boman single exon nucleic acid probes
                              Peptide #1396 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      edpe (a)
                                                             Probe; human; microarray; gene expression; cervidal epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic and probes useful for analyzing gene expression in human cervical epithelial cells \gamma
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 19788; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                        200098-0632366.
200008-0234687.
200008-0236359.
                                                                                                                                                                                                         30-JAN 2001; 2001WO-US00670.
                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312.
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                                                                               cervical cancer.
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                                                                                                              Homo sapiens,
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                    Protein #1373 encoded by probe for measuring heart cell gene expression.
                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing yene expression in human
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Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human fetal liver -
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                               Claim 27; SEQ ID No 26573; 53%pp · sequence listing, Enginsh.
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                                                                                                                                                                                                         DB 22; Length 42;
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                                                                                                                                                from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                   ABB19374 standard; Protein; 42 AA.
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                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                       Sequence 42 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe enceded protein SPQ 10 NO: 26806.
By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and proquosing diseases of the human heart and vascular system e.g. cardiovascular disease, hyperteision, aradian arrhythmias and rengenital heart disease. Note: The sequence data for this patcht did not form part of the printed specification, but was obtained in electronic formal directly from WIPO at fib.wipo.int/pub/published_pct_sequences.
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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Matches 7; Conservative 0; Mismatches
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Pred. No.
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2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-484446/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer.
                                                                                                                                                                                                                                              Sequence 42 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RKKKEGE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 rkkkege 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04 - PEB - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
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DB 22: Length 42;

Score 7:

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the invention relates to isolated polynucleotide (i) and polynetide (II) sequences. (I) is useful as hybridisation probes, polymentase chain reaction (PCR) primers, obligances, and for edromosome and gene mapping, and in recombinant production of III. The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed enters. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful to generating antibodies adainst it detecting or quantitating a polypotide in tissue, as molecular weight markers and as a tood supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging alerrant profesion or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ċ
                                                                                                                                                                                                                                                                                                 The polypeptide and polynacieotide Sequences have applications in diagnostics, forensies, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #1402 encoded by breast cell single exon nucleic acid probe.
responsible tor denetic disorders or other traits and to assess
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Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O, Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_prt_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ac.
                                                 Claim 20; SEQ ID No 31113; 103pp; English.
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40-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8. Conservation
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Hest Local Similarity
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288 (d)1nnki 295
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27 - SEP - 2000;
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                  brodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04 FER-2000;
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agents on cells, the microarray of this invention prosents a far areater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information trum genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                    nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled involves contacting derived from miRNA of human breast, and then measuring the label bound to each probe of the microatray. The probes are useful for verifying the expression of regions of genomic bNA predicted to encode proteins. They are useful for quene discovery, and for determining predisposition and/or prognosing breast disease, Gene expression analysis is useful for assessing the toxicity of chemical
                                                                                                                                                                                                                                                                                                                                                                                                   protect The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPO at ftp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; foctal liver; gene expression, single exon nucleic acid probe
                                                                                                                       The invention relates to a spatially-addressable set of simple exem
                                  sample derived from human
             New spatially-addressable set of single exon nucleic acid probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #1444 encoded by human foetal liver single exon probe.
                                                                                   Claim 27; SEQ ID NO 11719; 327pp · sequence listing: English
                                                 breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7: DB 22; Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Mismatches
                                  useful for measuring gene expression in
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20000S-0608408
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20000S-0234687
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Best Local Similarity Touse
Tr. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RKKKEGE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 rkkkege 24
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\mathbf{x} = \mathbf{1} \mathbf{1} \mathbf{1} \mathbf{2} \mathbf{3} \mathbf{3} \mathbf{3}
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Sednence
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or Vital infections. The peptides, nucleotides, antibodies, adopted an adjoint and antegorists may be also be used in drug serects. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynuciectides, polypeptides, antibodies, agonists and untagonists from
the present invention may be used to treat immune disorders by activating
or inhibiting the proliferation, differentiation or mobilisation of
immune cells, to treat disorders of harmanopoletic cells, autoimmune
disorders, allergic reactions, graft versus host disease and organ
rejection, modulate harmanostatic or thrombolytic activity, modulate
                                                                                                                                                                                                                                                                                                                                            include: cytostatic; profilerative, vulnerary; immincumodulator; antidatebucte, antidathumatic, antifheumatic, antifheumatic, antidathumatory, antithyroid, antidicyjic; antiboterial; antivital, dermatological, neuroprotective, cardiant, thrombolytic; coagulant; neuropropic; antiporropic; antiporropic; antiporropic; antiporropic; antiporropic; antiporropic antidatic and antiangloganic. The polynocleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                              in AAB43398 to AAB44239. The proteins can have activities based on the Lissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                         AAC77607 to AAC78448 encode the human cancer associated proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                  Novel isolated nucleic acids comprising sequences encoding peptides
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                                                                                                       useful for treating or diagnosing e.g. cancer
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                                                                                                                                                                      Claim 11; Page 1904-1906; 2352pp; English.
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100 0%; Pred No
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23-AUG-2000; 2000UG-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
1-15 8; Couserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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The invention relates to isolated polynucleotide (1) and polypeptide (i1) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PTP) primers, chicamers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in your thorapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it detecting or quantifating a polypeptide in tissue, as molecular weight markers and as a food supplement (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving observat protein, expression, or biological activity. The polypeptide and polyuchectide sequences have applications in diagnostics, forensies, gene mapping, identification of muchtions responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. And 000 (0.5MS 3037 represent novel human Nete: The sequences And of this patent did so appear in the printed specification, but was obtained is electronic format directly from With II print int/pub/published_pcl_sequences.
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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food supplement, medical imaging, diagnostic, genetic disorder.
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100 0%; Pred No 47;
tive 0; Mismatches
                                                                                                                                                                Claim 20; SEQ ID No 58077; 103pp; English.
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23 AMG-2000; 2000MS-0649167.
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Best Loral Similarity 100
8: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 AA;
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                                                                                        biodiversity
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
                                                                                                                                                                                                                                               uses, since the proteins are stable at very high temperatures, some up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory, cytostatic, neuroprolective, valuerary, moutopic; anticonvulsant; antiathritic; cerebroprotective; antiungal; antiviral; antibacterial; antiallergic, demandoparal; hacmostatic, antiathmatic; thrombolytic; immunogen; antibudy, gene therapy; neurological disorder; Parkinson's dievise; inflammatery disorder; cancer; asthma; osteoporosis,
                                                                                                                                                                                                          hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypepides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                                                            Note: This patent is in the same patent family as W0200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75920 and AAG65436.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
                                                                     New nucleotade sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                            a hyperthermophilic archaeon, which is isolated from deep-sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides encoding novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Querellow J, Weissembach J, Saurin W.
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                                                                                                                     Maim 7: Page 1130; 1657pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                    Hest Local Similarity 100.0%; P. Matches 8. Conservative 0;
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                                                                                     proteins useful in industry
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                                                                                                                                                                                                                                                              110 degrees centigrade.
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                                    WPI; 2001-126236/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 KKKEGERE 69
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proteins or their active domains. The polypeptides, polyburied ides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production, the polypeptides are used to identify compounds which bind to the polypeptides. Polynucleides to the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti sense DNA or target dids; to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative
                                                                                                                                                                                                                                                                                                                                                                                                                                     sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
fungal infection of from autoimmunity, cancer, allergy, asthma,
                                                                                                                                                                                                                                                                        protein levels, as tissue markers, and to isolate receptors or liquids. Oblygeptides of the invention may also be useful in treating platelet disorders, regenerating bone, cartilage, fendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliforation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthis, andemia. Altheimer's, Parkinson's and inntington's diseases, amylotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasctropic, antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; harmatopojetic cell disorder; autoimmune disorder; altergic reaction, graft versus host disease; ordan rejection; haemostalic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cancer associated gene, cancer antiden, detection, cancer, diagnosis, cytostatic, proliterative, vulnerary; immunomodulator, antidabetic, antiastimatic; antichemmatic; antiastimatic; antiastimatic; antiastimatic; antibacterial; cardiant, antinfiammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft-versus-host disease, eczema, haemophilia, rhrombosis, anti-inflammatory diseases, nervous system disorders, and intection. The present sequence represents a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 8; DH 22; Longth 307;
100.0%; Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LDLLINNKI, 34
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                                                                                                                                                                                                                                                                                                                                                                  a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abernant protein expression or bin majoral activity. The polypetide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and to produce other types of data and products dependent on DNA and amino acid sequences. ABC00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention or the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                       New isolated polynomization and encoded polypeptides, useful in
diagnostics, ferensies, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lood supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 22, Length 1569,
Pred. No. 6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at Itp.wipo int/pub/published_prt_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                          Claim 20: SEQ ID No 45591; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #2451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG02460 standard, Protein, 68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.85,
100.08; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-HSOR631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
2001-639362,73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                    N-PSDB; AAS79419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAP-2000;
23-AUC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1568 rk 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG02460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal attivity of (11) or to treat disease states involving quantitating a polypoptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical adsorders involving aberraan protein or itself in restored in the polypoptide and protein expressing or involving aberraan protein expressing or highly for treating dissorders involving aberraan protein expression or highly including the polypoptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences Abstrantion represent movel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did incl appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oliquments, and for chromosome and gene mapping, and in recombinant production of (II). The polymorlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o; Caps
                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mulations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%; Score 8; DB 22; Length 68; 100.0%; Pred. No. 8.7; Unders 0; Mismatches 0; Indeis
                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putalive F. abyssi pseudouridine synthase #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                          Claim 20; SEQ ID No 32819; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB96435 standard; Protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CNRS ) CNRS CENT NAT RECH SCI
                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99FR-0005034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bost_Local Similarity 100.0
Matches 8; Conservative
                   Drmanac RT, Liu C,
                                                          WF1, 2001-649462/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 KKKEGEEE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11111111
29 kkkeqeee 36
                                                                                N-PSDB; AAS66647
                                                                                                                                                                                      biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-00T-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB96435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention is directed to BAP28 polymeptides, BAP28 polymoleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 colding region. He BAP28 polymoleotides can be expressed by standard recombinant methodology BAP28 polymoleotides and polymeptides have been found to be over expressed in prostate tumenr cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suttering from or susceptible to useful as diagnosite reagents. Biallelic markers of the BAP28 per are useful as diagnostic reagents. Biallelic markers of the BAP28 per are useful any genetic analysis. The present sequence represents a protein enroded by a first cDMA sequence of the BAP28 gone consisting of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New MARZB polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 REKERFGFERGAINPQTALVTLELLOENFGAENPOPFVPVLXTAVELIAPERREERNVLGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALLOTARVISTITATATIVOTENIMPSTETIMKNISELVSEVVITSALAALOKVVETENH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LEPTETETPVIRGINGNPLPSVRRKALDELNNKLQQNISWKKLIVIRELKLVPPDLLATVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BARD1: ring protein; BRCA1; breast cancer; risk; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                   Rouqueleret L, Chumakov I, Cohen-Akenine A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 200; DB 22; L
Pred. No. 1.4e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
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                                                                                                                                                                                                 Claim 14; Page 297-304; 449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW54099 standard; Protein; 515 AA
                                                                                                                                                               polymerase chain reaction assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1774 fispylegilsqvihlekits 1794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       970S 0042985.
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970S - 0042611,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47W0-11416842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186.55
                                                                             PSI-H; AAFB 1909, AAFB 1910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                       WP1: 2001 467032/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exons 1 to 45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 - SFP - 1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                   Barry C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW54099;
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Rest Local s
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Gaps

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The sequence is that of a protein which can be used in the preparation of the recombinant breast cancer antigen, HRCA1, binding preparation of the recombinant breast cancer antigen, HRCA1, binding epictucins BARD1, Bi23, BE2, BE14, BE33 or BE445, or a composition for the detection of a BARD1, Bi23, BE2, BE31 or BE445 nucleic acid sequence, specifically a wild type BARD1 composition for the detection or purification of BARD1, and the detection and purification of a HRCA1 cancer BARD1 antibody, and in the detection and purification of a HRCA1 antiBARD1, BI23, BE2, BE14, BE31 or BE445 can be used in the detection and complex that alters the binding of BARD1, BI23, BE2, BE14, BE31 or BE445 to BRCA1 or the binding of BARD1, B123, BE2, BE14, BE31 or BE45, BE31 or BE45, BE31 or BE45, BE31 or BE45, a specific anti-BARD1 antibody can be used to identify a patient having or at risk of developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 TAVKLIAPERKEEKNVLGSALLCIAEVTSTLEALATPOLPSIMPSHITTMKNTSELVSSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: chromosome mapping; gene mapping; gene therapy; torensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                          DNA sequence encoding BAPD1, B123, BE2, BE14, BE31 or BE445 wh as breast cancer antigen, FRCA1, binding proteins are useful to identify patient having or at risk of developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 100; DB 19;
Pred. No. 7.7e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. nc.
                                                                                                                                                                           Disclosure; Page 287-288; :48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #15223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG15232 standard; Protein: 1569 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WD-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000US-0649167.
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(TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                          WPI; 1998-230317/20.
                                Bowcock AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                               N PSDB; AAV24135.
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                                Baer R,
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GenCore version 4.5
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OM protein . protein search, using sw model

July 2, 2002, 16:03.03 , Seatch time 117.59 Seconds Run on:

(without alignments) 189.862 Million cell updates/ser

US-09-603-665-5\_COPY\_1594\_1794 201

ISPYLEGILSQVIHLEKITS 201 1 LLPTETFIPVIRGLVGNPLP.. Perfect score: Sequence:

Gapop 60 0 , Gapext 60.0 Scoring table:

747574 seqs, 111073796 residues

Searched:

Word size :

Total number of hits satisfying chosen parameters:

1911

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Listing first 45 summaries

Database ·

/SIDSI/qcqdata/hold-geneseq/geneseqp-embl/AAI995\_IAT:\*/SIDSI/dcgdata/hold-geneseqp-embl/AAI996\_DAT:\*/SIDSI/dcgdata/hold-geneseqp-embl/AAI996\_DAT:\*/SIDSI/gcgdata/hold-geneseqp-embl/AAI999\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI999\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI999\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI999\_IAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI999\_IAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2000\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2000\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI2001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI3001\_DAT:\*/SIDSI/gcgdata/hold-geneseqy-embl/AAI3 /SIDS1/qcqdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*/SIDS1/qcqdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\* \*: LAU. /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT;\* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:\* /SIDS1/409data/hold-geneseq/genesegp-emb1/AA1994,DAT:\* /STIST/Arcidata/holid-remasseg/genessegp-embl/AAT940\_DAP+\* /SDST/gradata/holid-genesseg/genessegp-embl/AAT942\_DAT;\* /SDST/gradata/holid-genesseg/genessegp-embl/AAT942\_DAT;\* /SIDSI/gegdata/hold genese4/genese1p .ambl/AA1991 A\_Geneseq\_032802:\*

Pred. No. is the number of results predicted by chance to have a scorr greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Probein encoded by | Home Sapiens BAP28 | Novel human diagno | MOVO human diagra | Putative P abysei | Human novel protei | Human cancer assoc | Novel human diagno | Novel human diagno | Peptide #1402 enco | Peptide #1444 enco |
|-------------------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES                     | AAB85029           | AAW54099           | ABG15232           | ARC02460          | AAB96435          | AAU14137           | AAB43826           | ABG27718           | ARG00754           | ABB28751           | ABB33938           |
| 58                            | 딉                  | 13                 | CI<br>CI           | C                 | 22                | C1                 | 21                 | C1                 | C1                 | CI<br>CI           | C1                 |
| %<br>Query<br>Match Length DB | 2144               | 515                | 1569               | <b>α</b>          | 108               | 307                | 363                | 435                | 505                | 4.2                | Ç                  |
| %<br>Query<br>Match           | 99.5               | 49.8               | 30                 | 4                 | 4.0               | 4.0                | 4.0                | 4.0                | 4.0                | 3.5                | 3.5                |
| Score                         | 200                | 100                | 62                 | <b>∞</b>          | <b>&amp;</b>      | 90                 | œ                  | 8                  | œ                  | 7                  | 7                  |
| Result<br>No.                 |                    | 2                  | æ                  | 4                 | ır.               | 9                  | 7                  | œ                  | 6                  | 10                 | 11                 |

| Protesta #1373 enco | 2 CX     | Buman bone marrow | Peptide #1396 enco | #1433    | #1370    | opoolo   | pereted  | - a      | #2026    | #1931    | rain ex  | Human bone marrow | Peptide #1948 enco | 2002#          | #1949    | FX ORF   | i mmu    | Atabidopsis thalia | n        |          | Arabidopsis thalia |          | Drosophila melanoq | Eimeria merozoite | Drosophila melanog | Cotton fiber-speci | RosB related gene | related  |           | 51.5     | s that   | is thall     | is thali |  |
|---------------------|----------|-------------------|--------------------|----------|----------|----------|----------|----------|----------|----------|----------|-------------------|--------------------|----------------|----------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|-------------------|--------------------|--------------------|-------------------|----------|-----------|----------|----------|--------------|----------|--|
| ABB19374            | AAM54701 | AAM67101          | AAM14962           | AAM27396 | AAM02688 | AAP70093 | AAC02287 | ABB29349 | ABB34520 | ABB19932 | AAM55307 | AAM57706          | AAM15514           | AAM28005       | AAM03267 | AAB40973 | C 4      | AAC25155           | AAG07135 | ABG04745 | AAG25154           | AAG25153 | ABB63428           | AAR13165          | AHH69008           | AAR86913           | AAR36605          | AAR36606 | AAR 31999 | AAC37029 | AAG46615 | AAG 37028    | AAG46614 |  |
| 11                  | c;       | <u></u>           | CI                 | C        | CI       | æ        | 5        | C1<br>C1 | -1<br>-1 | C1       | 22       | (1<br>(1          | 디                  | CI             | C‡<br>C‡ | -4<br>-4 | 럲        | 5                  | 7        | 22       | 21                 | Ξ.       | C1                 | Ci                | C1                 | 17                 | 14                | 14       | 14        | 5        | 54       | -1           | đ        |  |
| 4                   | 42       |                   | 4.2                | 4.2      | 42       | 65       | 7.0      | 7.3      | 73       | 73       | 73       | 73                | 73                 | 73             | 73       | 113      | 118      | 136                | Š        | 3        | 144                | 187      | 195                | 200               | 200                | 214                | 216               | 216      | 216       | 230      | 2.50     | 13.2<br>13.2 | 232      |  |
| 3.5                 | 3.5      |                   |                    |          | 3,5      |          |          |          |          | 3.5      |          |                   |                    |                |          |          | r:<br>c: |                    |          |          |                    |          |                    |                   |                    |                    |                   |          |           |          | 3.5      |              |          |  |
| 7                   | 7        | 7                 | 7                  | 7        | 7        | 7        | ~        | 7        | 7        | 7        | 7        | 7                 | 7                  | ٢              | 7        | 7        | 7        | Ĺ                  | 7        | 7        | 7                  | 7        | 7                  | 7                 | 7                  | 7                  | 7                 | 7        | 7         | į.       | 7        | 7            | ۲-       |  |
| 12                  | 13       | 14                | 15                 | 16       | 17       | 18       | ۷.       | 20       | 21       | 22       | 23       | 24                | ኒን                 | 5 <sub>6</sub> | 27       | 28       | 50       | 30                 | 31       | 32       | en :               | 34       | 35                 | 36                | 3.7                | 38                 | 39                | 40       | 41        | 7        | £        | 7            | L'i      |  |

## ALIGNMENTS

RESULT

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BAP28; prostate; tumour; cancer, diagnostic; genetic analysis.
                                                                                                                                                                                Protein encoded by BAP28 cDNA consisting of exons 1 to 45.
                        AABB5029 standard, Protein; 2144 AA.
                                                                                                                         06-Aug-2001 (first entry)
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                          AAB85029;
AAB85029
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Location/Qualifiers /label- Ser or Asn 'label- Ala or Val /label= Asp or Asn /label= Gly or Glu Misc-difference 1694 Misc-difference 1854 Misc-difference 1967 Misc-difference 2017 

WOZÜÖlÜMER9-A2

23-JUN-ZUUU; 2000WO-IB01183 04 - JAN-2001.

25-JUN-1999; 99HS-0141323 18-JAN-2000; 20009S-0175880

(CEST ) CENSET.

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
CURRENT FILING DATE: 2002-02-21
NUMBER OF SAO ID NOS: 47374
ILENGTH: 1133
TYPE: PRT
CORGANISM: Neurospora crassa
FRATURE:
NAME/KEY: unsure
ILENGTH: 1133
TYPE: PRT
NAME/KEY: unsure at all Xaa locations
COCATION: (1)..(1133)
COTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-4112

QUETY Match
SIMILATITY 100 09, Prod No. 2 40:02;
Matches 7; Conservative 0: Mismatches 0; Indels 0; Gaps 0;
DD 362 SALAALQ 12
DD 362 SALAALQ 368
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Search completed: July 2, 2002, 15:16:45 Job time: 822 sec Gaps

.; C

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APPLICANT: SOLOYTEV, Victor and TROUKHAN, Maxim
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Phereby
FILE REFERENCE: 2750-0876P
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwel
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Green, Green
APPLICANT: Hinkle, Green
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PROJUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROFERIES
FILE REPRENCE: 38 10(5.052)A
CURRENT APPLICATION NUMBER: (15/60/360.039
CURRENT APPLICATION NUMBER: 2602-02:21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 7; DB 5; Length 1057; 100.0%; Pred. No. 2.2e+62; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.5%; Score 7; DB 7; Length 883; 100.0%; Pred. No. 1.5+02; dlive. 0; Mismatches of Inders
                           3.5%: Score 7; DB 5; Length 876; 100 04; Pred; No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1.8/09/573,655B CURRENT FILING DATE: 2000-05-18 NUMBER OF SEQ ID NOS: 3281
                                                                                                                                                                                                                                                             US-60-34n-039-23646
; Sequence 23646, Application US/60360039
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Sequence 1734, Application US/09573655B ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4112, Application US/60360039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFFWARE: Patentin version 3.0 SEQ ID NO 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
US-60-360-039-23646
                                                  Best Local similarity 100 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 7, Conservative
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Matches 7; Conserv
                                                                                                                      131 NDLEEVG 137
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                                                                                                                                                                     79 NDLEEVG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TTLAPRV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-573-6558-1734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-60-360-039-4112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 23646
LENGTH: 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057
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                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1001-0030-004-00
CURRENT APPLICATION NUMBER: US/09/540, 2098
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: 60,240 - 647- 64,240,414- 64,240,048: 64,241,240, 64,291,849,
60/291,829: 66,240,428: 66,448: 64,244,776

BRIOR FILING DATE: 2004-04,28: 66,448: 64,244,776

PRIOR FILING DATE: 2004-04,29: 2201-03-29: 2201-03-29; 2201-05-17,
2004-05-17: 2201-05-17: 2201-05-20; 2004-06-29

NUMBER OF SEQ ID Nes: 792

SUFINARE: PERI: Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LO, Audroy
APPLICANT: LAN Ruth Y.
APPLICANT: URASHRA, Michael E.
ATTER OF INVENTION MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: P1-12-11 PCT
CURRENT APPLICATION NUMBER: PCT/US02/09944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: II:218849.24.or12:2001MAYL7
PYT-US02-09-044-649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 7; DH 1; Length 727; 100.0%; Pred. No. 1.6e.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 7121, Application US/09540209B
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     GERSTIN, JR., Edward H.
PERALFA, Careyna H.
FRAN, Alanna-Phung B.
DAHL, Christopher R.
                                                                                            DUFOUR, Gerard E.
HILLMAN, Jernifer L.
                                                                                                                                                                                                                                                                                                          NGHYEN, Duy-Viet An
KLEEFELD, Yael
                                                                                                                                                              TUASON, Olivia
YAP, Pierre E.
AMSHEY, Stelan R.
DAUGHERIY, scan C.
                                                                                                                                                                                                                                                                                                                                                                                                          DAVID, Marie H.
LEWIS, Samantha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANZER, Scott R.
HARRIS, Bernard
FLORES, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hest Local Similarity 100.0
Matches 7, Conservative
                                                  GIETZEN, Darryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MARWAHA, Rakesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEN, Alice J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gary L. Breton
                                                                                                                                                                                                                                                                                    Formmy F.
                                                                      CHINN, Joyce
                                                                                                                                            YU, Jimmy Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                DAM, Tam G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: B.fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 TLPHFIS 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-540 2098-7121
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT
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Gaps

0

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APPLICANT: GLIDAIA, BALTY S.
APPLICANT: HINKLE, GREGOLY J.
APPLICANT: HINKLE, GREGOLY J.
APPLICANT: HINKLE, GREGOLY J.
APPLICANT: SLACT, SLEVENC.
TITLE OF INVENTION: EXPRESSION OF MICROHIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/60/346,039
CURRENT APPLICATION NUMBER: US/60/346,039
CURRENT APPLICATION NUMBER: US/60/346,039
SEQ ID NOS: 47374
SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                   APPLICANT: Hart, Elizabeth A.
IITLE OF INVENTION: Diterpene-Producing Unicellular Organism
FILE PEFFFFNCE: P020ROUS1/10025547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%, Score 7, DH 6, Longth 579, 100.0%; Prod No. 1 36+02, tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7, Length 688;
5. 1.5e+02;
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                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/041,018 CURRENT FILLING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: US 60/259880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6112, Application US/60360039; GENERAL INFORMATION:
                                                                                                                                                                    ; Sequence 261, Application US/10041018; GENERAL INFORMATION:
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                                                                                                                                                                                                                   APPLICANT: Matsuda, Seiichi P.T.
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                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 413
SOFTWARE: Patentin version 3 1
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Best Local Similarity 100.00
7, Conservative
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Rest Local Similarity Turson
7: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays
US-10-041-018-261
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                                                              414 OTEKNWK 420
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                    79 QIEKNWK 85
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US-60-360-039-6112
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TITLE OF INVENTION: NUCLEIC ACID AND AMING ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1001
CURRENT APPLICATION NIMBER: US/09/540, 209B
CURRENT FILING DATE: 2000-04-04
NIMBER OF SEQ ID NOS: 10444
SEQ ID NO 9330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Binkle, Gregory J.
APPLICANT: Binkle, Gregory J.
TITLE OF INVENTION: EXPRESSION OF WICKOBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38 10(5202)A
CURPENT APPLICANTION NUMBER: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5032
LENGTH: APPLICANTION NUMBER: 2002-02-21
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100 0%; Pred No 94;
7ative 0, Mismatches 0, Indels
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100.0%, Pred. No. let02,
Live 0; Mismatches 0; Indels
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  FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: FOR DIAGNOSTICS AND THE FILE REFERENCE: 2709-1001-001
CURRENT APPLICATION NUMBER: US/09/540,209H
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-540-209B-9330; Sequence 9330, Application US/09540204B; GENERAL INFORMATION:
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Host Local Similarity 100.v
The 7; Conservative
                                                                                                                                                                                                                                                                                 Best Local Similarity 100 Matches 7; Conservative
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US-09-540-209B-9330
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; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMIND ACID SEQUENCES RELATING TO BACTEROIDES
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FOR SEPTION NUMBER 60,287 151; 60,290,516; 60,291,217; 60,311,752; 60,729,217, 60,741,718; 60,744,718; 60,744,718; 60,744,718; 60,744,718; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,111; 20,11; 20,11; 20,11;
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o. 75;
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TITLE OF INVENTION G-PROTEIN CHIPLED PECEPTORS
FILE REPERENCE: PI -0.415 PGT
CUPRENT APPLICATION NUMBER POT/CS02/13329
CUPRENT FILING DATE: 2002 04 25
                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                              3.5%; Score 7; DB 5
100.0%; Pred. No. 39;
tive 0; Mismatches
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100.0%; Pred. No. 75;
Live 0; Mismatches
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PCT-US02-13329-8
         OTHER INFORMATION: Xaa is ary amino acid
                                                                 : NAME/KEY: misc_leature
: Locatron: 1.158
: OTHER PHYPRMATION: Ceres Seq. ID 1393051
US-09-620-393B-6605
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; Sequence 9466, Application US/N9849209B
; GENERAL INFORMATION:
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// GENERAL INFORMATION:
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RICHARDSON, Thomas W.
BOROWSKY, Mark L.
GRAUL, Richard C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCYTE GENOMICS, INC.
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YAO, Monique G.
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WARREN, Bridget A.
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Host Local Similarity 100...
Eng 7: Conservative
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Matches 7; Conservative
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                                       FEATURE:
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TITLE OF INVENTION: SPOUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERBY
FILE REFERENCE: 2750-1068P
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CURRENT FILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: Patentin Version 3.0
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                                                                                                                     : LOCATION: 1..105
; OTHER INFORMATION: Ceres Seq. ID 1393053
US 09-620-3938-6607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : NAME/KEY: misc_leature
: IntATTON: 1 121
: OTHER INFORMATION: Ceres Seq. ID 1393052
US-04-620 3438 6606
                                OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Sequence 6606, Application US/09620393B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Sequence 6605, Application US/09620393B ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALEXANDROV, Nickolai et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100
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LoCATION: 1..121
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LOCALTON: 1..105
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July 2, 2002, 74.16.44 , Search time 59,39 Seconds

(without alignments) 338 459 Million cell updates/sec

US-04-603-665-5\_00PY\_1754\_1954 Title: Perfect score:

TEYNLAD LARKING LETTE 201 1 EVYLLSALAALQKVVFTLPH Sequences

Gapop 60 0 , Gapext 60 0 Scoring table:

307805 segs. 101015595 residues Searched

Word size :

1089 Total number of hits satisfying chosen parameters:

Maximum DR sog longth. Zungmonnd Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|             |       | ф              |           |          | SUMMARIES            |                        |
|-------------|-------|----------------|-----------|----------|----------------------|------------------------|
| Result.     | Score | Query<br>Match | Length    | DB       | ID                   | Description            |
|             | 80    | 4.6            | Ç.        | 7        | LS 60 460 034 206.45 | S. (10.00) (2.06.35) A |
| c           | 7     | ج.<br>ب        | 105       | ď        | US-09-620-3938-6607  | Seguence 6607, Ap      |
| ĸ           | 7     | 3.5            | 121       | ıc:      | US-09-620-393B 6606  |                        |
| 4           | 7     | 3.5            | 158       | S        | US-09-620-393R-6605  |                        |
| J.          | 7     | 3.5            | 323       | 7        | PCT-US02-13329-8     | - 52                   |
| œ           | 7     | 3,5            | 417       | S        | US-09-540-209B-9466  |                        |
| 7           | 7     | 3.5            | 452       | 2        | US-09-540-209B 9330  | Sequence 9330, Ap      |
| 89          | 7     | 3.5            | 488       | 7        | US-60-360-039-5032   |                        |
| 90          | 7     | 3.5            | 579       | 9        | US-10-041-018-261    | 261, A                 |
| 10          | 7     | 3.5            | 688       | 7        | US-60-360-036-6112   | 1 ]                    |
| 11          | 7     | 3.5            | 727       | -        | PCT-US02-09944-649   | 6.49                   |
| 12          | 7     | ur<br>or       | R76       | U        | HS 09 540-209B-7121  | 7121,                  |
| 13          | 7     | 3.5            | 883       | 7        | US-60-360-039 23646  | 23646,                 |
| 14          | 7     | 3.5            | 1057      | S        | US-09-573-6558-1734  | Sequence 1734, Ap      |
| 1.5         | 7     | 3.5            | 1133      | 7        | US-60-360-039-4112   | -                      |
| 16          | 7     | ۍ<br>۲         | 161       | 7        | HS-60-460-044-1628   |                        |
| 17          | y.    | 3.0            | ¥         | ^        | 715-60-380-336-395   | α,                     |
| 18          | ¥     | C<br>*         | <b>.4</b> | Æ        | DS-10-105-299-3818   | 4818,                  |
| 19          | ę     | 3. Ú           | 4 1       | S        |                      | Sequence 1761, Ap      |
| 50          | ٩     | 3.∪            | 55        | ٥        | US-10-155 881 9573   | Sequence 9573, Ap      |
| 5           | 9     | 3.0            | 57        | S        | US-09-620 393H-550   |                        |
| 2.5         | œ     | ر<br>ح         | _         | <u>.</u> | п8-10-155-ян1-21249  | 21239                  |
| 23          | 9     | 3.0            | 64        | عا       | US-10-155-881-9610   | Sequence 9610, Ap      |
| <b>\$</b> 2 | 9     | 3.0            | 73        | ıΣ       | US-10-002 344A 246   | Sequence 240, App      |
| 25          | B     | 3.0            | 73        | 9        | US-10-002-344A 241   | Sequence 241, App      |
| 26          | ٥     | 3.0            | 8.5       | چ.       | US-10-137 337 730    | 730,                   |
|             |       |                |           |          |                      |                        |

| 128<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130 | 3.0       | 103  | 9  | US-10-023 171 47                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence  | 47, Appl |
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|                                                                           | C         | 109  | ĸ, | US-09-882-227-546                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence  | 546, Apr |
|                                                                           | C .       | 110  | ď  | HS-10-021-577A-2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence  | 2, Appli |
| Q                                                                         | 3.0       | 114  | ٥  | US-10-155 881 20586                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence  | 20586, A |
|                                                                           | 3.0       | 115  | 9  | US-10-155-881-8470                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence  | 8470, Ap |
|                                                                           | 3.0       | 139  | ۵  | US-10-125-540-431                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence  | 431, App |
|                                                                           | 3.0       | 119  | ٥  | US-10-137-337-413                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence  | 413, App |
| ¥                                                                         |           | 121  | v. | TIS-09-969-528-8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence  | 8, Appli |
|                                                                           | 3.0       | 124  | 9  | US-10-155-881-6986                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |           | 6986, Ap |
|                                                                           | _<br>.≁   | ÷ ÷  | 7  | 4858-610-698-69-8H                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Serinence | ALBE, AL |
| ۵                                                                         | 5.0       | 137  | 'n | US-09-852-659A-97                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence  | 97, Appl |
|                                                                           | 3.0       | 138  | S  | US-09-540-209B-8614                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence  | 8614, Ap |
| ¥                                                                         |           | 14∩  | Œ  | HS-10-104-047-2436                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |           | 2436, Ap |
| 9                                                                         |           | 16.2 | 'n | US-09 852 559A 63                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequences | 53. Appl |
| ¥                                                                         | 3.0       | 162  | v  | US-10-194-947 3724                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence  | 3724, Ap |
| 9                                                                         | 3.0       | 163  | 9  | US-10-155-881-8628                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |           | 8628, Ap |
| 45                                                                        | · · · · · | 7 5  | 7  | US-60-465-284-255                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |           | 255, App |
|                                                                           |           |      |    | ALIGNMENTS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |           |          |

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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinling Green Y.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
SEQ ID NOS: 47374
SEQ ID NO 20535
LENGTH: 543
Sequence Zubis, Application US/50350039 GENERAL INFORMATION:
                                                                   APPLICANT: Cao, Yongwei
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ORGANISM: Rhodopseudomonas palustris US-60-360-039-20635 TYPE: PRT

0 Caps 0 4.0%; Score 8; DB 7; Length 543; indels. 100.0%, Pred. No. 12; tive 0, Mismatches Best Local Similarity 100.0 Matches 9, Conservative Query Match

177 LLSALAAL 184 4 LLSALAAL 11 οp ó

, Sequence 6607, Application US/09620393B . GENERAL INFOPMATION. ; APPLICANT: ALEXANDROV, Nickolai et al. 185-114-4711-343B-6607

TITLE OF INVENTION: SEQUENCE-DEPERMINED DNA FRAGMENTS AND CORPESPONDING POLYDEPTID TITLE OF INVENTION: THEREBY 2750-1068P FILE PEFEPENCE

CUPPENT APPLICATION NUMBER: US/09/620,393B CUPFENT FILIN: DATE \_\_cum+07-21 NUMBER OF SEQ ID NOS: 9948 SSOFWARE, DALGALIN VELSION 3.0 SEQ ID NO 6607 LENGTH: 105

ORGANISM. Arabidopsis thallana TYPE: PRT

NAME/KEY: misc\_feature FEATURE:

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                                                       4.0%; Score 8: DB 21: Length 23;
100.0%; Pred. No. 7.3;
tuye 0: Mismatches 0; Indels
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APPLICANT: Klud, Aaron
APPLICANT: Isalan Mary
FILE OF INVENTION: Nuc.elc Acid Binding Proteins
FILE PROFERING: P2500USM
CURRENI APPLICATION NUMBER: US.Ong./224 OKQ
FRIOR FILING DALE: 2000-11 28
PRIOR PLILING DALE: 1997 05-23
NUMBER OF SEQ ID NOS: 14-07122
SOFTWARE: MacAlluister
SFO ID NO 1234483
LENGIH: 23
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APPLICANT: Klod, Aaron
APPLICANT: Isalan, Mark
TILLE OF INVENTION: Nucleic Acid Minding Proteins
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CURRENT ADMITYATIVA NUMBER: CS/CQ/724,059
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GR9710809.5
PRIOR FILING DATE: 1947-05-23
NUMBER OF SEQ 10 NOS: 1407122
SOFTWARE: MACALILISTEE
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  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       : Sequence 1235483, Application HS/09724059
; GENERAL INFORMATION:
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US-09-724-059-1235483
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US-09-724-059-1235861
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Best Local Similarity 100.0%
Matches 8; Conservative
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Best Local Similarity
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                                                                             Best Local Similarity
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US-09-724-059-1235483
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05-09 724 059-1245105
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35.8%; Score 72; DB 21; Length 135; 100 0%; Pred. No 1 5e 62;
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                                           Indels
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TITLE OF INVENTION: Nucleic Acid Binding Proteins
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                                           Mismatches
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CURRENT FILLING DATE: 2000-11-28
PRICH APPLICATION NUMBER: CR0710R09 6
PRIOR FILLING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 1407122
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CURRENT FILING DATE: 2001-01-09
PRIOF APPLICATION NUMBER: 60/179,065
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PRIOR APPLICATION UNBHER: 50/18U, 528
PRIOR FILING DATE: 2000-02-04
NUMBER OF SPO ID NOS: 2666
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                                                                                                                                                                          73 IKKTYKQIEKNW 84
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Matches 59, Conserva
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                  Best Local Similarity
Matches 72, Conserv
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APPLICANT: Isalan, Mark
TITLE OF INVENTION: Nucleic Acid Binding Proteins
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APPLICANT: Isalan, Mark
HILLEGENT: Nucleic Acid Binding Proteins
FILE PEPPENEY: P2500USM
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US-09-724-059-1234367
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PRIOR APPLICATION NUMBER: GB9710809.6
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID MOS: 1407122
SOFTWARE: MACALLLISTER
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NUMBER OF SD. ID NOS: 1407122
SOFTWARE: MacAllLister
SEQ. ID NO 1234745
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Best Local Similarity 100.0
Matches 8, Conservative
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SOFTWARE: MacAllLister
SEQ ID NO 1234367
LENGTH: 23
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LENGTH: 23
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                                                                        TYPE: PRT
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OTHER INFORMATION: potential membrane-spanning segment, lopPred Program

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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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APPLICANT: Bouqueleret, Lydie
APPLICANT: Chumakov, Lilva
IITLE of INVENTION: A NOVEL BAP28 GENE AND PROTEIN
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Matches 100; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: USZACZ141 323
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 08 097549,217
PRIOR APPLICATION NUMBER: 08 097649,167
PRIOR FILIN: DATE: 2000 08-23
PRIOR APPLICATION NUMBER: PCT7US51/28651
PRIOR FILINS DATE: 2001 03-40
                                              port/men1,764927
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PRIOR FILING DATE: 2000 05·19
PRIOR APPLICATION NUMBER: PCT/0501/04941
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PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR APPLICATION NUMBER: US (97577,409)
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: PCT/99501/04027
                                                                    PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US-04/519,705
PRIOR FILING DATE: 2000-03-07
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PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000 03 31
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PRIOR FILING DATE: 2000 04-18
PRIOR APPLICATION NUMBER: US 09/770,160
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: GENERAL INFORMATION:
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NUMHER OF SEQ ID NOS: 4:2
SOFTWARE: PI_FI_qenes Version 6:0
SEQ ID NO 167
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98-60-339-453-167
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LOCATION: 911..931
OTHER INFORMATION: potential membrane-spanning segment, lopPred Program
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OTHER INFORMATION: potential membrane spanning segment, TopPred Program
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UTHEK INFORMATION: potential membrane:spanning segment, TopPred Program
                                                                                                                     LOCATION: 884..904
OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Printiam
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OTHER INFORMATION: potential membrane-spanning segment, TopPred Program
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OTHER INFORMATION: Potential membrane-spanning segment, TopPred Proglam
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CITHER INFORMATION: potential membrane-spanning segment, TopPred Program
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; UTHER INFORMATION: potential leucine zipper pattern, BLA Program
US-60-141-323-3
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TITLE OF INVENTION. Nucleic Acids, Froteins, and Antibodies
FILE REFERENCE: PMO01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1814 ATTLAPRVLLPAIKKTYKQIEKNWKNIIMGPFMSILQEHIG 1853
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CURRENT FILLING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILLING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
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SEQ ID NO 2590
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Matches 100; Conservative
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US-09-757-028-2590
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NAME/KEY: TRANSMEM
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COUNTRY:
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                                                                                                                                                                        APPLICANT: Bowcock, Anne M.
APPLICANT: Baer, Richard
TITLE OF INVENTION: Compositions and Methods Comprising
TITLE OF INVENTION: HARDI and Other BRCAI Binding Proteins
NUMBER OF SROUENCES: 115
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: BARDI and Other BRCAL Binding Proteins
NUMBER OF SEQUENCES: 115
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                61 ATTLAPRVLLPAIKKTYKQIEKNWKNHMGPFMSILQEHIG 100
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100 OM; Prod No. ...
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TELECOMMUNICATION INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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; GENERAL INFORMATION:
                                                                                                                                      Sequence 52, Application US/60042611 GENERAL INFORMATION:
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NAME: Hibler, David W.
REGISTRATION NUMBER: P-41,071
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                   Houston
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US-60-042-611-52
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STATE:
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125 EVYLLSALAALQKVVETLPHFISFYLEGILSQVIHLEKITSEMGSASQANIRLTSLKKTL 184
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                                                                                                Patentin Release #1.0, Version #1.30
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100.0%; Pred w.
tive 0; Mismatches
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UTSD-499PZ3
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/60/339,453
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PRIOR PLINO DATE: 2000-04-25
PRIOR FILING DATE: 2000 12:22
PRIOR APPLICATION NUMBER IS 09/491,404
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ING DATE: 2001-01-25
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PRIOR APPLICATION NUMBER: PCI/US01/03800
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APPLICATION NUMBER: US 09/515,126
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PRIOR APPLICATION NUMBER, US 39/488,725
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PRIOR APPLICATION NUMBER: US 09/552,317
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                                                                              PC-DOS/MS-DOS
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                                                                                                                                                                                                                         NAME: Hibler, David W.
REGISTRATION NUMBER: P-41,071
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                     515 amino acids
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Best Local Similarity 100.0
Matches 100; Conservative
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Weng, Gezhi
                                                                                                                  CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
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Wang, Jian-Rui
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                                                                                                                                          APPLICATION NUMBER
                                                                            OPERATING SYSTEM:
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US-60-042-985-52
                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                                                                                                                       61 ATTLAPRVITPATKKTYKQIFKNWKNHMOPFWSILQEHIGXMKKEFITSHQSQLIAFFLE 120
                                                                                                                                                                                                                                                                                                                                                                                                   121 ALDFRAUHSENDLEEVG*TENTITOTAVAMVYKLSEVTFRPLFFKLFDWAKTEDAPKDRL 180
                                                                                                                                                                                                                                      1 EVYLLSALAALOKVEL PHETSPYLESZINGOVIELEKTISEMGSASQANIKUTSIKKILL 60
                                                                                                                                                                                                      Gaps
                                                                                                                                                             Length 2144,
                                                                                                                                                                                                    Indels
                                                                                                                                                           99.5%; Score 200; DB 26; L
ilarity 140.0%; Pred. No. 3.3e-188;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barry, Caroline
APPLICANT: Bouqueleret, Lydie
APPLICANT: Choumakov, 11ya
1111E CE'INVENTION: A NOVEL BAP28 GENE AND PROTEIN.
FILE REFERENCE: 67.US2.PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT AFFLICATION NUMBER: USABUZIS 880 CURRENT FILING DATE: 2000-01-18 EARLIER AFFLIANTION NUMBER: US 60/141,323 EARLIER FILING DATE: 1999-06-25 NUMBER OF SEQ ID NOS: 12
                                                                            7 OTHER INFORMATION: Xaa-Sly or Glu US-09-604-665-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/60176880 GENERAL INFORMATION:
              CHER INFORMALION: XAATASP OF ASD NAME/KEY: VAPIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1694
OTHER INFORMATION: Xda-Ser or Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa+Asp or Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STHER INFORMATION: Xaa-Gly or Glu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1934 LTFYNLADCIAEKLKGLFTLF 1954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                              Best Local Similarity
Matches 201: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patent.pm
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1967
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LOCALLINE 1967
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US-60-176 880-4
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LOCATION:
                                                                                                                                                         Query Match
Best Local v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                           LOCATION:
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1754 EVYLLSALAALQKVVETI PHETSPYLEGTLSOVTHLEKTI SEMGSASOANTHLI SLKKTT 1813
                                                          61 ATTLAFRVLLPAIKKTYKQIEKNWKNHMCPFMSILQEHIGXMKKEELTSHGSGLTAFTLE 120
                                                                                                              121 ALDERAQHSENDLEEVGKTENCLIDGLVAMVVKLSEVTERPLEEKLEDAWAKTEDAPKDRL, 180
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                                                                                                                                                                                                                                                                                                                                                                                                  TIILE OF INVENTION: Compositions and Methods Comprising TIILE OF INVENTION: BARD1 and Other ERCAL Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Detentin Holease #1.0, Version #1.40 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/CB/936.487 FILING DATE: CONCURRENTLY Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.60,
100.0%, Pred. no.
*ive 0, Mishatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/025,296
FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US £0/042,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  RESULT 3
US-08-936-487-52
; Sequence 52, Application US/08936487
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-41,071
                                                                                                                                                                                                                           1934 LTFYNLADCIAEKLKGLFTLF 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-41,0
PEFEPENTE/TWOKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         181 LIFYNLADCIAEKLKGLFTLF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOWCOCK, Anne M. APPLICANT: Baer, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512/418-3000
512/474-7577
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hibler, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-APF-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houston
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Indels 0; Gaps

Longth 2144;

59.5%: Score 200: DB 26: 1. 100.0%: Pred. No. 3.36-188: 17e (): Mismatches ();

Conservative

Matches 201,

5

Local Similarity

Ouery Match Best Local 9 | FVVI | SALAALQKVVETLEHFTSPYTEGT | SQV PERKETSEMESASGANTELTSEKET, KO

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(without alignments)
140.012 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                           1 EVYLLISALAALOKVVETLPH.....TEYNLADCTAEKLKGLETLE 201
                                                                                                                                                                                        July 2, 2002, 14-14-34; Scarch time 505,3 Scounds
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/cqn2_6/ptodata/2/paa/US087_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_b/ptodata/z/paa/uSu89_COMB.pep:*
/cgn2_6/ptodata/2/paa/US090_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cqn2_6/ptodata/2/paa/US/dal_coMB_pep++
Csqn2_6/ptodata/2/paa/US/dal_coMB_pep++
/cqn2_6/ptodata/2/paa/US/094_COMB_pep+
/cqn2_6/ptodata/2/paa/US/094_COMB_pep;+
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/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/cgn2_6/ptodata/2/paa/US097_COMB.pep:*
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/cgn2_6/prodata/2/paa/uSt01_coML.pep.*
/cgn2_6/prodata/2/paa/uS60_00MH pep.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgm2 6/ptodata/2/paa/rcrus_cown_pep:+
/cgm2 6/ptodata/2/paa/rison_cown_pep:+
/cgm2 6/ptodata/2/paa/rison_cown_pep:+
/cgm2 6/ptodata/2/paa/rison2/paa/rison2/pep:+
/cgm2 6/ptodata/2/paa/rison3/rison3/pep:+
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/cgn2_6/ptcdata/2/paa/US083_COMB.pcp:*
/cgn2_6/ptcdata/2/paa/US084_COMB.pcp:*
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                           Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satistying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3502263 scqs, 351980561 residues
GenCore version 4 5
                                                                                                                                                                                                                                                                                                                        US-09-603-665-5_COPY_1754_1954
                                                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 60 0 , Gapext, 60,0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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and is derived by analysis of the total score distribution

| *<br>Query<br>ore Match Length DB ID | 99.5  | 99.5 2144 26 | 49.8 515 13 | 49.8 515 26 | 49 8 515 26 | 1149  | AC ANIC R PA |
|--------------------------------------|-------|--------------|-------------|-------------|-------------|-------|--------------|
| #<br>Query<br>Match                  | 9.66  | 1.66         | 4.0         | 49.5        | 49 5        | 4.9   | ₹<br>7       |
| Result<br>No. Score                  | 1 200 | 2 200        | 3 100       | 4 100       | 5 100       | 9 100 | 7 100        |

| 028-2590 Sequence 2590, A | 1234367 Sequence 12 | 1234745 Sequence 12 | 1235105 Sequence 12 | -1235483 Sequence 12 | 1235861 Sequence 12 | 1236203 Sequence 12 | -1236617 Sequence 12 | 1236959 Sequence 12 | -1237319 Sequence 12 | 1237697 \$cquence 12 | 1242341 Sequence 12 | 1242593 Sequence 12 | 1242833 Sequence 12 | -1243085 Sequence 12 | -1243337 Sequence 12 | 1243565 Sequence 12 | 1243841 Sequence 12 | 1244069 Sequence 12 | 1244309 Sequence 12 | -1244561 Sequence 12 | -1265676 Sequence 12 | 1268196 Sequence 12681 | 1270596 Sequence 127059 | 1273116 Sequence 127311 | -1275636 Sequence 12756 | -1277916 Sequence 127791 | 1280676 Septence 128067 | 1282956 Sequence 12829 | 128635 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 1287971 Sejucious 3787971 | .212469 sequence 21240 | JIJ649 sequence 2126 | -212889 Sequence 21288 | 212913 Sequence 212 | 213369 Sequence 21446 | 213393 Sequence 213 |
|---------------------------|---------------------|---------------------|---------------------|----------------------|---------------------|---------------------|----------------------|---------------------|----------------------|----------------------|---------------------|---------------------|---------------------|----------------------|----------------------|---------------------|---------------------|---------------------|---------------------|----------------------|----------------------|------------------------|-------------------------|-------------------------|-------------------------|--------------------------|-------------------------|------------------------|--------------------------------------------|---------------------------|------------------------|----------------------|------------------------|---------------------|-----------------------|---------------------|
| US-09-757-0               | 69 724              | -09-724-            | -09-724-            | -09-724-             | -09 724             | 0.9 724             | -09-724-             | -09 724             | -09-724-             | -00-724-             | -08-724             | 09 724              | 09 724              | -09-724-             | -09-724-             | -09 724-            | 09 724              | .09 724             | +                   | - 09 - 7.14 -        | -09-724-             | -09 724                | 09 724                  | 09 724                  | -09-724-                | -09-724-                 | 09 724                  | -09-724                | 09 724                                     | 09 724                    | - PCZ - 50-            | \$77 KO              | - 08-724-              | <b>~</b>            | 09 724                | 109 724             |
| 135 21                    | m<br>C              | n                   | m                   | æ                    | œ                   |                     | æ                    | ٠.                  | ~                    | ~                    | ٠.                  | ,~.                 | ~                   | m                    | m                    | ~                   | œ                   | ~                   | ~                   | m                    | m                    | æ                      | ~                       | ~                       | m                       | æ                        | m                       | œ                      | ~                                          | ~                         | _                      | <b>~</b> }           | ~                      | æ                   | ~                     | c                   |
| 35.8                      | 4                   | 4                   | 4                   | 4                    | 4                   |                     | 4                    | 4                   | 4                    | 4                    | 4                   | ÷                   | 77                  | ₹*                   | 4                    | Ψ.                  | Ψ.                  | ÷                   | 4                   | 4                    | 4                    | ₹*                     | ₹\$                     | Ψ.                      | 4.                      | 4                        | 4                       | ~                      | ν.                                         | <del></del>               | ₹7                     | 4                    | 4                      | 4                   | 4                     | ~                   |
| ж<br>С                    | - 01                | 11                  | 1.2                 | 13                   | 1.4                 | 1277<br>17          | 16                   | 17                  | 18                   | 16                   | 50                  | 54                  | c:<br>c:            | 23                   | ₹ <sup>#</sup>       | 25                  | 26                  | 27                  | 58                  | 67                   | 3.0                  | 3.1                    | 32                      | 3.3                     | 34                      | 3.5                      | 36                      | 3.7                    | 3.8                                        | 34                        | - 4                    | 7 <b>5</b>           | 4.0                    | 43                  | 4.1                   | 4 =                 |

## ALIGNMENTS

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TITES OF INVENTION. A NOVEL BARDS GENE AND PROTEIN FILE REFERENCE. GENSET.063AUS
                                                                                                                                                                                           CHRRENT APPLICATION NUMBER 115/19/603,665
CUBRENT FILLING DATE: 2000-06-23
PRICE APPLICATION NUMBER: US 60/141,323
                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-06-25
PELO APPLICATION NUMBER: 18 50/176,880
PRIOR FILING DATE: 2000-01-18
                    Sequence 5, Application HS/04603665; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1694
OTHER INFORMATION: Xaa-Ser of Asn
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1854
OTHER INFORMATION, Xaamala or Val
                                                                                                       Chumakov, llya
Cohen-Akenine, Annick
                                                          APPLICANT: Barry, Caroline
APPLICANT: Hougueleret, Lydic
                                                                                                                                                                                                                                                                                                                           NIMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Patent.pm
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115-114-404-465-5
                                                                                                         APPLICANT:
APPLICANT:
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